| 5  | RGTTFSILSD<br>NEREKFAFCS<br>TKDHFLEVKM<br>NSILQGIPWQ<br>GPKGSFRPIW                                       | VHNRLLKQTS<br>MKGCERIKIK<br>ESSKQHFFHL<br>LFNYVATIPD<br>VTLDTEDHKA | VVTLQKGYTI<br>KTGVFVRTLQ<br>ALIPKNAGVS<br>WNDFAYIEVD<br>NSIVLMASKG<br>KIFQVVPIPV | HWDQTAPAEL<br>MDKVEQSYPG<br>DCTATAYPKF<br>GKKYPSSEDG<br>RYVSRGPWTR | AIWLINFNKG<br>RSHYYWDEDS<br>TERAVVDVPM<br>IOVVVIDGNO | MKIIKNDFPS<br>DWIRVGLCYP<br>GLLFLKLKAQ<br>PKKLFGSQLK<br>GRVVSHTSFR<br>LKLKEQMAFV   | 660<br>720<br>780<br>840<br>900<br>960 |  |  |
|----|--|--|--|--|--|--|--|--|--|
| 10 | Seq ID NO: 141 <u>DNA sequence</u><br>Nucleic Acid Accession #: Eos sequence<br>Coding sequence: 2612861 |  |  |  |  |  |  |  |  |
|    | 1  | 11   | 21   | 31   | 41   | 51   |  |  |  |
| 15 | GAGCTAGCGC   | TCAAGCAGAG   | CCCAGCGCGG   | TGCTATCGGA   | CAGAGCCTCG   | Concente   |  |  |  |
|    | CGGCGCGGGG   | AGCCAGCGGG   | GCTGAGCGCG   | GCCAGGGTCT   | GAACCCAGAT   | TTYTYTACACT  | 60<br>120                              |  |  |
|    | AGCTACCACT   | CCGCTTGCCC   | ACGCCCCCGG   | AGCTCGCGGC   | CCCTCCCCCT   | CAGCGACCAG   | 180                                    |  |  |
| •• | AGAGGGAGCA   | CCGCTGCGCT<br>CACTGCCAGG   | ATGGGAGCTG   | CTGGGAGGCA   | ACTGTCTCGG   | CTACAGACCC   | 240                                    |  |  |
| 20 | TGCTGACCAT   | CAGCTGGCTC   | ACTCTGACCT   | GCTTCCCTCC   | GGCCACATCC   | A CACTOCOTO  | 300<br>360                             |  |  |
|    | CIGGGIGCCC   | TGACCAGAGC   | CCTGAGTTGC   | AACCCTGGAA   | CCCTGGCCAT   | CACCAAGACC   | 420                                    |  |  |
|    | CCATCCACAT   | TATCGGCCAG<br>CTCAGAGGGA   | GGCAAGCTGG   | TCATTANAGA   | CCACCACCAC   | COLD DESCRIPTION   | 480<br>540                             |  |  |
| 25 | TGCGAACCCG   | GCACATCCTG   | ATTGACAACG   | GAGGAGAGCT   | GCATGCTGCG   | P CALCACACAL CALL  | 600                                    |  |  |
| 23 | CGGATCCTTA   | GGGCAATTTC<br>CTATGGTCTG   | ACCATCATTT   | TGTATGGAAG   | GGCTGATGAA   | GGTATTCAGC   | 660                                    |  |  |
|    | ATGGACAGAA   | AAAGCTCTCC   | TGGACATTTC   | TGAACAAGAC   | CCTTCACCCA   | COTOCCATOC   | 720<br>780                             |  |  |
|    | CAGAAGGAGG   | CTATTTTTTT   | GAAAGGAGCT   | GGGGCCACCG   | TECACTTATT   | CTTCNTCTCN   | 840                                    |  |  |
| 30 | AAGAGAGTGA   | ATCAGGCACA<br>ACGTCTGGTC   | CACCATCCATT  | CTGACCGGTT   | TGACACCTAT   | AGATCCAAGA   | 900                                    |  |  |
|    | TIGCAGIGAA   | TGATGAAGGT   | TCTCGAAATC   | TGGATGACAT   | GGCCAGGAAG   | GCCATCACCA   | 960<br>1020                            |  |  |
|    | AATTGGGAAG   | CAAACACTTC   | CTGCACCTTG   | GATTTAGACA   | CCCTTGGAGT   | ጥጥጥር ጥል አርጣያን  | 1080                                   |  |  |
|    | CTGCTGCTGC   | TCCATCATCT<br>CCGGGTATTC   | TCAGTGGAAG   | ACCATATTGA   | ATATCATGGA   | CATCGAGGCT   | 1140                                   |  |  |
| 35 | CTTTGTCCAG   | TGAGTGGGTT   | CAAGACGTGG   | AGTGGACCCA   | CTCCTTCCAT   | CATCATTALAC  | 1200<br>1260                           |  |  |
|    | TATCTCAGAC   | TAAAGGTGGG   | GAGAAAATTT   | CAGACCTCTG   | GAAAGCTCAC   | CCAGGAAAAA   | 1320                                   |  |  |
|    | AGGTTGTCTA   | TCCCATTGAT   | CAGGATTATA   | CTACAATGGA   | TGGAGTTAAC   | CTCAGCACCG<br>GGCAGAGCCT   | 1380                                   |  |  |
| 40 | GCCGGAGCTA   | CCGTGTACGG   | TTCCTCTGTG   | GGAAGCCTCT   | GAGGCCCCAAA  | CTCACACTCA   | 1500                                   |  |  |
| 40 | CCATTGACAC   | CAATGTGAAC   | AGCACCATTC   | TGAACTTGGA   | GCATAATCTA   | CACTCATCCA   | 1560                                   |  |  |
|    | TCCAGGTGCT   | TACCCTGGTC<br>TCCCTGCAGA   | TCCTGCGCCC   | CCAACCAGGT   | CAAAGTGGCA   | CCCAAACCAA   | 1620<br>1680                           |  |  |
|    | TGTACCTGCA   | CATCGGGGAG   | GAGATAGACG   | GCGTGGACAT   | GCGGGGGGAG   | CTTCCCCCTTC  | 1740                                   |  |  |
| 45 | ACATCTGCAA   | CATCATAGTG<br>TTTCTTTGAC   | ATGGGGGAGA   | TGGAGGACAA   | ATGCTACCCC   | TACAGAAACC   | 1800                                   |  |  |
|    | TTAAGGCAGC   | ACACTTGGAG   | GGCACGGAGC   | TGAAGCATAT   | GGGACAGCAG   | CTCCTCCCTC   | 1860<br>1920                           |  |  |
|    | AGTACCCGAT   | TCACTTCCAC   | CTGGCCGGTG   | ATCTACACCA   | AACCCCACCT   | TATOMORA   | 1980                                   |  |  |
|    | GCTCCAATGG   | CAGGGACCTC<br>CTTGTTGATC   | AAGGACGTTG   | ATACATTCTC   | TCGCTGCGTC   | ACAGTCCATG   | 2040                                   |  |  |
| 50 | TCACGGAAGA   | TGGGCCGGAG   | GAACGCAACA   | CTTTTTGACCA  | CHARTELANCE  | CTCCTTCTCT   | 2100<br>2160                           |  |  |
|    | AGTUTGGAAC   | CCTCCTCCCC   | TCGGACCGTG   | ACAGCAAGAT   | GTYCCAACATYC   | ATCACAGACC   | 2220                                   |  |  |
|    | GGATGGCCAA   | AGGGTACATC<br>TCCCAACAAC   | AACCTCATCA   | ACTGTGCCC  | TECACEATOR   | CACCABACTO   | 2280                                   |  |  |
| 55 | GATTTTGGTT   | TATTTTTCAC   | CACGTACCAA   | CGGGCCCCTC   | CETCEGAATC   | TACTCCCCAC   | 2340<br>2400                           |  |  |
| 55 | GITATTCAGA   | GCACATTCCA   | CTGGGAAAAT   | TCTATAACAA   | CYCACCACAT   | TCCAACTACC<br>AAGGACAAGC   | 2460                                   |  |  |
|    | GGCCGTTCCT   | CTCAATCATC   | TCTGCCAGAT   | ACAGCCCTCA   | CCAGGACGCC   | CACCCCCTCA   | 2520<br>2580                           |  |  |
|    | AGCCCCGGGA   | GCCGGCCATC   | ATCAGACACT   | TCATTGCCTA   | CAAGAACCAG   | GACCACGGGG   | 2640                                   |  |  |
| 60 | AAGGCTTCTT   | GCTTACAGGA   | ATGAAGGCTG   | ACAGCTGCCA   | TTTCAGAGGG   | GAGGCTCAGG<br>GATGAGGCAG   | 2700                                   |  |  |
|    | CCTCTGGAAT   | GGCTCAGGGA   | TTCAGCCCTC   | CCTGCCGCTG   | CCTGCTGAAG   | CTGCTTCA CTA   | 2760<br>2820                           |  |  |
|    | CGGGGTCGCC   | CTTTGCTCAC   | GTCTCTCTGG   | CCCACTCATG   | ATCCACAACT   | CTCCTCACAC   | 2000                                   |  |  |
|    | CTCTGACTCC   | AAGAGGGTGA   | AGTCCACAGA   | AGTGAGCTCC   | TOCOTTAGGG   | GCAGCCCTGC<br>CCTCATTTGC   | 2940                                   |  |  |
| 65 | TUTTCATCCA   | GGGAACTGAG   | CACAGGGGGG   | CTCCAGGAGA   | CCCTT A CT TYCH                                      | CORCORNORC   | 3000<br>3060                           |  |  |
|    | CUTCGGCCTG   | GGATTTCAGA   | GCTGGAAATA   | TAGAAAATAT   | CTACCCCAAA   | GCCTTCATTT<br>AGGGAGGGCC   | 2120                                   |  |  |
|    | TGGGGAGCCC   | CACCCTAGCC   | CTTGCTGCCA   | CACCACATTG   | CCTCABCAAC   | CCCCCCCACA   | 2240                                   |  |  |
| 70 | GIGCCCAGGC   | ACTCCTGAGG   | TAGCTTCTGG   | AAATGGGGAC   | AAGTCCCCTC   | GNACCANACC   | 2200                                   |  |  |
| 70 | AAATGACTAG   | AGTAGAATGA   | CAGCTAGCAG   | ATCTCTTCCC   | TCCTGCTCCC   | AGCGCACACA<br>ACTACCTGTC   | 3360                                   |  |  |
|    | AGCCCAGCCT   | GGGTGCACAG   | TAGCTGCAAC   | TCCCCATTCC   | שביריים מידים ביי                                    |  | 3400                                   |  |  |
|    | TUTGUAGUTC   | TACAGGTGAG   | GCCCAGCAGA   | GGGAGTAGGG   | CTCCCCATCT   | יון איניותים ביותים איני   | 3540                                   |  |  |
| 75 | CCAATTIGGC   | TGATCTTGGG   | TGTCTGAACA   | GCTATTGGGT   | CCACCCCACT   | CCCTTTCAGC<br>AGAGCTCCTG   | 3600                                   |  |  |
| _  | TAAGAGGGAG   | AACTCTATCT   | GTGGTTTATA   | ATCTTCCACC   | <b>ACCCA CCACA</b>                                   | Cultural Company   | 2720                                   |  |  |
|    | GICTIGIGAT   | GAACTACATT   | TATCCCCTTT   | CCTGCCCCAA   | CCBCBBBCTC   | THE PROPERTY OF THE PARTY OF TH | 2220                                   |  |  |
|    | AGAGGGCCTG   | CCTGGCTCCC   | TCCACCCAAC   | TGCACCCATG   | AGACTCCCTC   | CAAGAGTCCA<br>TTCAGCTGCT   | 2040                                   |  |  |
| 80 | GGGAGGTGAC   | CATAGGGCTC   | TGCTTTTAAA   | GATATGGCTG   | CTTCAAAGGC   | CACACTCACA   | 2060                                   |  |  |
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                                                                                          900
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PCT/US02/36810

|    |            | CTGGTCACAA   |                          | a C== a C== C= a C= a | ANTOTODAGA                | CATTGATGAG                   | 960          |
|----|------------|--------------|--------------------------|-----------------------|---------------------------|------------------------------|--------------|
|    | AGATGCCCTG | TTCCTGGGAT   | ACAGAGIGAA<br>ACCCCAAACC | CCTACTCAGA            | CONTRACTOR                | CCCAACCTAT                   | 1020         |
|    | TGCAGCATCA | GTCCACGTGG   | ATOTOANACT               | TCABCACATG            | CONCRETE                  | CATCGATCAG                   | 1080         |
|    | TTTTGTGTTT | TGTGTTTCTC   | CCCCCTCCTC               | A ATCCCCCCCT          | CTCCACAGA                 | GCTCCCGGGG                   | 1140         |
| 5  | AGAACAGGCA | AAATGCAGTG   | CTCCTCTCAC               | CONCACCACT :          | CCTCCCCCCAT               | CGGAACCATT                   | 1200         |
| ,  | AGAATGACGA | GTCCTGTCAG   | LIGCIGIGAG               | CANTATCCCA            | CACTTTCCAT                | CCATCCACTT                   | 1260         |
|    | CCTGAAGCCT | GAATTCCAGG   | AGGIICIGAG               | TOTAL TOTAL           | GVCIIIGCVI                | CCCAAATCCC                   | 1320         |
|    | CCAATGGGAG | GTGGCAATGG   | GAGIGCIGGI               | CCCCCCCCC             | CCACACCCCTT               | CATCCCCATC                   | 1380         |
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| 10 | CCTGGAGGCA | ATGGCTTTTC   | TCCTGGCGTT               | A A CONCINCA O        | MACATATOTC                | TARCCATCAT                   | 1500         |
| 10 | GGACCTATCA | TCACTGGACT   | AACAATTCTG               | AACCAGACAA            | TAGATATCIG                | AMOUNTON                     | 1560         |
|    | GCTAACCTTT | GTTTAAATGG   | ACGCTGTATA               | CCAACTGTCT            | CAAGCTACCG                | ATGIGAATGC                   |              |
|    | AACATGGGTT | ATAAGCAGGA   | TGCAAATGGA               | GATTGTATAG            | ATGITGATGA                | MIGCACATCA                   | 1620<br>1680 |
|    | AATCCCTGCA | CTAATGGAGA   | TTGTGTTAAC               | ACACCTGGTT            | CCTATTATIG                | OTTOONTOON                   | 1740         |
| 15 | GCTGGATTCC | AGAGGACTCC   | TACCAAGCAA               | GCATGCATTG            | ATATIGATGA                | CONCENTE                     | 1800         |
| 15 | AATGGGGTTC | TTTGTAAAAA   | CGGTCGATGC               | GTGAACTCAG            | ATGGAAGITI                | CCAGIGCAII                   | 1860         |
|    | TGCAATGCCG | GCTTTGAATT   | AACTACAGAT               | GGAAAAAACT            | GIGITGATCA                | TGATGAATGT                   |              |
|    | ACAACTACCA | ACATGTGTTT   | GAATGGAATG               | TGCATCAATG            | AAGATGGCAG                | CTTCAAGIGC                   | 1920<br>1980 |
|    | ATCTGCAAAC | CAGGATTIGT   | CITGGCTCCA               | AATGGGCGTT            | ACTOTACTOA                | CONCOUNTCOCC                 | 2040         |
| 20 | TGCCAGACCC | CAGGAATCTG   | CATGAATGGG               | CACTGCATCA            | ACAGIGAAGG                | GICCIICCGC                   | 2100         |
| 20 | TGTGACTGTC | CCCCAGGCCT   | GGCTGTGGGC               | ATGGATGGAC            | GIGIGIGIGI                | TGATACTCAC                   |              |
|    | ATGCGCAGTA | CCTGCTATGG   | AGGAATCAAG               | AAAGGAGTGT            | GIGIGCGICC                | TTTCCCCGGT                   | 2160         |
|    | GCAGTGACCA | AGTCCGAATG   | CTGCTGTGCC               | AATCCAGACT            | ATGGTTTTGG                | MCCACCACCAC                  | 2220<br>2280 |
|    | CAGCCATGCC | CTGCAAAAAA   | TTCAGCIGAA               | TTCCACGGCC            | TTTGTAGTAG                | I GONG I MOGI                | 2340         |
| 25 | ATCACTGTGG | ATGGAAGAGA   | TATCAATGAA               | TGTGCTTTGG            | ATCCTGATAL                | AIGIGCCAAI                   | 2400         |
| 25 | GGGATTTGTG | AAAACTTACG   | TGGTAGTTAC               | CGTTGTAATT            | GCAACAGIGG                | CIAIGAACCA                   | 2460         |
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|    | GATAACGGAT | TGTGCCGAAA   | CACGCCAGGA               | AGTTACAGCT            | GTACGTGCCC                | ACCAGGGIAI                   | 2580         |
|    | GTGTTCAGGA | CTGAGACAGA   | GACCTGTGAA               | GATATAAATG            | AATGTGAAAG                | CAACCCAIGI                   | 2640         |
| 20 | GTCAATGGGG | CCTGCAGAAA   | CAACCTTGGA               | TCTTTCAATT            | DOCCOLOGIC                | WECCOGGCAGC                  | 2700         |
| 30 | AAACTCAGCT | CCACAGGATT   | GATCTGTATT               | GACAGCCIGA            | AGGGGALCIG                | TIGGCICANC                   | 2760         |
|    | ATCCAGGACA | GCCGCTGTGA   | GGTGAATATT               | MATGGAGCCA            | CICIGAMAIC                | TACACCTTCC                   | 2820         |
|    | GCCACCCTCG | GAGCCGCCTG   | GGGGAGCCCC               | TGTGAGCGGT            | GIGAACIAGA                | COCOCO                       | 2880         |
|    | CCAAGAGGGC | TTGCCAGGAT   | TAAAGGTGTT               | ACGIGIGAAG            | AIGIIAAIGA                | GIGIGAGGIG                   | 2940         |
| 35 | TTCCCTGGCG | TTTGTCCAAA   | TGGACGCTGT               | GTCAACAGTA            | AGGGATCITI                | TOCCATCGAG                   | 3000         |
| 33 | TGCCCTGAAG | GCCTTACGTT   | GGATGGGACT               | GGCCGTGTAT            | COCCECC                   | ANACTTCCCC                   | 3060         |
|    | CAGTGTTACT | TGAAGTGGGA   | TGAAGATGAA               | TGCATCCACC            | CCGITCCIGG                | CCACTCCCCC                   | 3120         |
|    | ATGGATGCCI | GCTGCTGTGC   | TGTCGGGGCG               | GCTTGGGGCA            | CCGAGIGIGA                | mccma a ccca                 | 3180         |
|    | AAACCTGGCA | CCAAGGAATA   | CGAGACACTG               | TGCCCCCGCG            | GGGCTGGCTT                | ACCAMENCE                    | 3240         |
| 40 | GGGGATGTTC | TTACTGGGCG   | GCCATTTTAC               | AAAGACATCA            | ATGAATGCAA                | COCCECCA                     | 3300         |
| 40 | GGGATGTGC  | CTTATGGGAA   | GTGCAGAAAT               | ACAATCGGAA            | GCTTCAAATG                | CTCCACCATT                   | 3360         |
|    | AGTGGCTTTC | CTCTAGACAT   | GGAGGAAAGA               | AACTGCACGG            | ACATCGACGA                | GIGCAGGAII                   | 3420         |
|    | TCTCCTGAC  | TCTGTGGCAG   | TGGAATCIGC               | GICAATACAC            | * COCCAGCII               | TOMOTOCOMO                   | 3480         |
|    | TGCTTCGAAC | GCTATGAAAG   | TEGCTTCATE               | ATGATGAAGA            | ACTGCATGGA                | CCCCACCTTT                   | 3540         |
| 15 | TGTGAACGTZ | ACCCTCTCCT   | TIGTAGGGGI               | GGCACCTGTG            | IGAACACIGA                | MODEL AND CALL               | 3600         |
| 45 | CAGTGTGAC  | r GCCCACTGGG | ACACGAGCTG               | TCACCATCCC            | GIGAGGACIG                | , IGIGGWIWII                 | 3660         |
|    | AATGAATGC: | r ccctgagtga | CAATCTCTGC               | AGAAATGGAA            | AAIGIGIGAA                | CAIGAIIGGA                   | 3720         |
|    | ACCTATCAG: | r GCTCTTGCAA | TCCTGGATAT               | CAGGCTACGC            | CAGACOGCCA                | A PARTICIACA                 | 3780         |
|    | GATATTGAT  | S AATGTATGAT | AATGAACGG                | GGCTGTGACA            | TOOMS TOOMS               | . AAAIICAGAG                 | 3840         |
| 50 | GGAAGCTAC  | 3 AATGCAGCTG | CAGTGAGGG                | TATGUCCTGA            | TGCCAGATGC                | ONCALCULUI                   | 3900         |
| 30 | GCAGACATT  | ATGAATGTGA   | AAACAATCC                | GATATCTGTG            | MIGGEGGE                  | CONCRECANC                   | 3960         |
|    | ATTCCTGGA  | G AGTATCGCTG | CCTCTGCTA                | GAIGGUITUA            | TGGCTTCCAT                | T TOCCOUNTER                 | 4020         |
|    | ACATGCATT  | G ATGTCAATGA | ATGTGACCTA               | AATTCAAATA            | TUIGCAIGI                 | CARCARCOC                    | 4080         |
|    | GAGAACACA  | A AGGGATCCTT | CATTIGCCAC               | TGTCAGCTGG            | GITACICAG                 | CONTRACTOR                   | 4140         |
| 55 | ACCACAGGA  | T GTACAGATGT | GGATGAGTG                | GAAATTGGTG            | CICAIAACIO                | CONCRINENT                   | 4200         |
| 33 | GCCTCATGT  | C TGAATATCCC | AGGAAGCTT                | AAGTGTAGCT            | GCAGAGAAGC                | CIGGATIGGA                   | 4260         |
|    | AACGGCATC  | A AGTGTATTGA | TCTGGACGA                | TGTTCTAATC            | GAACCCACC                 | A GIGIMOCAIC                 | 4320         |
|    | AATGCTCAG  | T GTGTAAATAC | CCCGGGCTC                | TACCGCTGTC            | CCIGCICCG                 | A AGGIIICACI                 | 4320         |
|    | GGTGATGGC  | T TTACCTGCTC | AGATGTTGA                | C GAGIGIGCAC          | , voncection              | A CCTCTGTGAG                 | 4440         |
| 60 | AACGGACAG  | T GCCTTAATG  | CCCGGGTGC                | ATAICGCIGC            | HGIGIGNON                 | r gggcttcact<br>A AAACATTTGT | 4500         |
| UU | CCAGCCTCA  | G ACAGCAGATO | CIGCCAAGA                | L WILGHTOWN           | r centerice               | A TGATGGTTAT                 | 4560         |
|    | GTCTCTGGA  | A CATGIAATA  | CCIGCCIGG                | A CAMAMACAN           | NOTICE CAR                | A TCCTATAAAC                 | 4620         |
|    | GAATIGGAC  | A GAACAGGAGG | GAACIGIAC                | a comoconan           | AGIGIGO                   | G CCCACCCGAT                 | 4680         |
|    | TGTGTCAAT  | G GCCTATGTG  | CAACACGCC                | T GGICGCIAN           | AGIGIANCI                 | A CIGCTACCIG                 |              |
| 65 | TITCAGITG  | A ACCCAACIGO | TGIGGGTIG                | r Grigacaacu          | COCACATOC                 | a concector                  | 4800         |
| 05 | AAGTTTGGA  | C CICGAGGAGA | 1 TGGGAGTCT              | a recognic            | CANACCCCT                 | G GGTGGGCGTC                 | 4860         |
|    | AGTCGCTCT  | T CAIGCIGCIO | 5 CICICIGGG              | u varancaccian        | CACCTCAAC                 | G TGAGACATGC<br>G CTTCAGACCT | 4920         |
|    | CCCCCTGTC  | A ATAGCACTG  | ATATTACAC                | m chockage            | S GAGGIGAAG               | C AGGTCTCTGC                 | 4000         |
|    | AACCCCATC  | A CAATCATTT  | L AGAAGACAI              | T GWCGWWIGC           | r cacycacture             | C ACAAGGCTAC                 | 5040         |
| 70 | CAGGGTGGA  | A ACIGCATCA  | A CACTILIGG              | C CATATTCAG           | - ACTOMOTOCC              | C ACATCCTGGT                 | 5100         |
| 70 | TACCTCAGC  | O AGGATACCC  | J CAICIGIGA              | G CAGGGYYYA           | A WOTOTITIO               | T TTGCCCACCT                 | 5160         |
|    | GIGIGIGG   | CIGGGACCI    | - CIATAACAC              | C TOUGHAAT            | Y MCMCCIGCH               | G Children Course            | 5220         |
|    | GAGTACATO  | AGGTCAATG    | a AGGCCACAA              | T CACHTGGAC           | u ucatomica<br>P Tomoment | G CTTTTGCTAC<br>C AAAAAGGATG | 5220         |
|    | CGAAGCTAT  | A ATGGAACCA  | TIGIGAGAA                | n cocencer            | T TOWNIGION               | C WANNERD TO                 | 5340         |
| 75 | TGCTGCTGC  | A CATATAATG  | I GGGCAAAGC              | T CCARROAN            | C CIIGIGAAC               | C ATGCCCAACT<br>C CTTTGACATT | 5400         |
| 13 | CCAGGAAC   | G CTGACTITA  | A AACCATATG              | I GGAAATATT           | CIGGATICA                 | on delighted by an           | 2400         |
|    | CACACAGG   | A AAGCTGTTG  | A CATTGATGA              | A TUTAAAGAG           | M COCOMPOSO               | T TTGTGCAAAT                 | 2400         |
|    | GGTGTGTG   | A TTAACCAGA  | T TGGCAGTTI              | C CGCIGIGAA           | A CONTROCTO               | G ATTCAGTTAC                 | 552V         |
|    | AATGACCTC  | C TGTTGGTTT  | G TGAAGATAT              | A GATGAGTGC           | A GCAATGGTG               | A TAATCTCTGC                 | 5640         |
| 80 | CAGCGGAA'  | G CAGACTGCA  | T CAATAGICO              | I GGTAGTTAC           | C BARCERET                | G TGCCGCGGGT                 | 5040         |
| ٥٥ | TTCAAACT   | T CACCCAATG  | G GGCCTGTGT              | A GATCGCAAT           | G AAIGTTTAG               | A AATTCCTAAC                 | 5760         |
|    | GTTTGCAG.  | ATGCTTGT     | G TGTTGATCT              | O TOOLTOO             | T WOCKER                  | T CTGCCACAAT                 | 5/00         |
|    | GGCTTTAA   | CTTCTCAGG    | A CCAGACCAT              | G TGCATGGAT           | A TIGHTONG!               | G CGAGCGGCAC<br>T GTGCTACCCA | C200         |
|    | CCATGTGG   | AA AIGGAACTI | G TAAAAACAC              | C CTCCACATC           | C ATCACTOR                | G TTCCTTTTT                  | 5040         |
|    | GGGTTTGA   | AC TCACTCATA | A TAATGATT               | C CIGGACATA           | S AIGHGIGCE               |                              | 2240         |

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GGTCAGGTGT GCAGAAATGG ACGTTGTTTT AATGAAATTG GTTCTTTCAA GTGTCTATGT
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                                                                                  6060
        GCCCTTCCCG GCTCTTGCTC TCCTGGTACC TGTCAGAATT TGGAGGGATC CTTCAGATGC
                                                                                  6120
       ATCTGTCCCC CAGGGTATGA AGTAAAAAGC GAGAACTGCA TTGATATAAA TGAATGTGAT
                                                                                  6180
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       GAAGATCCCA ACATTIGTCT TTTTGGTTCC TGTACTAATA CTCCAGGGGG CTTCCAGTGC
        CTCTGCCCCC CTGGCTTTGT ACTATCTGAT AATGGACGGA GATGCTTTGA TACTCGCCAG
        AGCTTCTGCT TCACAAATTT TGAAAATGGA AAGTGTTCTG TACCCAAAGC TTTCAACACC
                                                                                  6360
        ACAAAAGCAA AATGCTGCTG TAGTAAGATG CCAGGAGAGG GCTGGGGGGA CCCCTGTGAG
                                                                                  6420
        CTGTGCCCCA AAGACGATGA AGTTGCATTT CAGGATTTGT GTCCATATGG CCATGGAACT
                                                                                  6480
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        TGTTCAAATG GTCAATGTAT CAACACCGAC GGATCTTTTC GCTGTGAATG TCCAATGGGC
                                                                                  6600
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CCGTGTGGAA ATGGTACATG CACCAATGTT ATTGGGAGTT TTGAATGCAA TTGCAATGAA
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                                                                                  6720
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                                                                                  6840
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        TTCACACAGC ATCACACTGC TTGTATCGAC AACAACGAAT GTGGGTCTCA ACCTTTGCTT
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                                                                                   7800
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        ANTICOTOTO GOTOTOCTTO CTGCTACAAC ACCCTGGGGA GTTACAAGTG CGCCTGCCCC
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                                                                                   8700
                                                                                   8760
        TCAAATCCTA GCACAGCCAG TCTGCAGAAG CATTTGAAAA GTCAAGGACT AATTTTAAAG
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                                                                                   8880
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        CTCACAGGGA GGGATAATTI AGACTCTGGT ATGGCCAAAG ATTTGAGCTC AAAGGCAACC GTGGTTACTG TATTTTTTAT ATAACTTCAT TTTAAAATAT ATTAAAAGAA ACCTAAATGT
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                                                                                   9000
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         CCAAACCTCA TATGTGAAAT GGCCAAAGCA CATGCAGGCT CCTGGTTGTT CCTCTCAAAC 10080
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         CTGTGCTGAC CAAGATTAG TAACCAGTTA TACCCAGTAT TTTGAGGTTT TATTGTTTTT 10140
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         MGRRRRLCLQ LYFLWLGCVV LWAQGTAGQP QPPPPPKPPRP QPPPQQVRSA TAGSEGGFLA
         PEYREEGAAV ASRVRRRGQQ DVLRGPNVCG SRFHSYCCPG WKTLFGGNQC IVPICRNSCG DGFCSRPNMC TCSSGQISST CGSKSIQQCS VRCMNGGTCA DDHCQCQKGY IGTYCGQPVC
                                                                                     120
 80
                                                                                     180
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480

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                                                                                    720
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       MDACCCAVGA AWGTECEECP KPGTKEYETL CPRGAGFANR GDVLTGRPFY KDINECKAFP
       GMCTYGKCRN TIGSFKCRCN SGFALDMEER NCTDIDECRI SPDLCGSGIC VNTPGSFECE
       CFEGYESGFM MMKNOMDIDG CERNPLLCRG GTCVNTEGSF OCDCPLGHEL SPSREDCVDI
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                                                                                  1260
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                                                                                   2100
                                                                                   2160
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       PCGNGTCTNV IGSFECNCNE GFEPGPMMNC EDINECAQNP LLCALRCMNT FGSYECTCPI
GYALREDQKM CKDLDECAEG LHDCESRGMM CKNLIGTFMC ICPPGMARRP DGEGCVDENE
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                                                                                   2340
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        GYIQHYQWNQ CVDENECSNP NACGSASCYN TLGSYKCACP SGFSFDQFSS ACHDVNECSS
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CYECKINGYP KKDSRQKRSI HEPDPTAVEQ ISLESVDMDS PVNMKFNLSH LGSKEHILBL
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        Coding sequence: 63..617
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                                                                                    300
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        GCCAGTGCAA CTCTTTCTAC ATCCCCAGGC ACATCCGGAA GGAGGAAGGT TCCTTTCAGT
                                                                                     480
        CCTGCTCCTT CTGCAGCCC AAGAAATTCA CTACCATGAT GGTCACACTC AACTGCCCTG
                                                                                    540
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65
                                                                                    960
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```

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|                                  | TCTGATTAAA   | CTTGGCCTAC   | TGGCAATGGC  | TACTTAGGAT   | TGATCTAAGG  | GCCAAAGTGC   | 2160  |
|----------------------------------|--|--|---|--|---|--|---|
|                                  |  |  | TACTTTGGAT  |  |   |  | 2220  |
|                                  |  |  | AATACTCTTT  |  |   |  |   |
|                                  | 1111111111   | AMCICCCIG  | AMIACICIII  | TIGCCTIGIA   | TUTTUTCHGC  | CICCIAGCCA   | 2280  |
| 5                                | AGICCIAIGI   | AATATGGAAA   | ACAAACACTG  | CAGACTTGAG   | ATTCAGTTGC  | CGATCAAGGC   | 2340  |
| )                                | TCTGGCATTC   | AGAGAACCCT   | TGCAACTCGA  | GAAGCTGTTT   | TTATTTCGTT  | TTTGTTTTGA   | 2400  |
|                                  | TCCAGTGCTC   | TCCCATCTAA   | CAACTAAACA  | GGAGCCATTT   | CAAGGCGGGA  | GATATTTTAA   | 2460  |
|                                  | ACACCCAAAA   | TOTTOCCUT  | GATTTTCAAA  | CTTTTTAAAACT   | CACTACTCAT  | CATTOTOLOG   |   |
|                                  | CTACCCCAAR   | TTOTTOOGICI  | **************************************  | CITITATACI   | CACIACIGAI  | GATTCTCACG   | 2520  |
|                                  |  |  | ACATAGTGTG  |  |   |  | 2580  |
| 10                               | CCAAATCTTT   | GTATTGTCCA   | CATTCTCCAA  | CAATAAAGCA   | CAGAGTGGAT  | TTAATTAAGC   | 2640  |
| 10                               | ACACAAATGC   | TAAGGCAGAA   | TTTTGAGGGT  | GGGAGAGAAG   | AAAAGGGAAA  | GAAGCTGAAA   | 2700  |
|                                  |  |  | GGAAAAATGA  |  |   |  | 2760  |
|                                  |  |  |   |  |   |  |   |
|                                  |  |  | CAAGAATGCA  |  |   |  | 2820-   |
|                                  | AGCAGTAATC   | TTCTTTTAGG   | AGCTTGTACC  | ACAGTCTTGC   | ACATAAGTGC  | AGATTTGGCT   | 2880  |
|                                  | CAAGTAAAGA   | GAATTTCCTC   | AACACTAACT  | TCACTGGGAT   | AATCAGCAGC  | GTAACTACCC   | 2940  |
| 15                               |  |  | AAGAGGGAAA  |  |   |  | 3000  |
|                                  | CACTACTACA   | AATCTYCCTYCT   | GTCTTCCAAC  | THICK OTTER  | **********  | CCIMINITIAN  |   |
|                                  |  |  |   |  |   |  | 3060  |
|                                  |  |  | ATGTAATGAT  |  |   |  | 3120  |
|                                  | TTATGGCAAG   | ATATTTGTGG   | TCTTGATCAT  | ACCTATTAAA   | ATAATGCCAA  | ACACCAAATA   | 3180  |
|                                  | TGAATTTTAT   | GATGTACACT   | TTGTGCTTGG  | CATTAAAAGA   | AAAAAACACA  | CATCCTGGAA   | 3240  |
| 20                               |  |  | TACTGTAGGT  |  |   |  |   |
|                                  |  |  |   |  |   |  | 3300  |
|                                  |  |  | ACTGTGTGGA  |  |   |  | 3360  |
|                                  | ATTTAATGTA   | ATTATTACTT   | CAAATCCTTT  | GGTCACTGTG   | ATTTCAAGCA  | TGTTTTCTTT   | 3420  |
|                                  | TTCTCCTTTA   | TATGACTTTC   | TCTGAGTTGG  | GCAAAGAAGA   | AGCTGACACA  | CCGTATGTTG   | 3480  |
|                                  |  |  | AGGGGAAACA  |  |   |  | 3540  |
| 25 ·                             | GAGTCACTCC   | CALCY VACALAN  | AAATTTTTA   | THENDER  | CONTRACTOR  | ALGICITOCI   |   |
|                                  | 1100100  | CIGARICITI   | WITTITIANW  | TIGAMIGITE   | CITAAAGGIT  | AACATTTCTA   | 3600  |
|                                  |  |  | TTAAATGTTA  |  |   |  | 3660  |
|                                  | ACGAATAGCA   | GATAATGATG   | ACTAGTTCAC  | ACATAAAGTC   | CTTTTAAGGA  | GAAAATCTAA   | 3720  |
|                                  | AATGAAAAGT   | GGATAAACAG   | AACATTTATA  | AGTGATCAGT   | TAATGCCTAA  | GAGTGAAAGT   | 3780  |
|                                  | AGTTCTATTG   | ACATTCCTCA   | AGATATTTAA  | TATCAACTCC   | ስጥተልጥ <u>የ</u> ምስጥተ   | MACHANCIAN   | 3840  |
| 30                               | AAATCATTTA   | AAAAAAAAA  | VOLUME TANK   | 1410440100   | ATTAIGIATT  | MIGICIOCII   |   |
| 50                               |  |  | AGAATTATAT  |  |   |  | 3900  |
|                                  |  |  | CTCATAAAAC  |  |   |  | 3960  |
|                                  | ACTAGAATTT   | AATTTTCACC   | CCAATAATGT  | TCTATATAGC   | CTTTGCTAAA  | GAGCAACTAA   | 4020  |
|                                  |  | CTATTCTTTC   |   |  |   | *  |   |
|                                  |  |  |   |  |   |  |   |
| 35                               | Com TD MO.   | 164 Dunbain  |   |  |   |  |   |
| 55                               |  | 164 Proteir  |   |  |   |  |   |
|                                  | Protein Acc  | cession #: 1   | TP_037504.1   |  |   |  |   |
|                                  |  |  |   |  |   |  |   |
|                                  | 1  | 11   | 21  | 31   | 41  | 51   |   |
|                                  | ī  | ï -  | ī-  | ī  | ī~  | 1  |   |
| 40                               | 1  | <u>.</u>   | !   | 1  | ŀ   | i  |   |
| 70                               | MSRTAYTVGA   | PPPPP  | AABGKKKGSQ  | GAIPPPDKAQ   | HNDSEQTQSP  | QQPGSRNRGR   | 60  |
|                                  | GQGRGTAMPG   | EEVLESSOEA   | LHVTERKYLK  | RDWCKTOPLK   | OTIHEEGCNS  | RTIINRFCYG   | 120   |
|                                  |  |  |   |  |   |  |   |
|                                  | QCNSFYIPRH   | IRKEEGSFQS   | CSFCKPKKFT  | TMMVTLNCPE   | LOPPTKKKRV  | TRVKOCRCIS   |   |
|                                  | QCNSPYIPRH   | IRKEEGSFQS   | CSFCKPKKFT  | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   | 180   |
|                                  | QCNSFYIPRH<br>IDLD   | IRKEEGSFQS   | CSFCKPKKFT  | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   |   |
| 45                               | QCNSFYIPRH<br>IDLD   | IRKEEGSFQS   | CSFCKPKKFT  | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   |   |
| 45                               | QCNSFYIPRH<br>IDLD<br>Seq ID NO:   | 165 DNA sec  | CSFCKPKKFT  | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   |   |
| 45                               | QCNSFYIPRH<br>IDLD<br>Seq ID NO:   | 165 DNA sec  | CSFCKPKKFT  | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   |   |
| 45                               | QCNSFYIPRH<br>IDLD<br>Seq ID NO:   | 165 DNA sec  | CSFCKPKKFT  | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   |   |
| 45                               | QCNSFYIPRH<br>IDLD<br>Seq ID NO:   | IRKEEGSFQS<br>165 <u>DNA sec</u><br>id Accession   | CSFCKPKKFT  Tuence  1 #: CAT cl   | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   |   |
| 45                               | QCNSPYIPRH<br>IDLD<br>Seq ID NO:<br>Nucleic Ac:  | 165 DNA sec  | CSFCKPKKFT  | TMMVTLNCPE   | LQPPTKKKRV  | TRVKQCRCIS   |   |
|                                  | QCNSFYIPRH<br>IDLD<br>Seq ID NO:<br>Nucleic Ac:  | IRKEEGSFQS  165 DNA sec id Accession   | CSFCKPKKFT TUENCE 1 #: CAT cl   | uster  | LQPPTKKKRV  | TRVKQCRCIS   | 180   |
| <b>45</b><br><b>50</b>           | QCNSPYIPRH<br>IDLD<br>Seq ID NO:<br>Nucleic Act  | IRKEEGSFQS  165 DNA sec id Accession  11   | CSFCKPKKFT  Tuence 1 #: CAT cl 21   TCGCCATGGC  | TMMVTLNCPE  uster  31   CGAGTTGCGC   | LQPPTKKKRV 41   | TRVKQCRCIS  51   CACTAACACT  |   |
|                                  | QCNSPYIPRH<br>IDLD<br>Seq ID NO:<br>Nucleic Act  | IRKEEGSFQS  165 DNA sec id Accession  11   | CSFCKPKKFT TUENCE 1 #: CAT cl   | TMMVTLNCPE  uster  31   CGAGTTGCGC   | LQPPTKKKRV 41   | TRVKQCRCIS  51   CACTAACACT  | 180   |
|                                  | QCNSPYIPRH<br>IDLD<br>Seg ID NO:<br>Nucleic Ac:<br>1<br> <br>GAATTGCATC<br>GCTACGTTTC  | IRKEEGSFQS  165 DNA sec id Accession  11    GGACAGAGCT CGCCTGAGCG  | CSFCKPKKFT  Tuence 1 #: CAT cl 21   TCGCCATGGC  | TMMVTLNCPE  uster  31  | LQPPTKKKRV 41   | TRVKQCRCIS  51   CACTAACACT  | 180   |
|                                  | QCNSPYIPRH<br>IDLD<br>Seg ID NO:<br>Nucleic Ac:<br>1<br> <br>GAATTGCATC<br>GCTACGTTTC  | IRKEEGSFQS  165 DNA sec id Accession  11    GGACAGAGCT CGCCTGAGCG  | CSFCKPKKFT  Quence 1 #: CAT cl 21 1 TCGCCATGGC TGGACCGAAC   | TMMVTLNCPE  uster  31  | LQPPTKKKRV 41   | TRVKQCRCIS  51   CACTAACACT  | 180   |
| 50                               | QCNSPYIPRH<br>IDLD<br>Seg ID NO:<br>Nucleic Ac:<br>1<br> <br>GAATTGCATC<br>GCTACGTTTC  | IRKEEGSFQS  165 DNA sec id Accession  11    GGACAGAGCT CGCCTGAGCG  | CSFCKPKKFT  Quence 1 #: CAT cl 21 1 TCGCCATGGC TGGACCGAAC   | TMMVTLNCPE  uster  31  | LQPPTKKKRV 41   | TRVKQCRCIS  51   CACTAACACT  | 180   |
| 50                               | QCMSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  1   GAATTGCATC GCTACGTTTC ACTGCGCACG  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGCT GGCCTGAGCG GAGAACGGGC  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21  1 TCGCCATGGC TCGCCCAAGC TCTGGCTCAA   | TMMVTLNCPE  uster  31  | LQPPTKKKRV 41   | TRVKQCRCIS  51   CACTAACACT  | 180   |
|                                  | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  1   GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO:  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT CGCCTGAGGG GAGAACGGGC 166 DNA sec  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21  1 TCGCCATGGC TCGGCCTCAA  TCTGGCTCAA  | TMMVTLNCPE  .uster  31   CGAGTTGCGC CCGCAAGGTG G   | LQPPTKKRRV 41   GTGGTTGTGG CGGCGGAAGC   | TRVKQCRCIS  51   CACTAACACT  | 180   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  1   GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac:  | 165 DNA sec d Accession  11   GGACAGAGGT CGCCTGAGGG GAGAACGGGC 166 DNA sec d Accession   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES   | TMMVTLNCPE  .uster  31   CGAGTTGCGC CCGCAAGGTG G   | LQPPTKKRRV 41   GTGGTTGTGG CGGCGGAAGC   | TRVKQCRCIS  51   CACTAACACT  | 180   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  1   GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac:  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT CGCCTGAGGG GAGAACGGGC 166 DNA sec  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES   | TMMVTLNCPE  .uster  31   CGAGTTGCGC CCGCAAGGTG G   | LQPPTKKRRV 41   GTGGTTGTGG CGGCGGAAGC   | TRVKQCRCIS  51   CACTAACACT  | 180   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  1   GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac:  | 165 DNA sec d Accession  11   GGACAGAGGT CGCCTGAGGG GAGAACGGGC 166 DNA sec d Accession   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES   | TMMVTLNCPE  .uster  31   CGAGTTGCGC CCGCAAGGTG G   | LQPPTKKRRV 41   GTGGTTGTGG CGGCGGAAGC   | TRVKQCRCIS  51   CACTAACACT  | 180   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  1   GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac:  | 165 DNA sec d Accession  11   GGACAGAGGT CGCCTGAGGG GAGAACGGGC 166 DNA sec d Accession   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES   | TMMVTLNCPE  .uster  31   CGAGTTGCGC CCGCAAGGTG G   | 41<br> <br>  GTGGTTGTG<br>CGGCGGAAGC  | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT   | 180   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  1   GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac:  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT GCCTGAGGG GAGAACGGGC  166 DNA sec dd Accession lence: 116  | CSFCKPKKFT  TUENCE  #: CAT cl  21  TCGCCATGGC TCGGCTCAA  TCTGGCTCAA  TUENCE  #: FGENES  550  21   | TMMVTLNCPE  .uster  31   CGAGTTGCGC GCGCAAGGTG G   | LQPPTKKRRV 41   GTGGTTGTGG CGGCGGAAGC   | TRVKQCRCIS  51   CACTAACACT  | 180   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:    GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequents  | IRKEEGSFQS  165 DNA sec id Accession  11   GACCAGAGGCT CGCCTGAGGG GAGAACGGGC  166 DNA sec id Accession sence: 116  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TCTGGCTCAA  TUENCE  1 #: FGENES  550  21   | TMMVTLNCPE  uster  31   GAGTTGCGC GCGCAAGGTG G  H predicted  | LQPPTKKKRV  41  j GTGGTTGTGG CGGCGGAAGC   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT   | 60<br>120   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  1   | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT GGCCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 116  11   TGCCATCCAG  | CSFCKPKKFT  TUENCE 1 #: CAT cl 21   TCGCCATGGC TGGACGAAC TCTGGCTCAA  TUENCE 1 #: FGENES 550 21   AATGTCTCGG   | TMMVTLNCPE  J1 CGAGTTGCGC GCGCAAGGTG G  H predicted  | LQPPTKKRRV  41  GTGGTTGTGG CGGCSGAAGC   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG  | 60<br>120   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG  | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec id Accession sence: 1(  11   TGCCATCCAG ACCGCCTGCT  | CSFCKPKKFT  TUENCE  #: CAT cl  21  TCGCCATGGC TCTGGCTCAA  TUENCE  #: FGENES  550  21  AATGTCTCGG GCACCTCCTG   | TMMVTLNCPE  J1  CGAGTTGCGC CGCCAAGGTG G  H predicted  J1  GGGCCCTCCT GGGCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  | 41 GTGGTTGTGG CGGCGGAAGC  41 TGGTGACAGG AGACGGCGTT  | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGGCATATAC   | 60<br>120   |
| 50                               | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA   | IRKEEGSFQS  165 DNA sec id Accession  11   GACAGAGGCT GCCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 11c  11   GACCATCCAG ACCGCCTGCT CCCTTCTCCT   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGACCGAAC TCTGGCTCAA  TUENCE  1 #: FGENES  550  21    AATGTCTCGG GCACCTCCTG CTTCCTGCTC  | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted  J1   GGGCCTCCT GGGCTGGAGA TTCTTCCTGT  | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGGCGTT TCCGCCTCCT   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC  | 60<br>120   |
| 50<br>55<br>60                   | Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGC GAGAACGGGC  166 DNA sec dd Accession ience: 11c  11   TGCCATCCAG ACCGCCTGCT CCCTTCCTC GCAGGAGCTT   | CSFCKPKKFT  TUENCE 1 #: CAT cl 21   TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550 21   AATGTCTCGG GCACCTCCTG CTTACATCACC   | TMMVTLNCPE  J1 CGAGTTGCGC GCGCAAGGTG G H predicted J1 GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCCCCGGG  | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGCGTT TCCGCCTGCT TGCGGTGGTT   | 51   CACTAACACT CGGAGCTCAT   | 60<br>120<br>60<br>120  |
| 50                               | Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGC GAGAACGGGC  166 DNA sec dd Accession ience: 11c  11   TGCCATCCAG ACCGCCTGCT CCCTTCCTC GCAGGAGCTT   | CSFCKPKKFT  TUENCE 1 #: CAT cl 21   TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550 21   AATGTCTCGG GCACCTCCTG CTTACATCACC   | TMMVTLNCPE  J1 CGAGTTGCGC GCGCAAGGTG G H predicted J1 GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCCCCGGG  | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGCGTT TCCGCCTGCT TGCGGTGGTT   | 51   CACTAACACT CGGAGCTCAT   | 60<br>120<br>60<br>120<br>180<br>240  |
| 50<br>55<br>60                   | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGCCGCACACAC  | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 11c  11   TGCCATCCAG ACCGCCTGCT CCCTTCTCT GCAGGAGGTT ACTGGCTGCT   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCCTG CTTCCTGCTC CTACATCACC GGGCCACCTG   | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted  J1   GGGCCCTCCT GGGCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCCGGC GGCATGTACC   | LQPPTKKRRV  41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCGTT TCCGCCTGCT TGCCCTGCTT TTCCAAATGA  | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCTT GGCGGCCCTT   | 60<br>120<br>120<br>180<br>240<br>300   |
| 50<br>55<br>60                   | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGGCGCA CAAAATGAAGA   | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 116  11   TGCCATCCAG ACCGCCTGCT CCCTTCTCCT GCAGGAGGTT ACGGCTGCT ACAGGAGGTACT ACAGGTACT ACAGGGTACT ACAGGTACT ACAGGGTACT ACAGGGTACT ACAGGTACT    | CSFCKPKKFT  TUENCE  #: CAT cl  21  TCGCCATGGC TCTGGCTCAA  TUENCE  #: FGENES  550  21  AATGTCTCGG GCACCTCTG CTTCCTGCTC CTTCCTGCTC CTACATCACC GGGCCACCTG GGGCACCTG GGGCACCTG GGGCACCTG GGGCACCTG GGGCACCTG GGGCACCTG GGGCACCTG  | TMMVTLNCPE  J1  GGAGTTGCGC CCGCAAGGTG G  H predicted  J1  GGGCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCGGC GGCATGTACC CACCATGTAC  | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGGCGTT TCCGCCTGCT TCCGCTGCT TCTCCAAATGA TCTTGGTATG  | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GGCGGGCCTT GGCGGGCCCT GATGGGACCT  | 60<br>120<br>60<br>120<br>180<br>240<br>300<br>360  |
| 50<br>55<br>60                   | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCCACG CCATCCACG CTGACGCTCT CCCCGCGCCA CAGATGAGA GTCCTGCCGC  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGC CGCCTGAGCG GAGAACGGGC  166 DNA sec dd Accession ience: 110  TGCCATCCAG ACCGCCTGCT CCCTCTCCT CCCTCTCCT CCAGGAGCTT ACTAGGTGCT TGTTGGTTCT TGTTGGTTCT  | CSFCKPKKFT  TUENCE 1 #: CAT cl 21   TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550 21   AATGTCTCGG GCACCTCCTG CTTCCTGCTC CTTACATCACC GGGCAACATG GGGCAACATG GGGCAACATG GGGCACCTC GGGCACCTC GGGCACCTC GGGCACCTC GGGCACCTC GGGCACCTC GGGCACCTC GGGCACCTC GGGCACCCCT  | TMMVTLNCPE  J1  GCGCTAAGGTG  GH predicted  J1  GGGCCTCCT GGGCTGGAGA TTCTTCCTGT TTCCCGCGGGC GGCATGTACC CACCATGTAC   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCCTT TCCCAAATGA TCTTGGTATG TCTTGTATG   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGCATATAC CCCCCAGCCT GCCGGGCCTT GATGGGACCTC GGGAGCCTC GGGAGCCTC GGGAGCCTC GGGAGCCTC GGGAGCCTC GGGAGCCTC GGGAGCCTC  | 60<br>120<br>120<br>180<br>240<br>360<br>420  |
| 50<br>55<br>60                   | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGCGCAC CAAGATGAGA GTCCTGCCGCGCAC GCTGCCGCGCGCGCTCCACACG GCTGCCGCCGC  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT GAGAACGGGC  166 DNA sec dd Accession dence: 11c   TGCCATCCAG ACCGCTGCT CCTTCCTT ACTAGGTACT TGTTGGTTCT TGTTGGTTCT TCCCCAAGGA  | CSFCKPKKFT  Dience  ##: CAT cl  TCGCCATGGC TCGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  CTTCTGCTC CTTCTGCTC CTTCTGCTC CTACATCACC CGGCACACTG GGACAACATG GGACAACATG GGTGCACCCT TGACCTCTTC   | TMMVTLNCPE  J1  GCGAGTTGCGC GCGCAAGGTG G  H predicted  J1  GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCCGGC GGCAGTGACC CACCATGTAC CATTACATCA TATGGCTTCC   | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGGCGTT TCCGCCTCCT TGCCCTGCTT TTCCCAAGTA TCTTGGTATG AACCCTTTT TAAAACCTTG   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GATGGGACCTT GATGGGACCTC GGGAGCCTTG GCTAGGGGAT   | 60<br>120<br>60<br>120<br>180<br>240<br>300<br>360  |
| 50<br>55<br>60<br>65             | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGCGCAC CAAGATGAGA GTCCTGCCGCGCAC GCTGCCGCGCGCGCTCCACACG GCTGCCGCCGC  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT GAGAACGGGC  166 DNA sec dd Accession dence: 11c   TGCCATCCAG ACCGCTGCT CCTTCCTT ACTAGGTACT TGTTGGTTCT TGTTGGTTCT TCCCCAAGGA  | CSFCKPKKFT  Dience  ##: CAT cl  TCGCCATGGC TCGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  CTTCTGCTC CTTCTGCTC CTTCTGCTC CTACATCACC CGGCACACTG GGACAACATG GGACAACATG GGTGCACCCT TGACCTCTTC   | TMMVTLNCPE  J1  GCGAGTTGCGC GCGCAAGGTG G  H predicted  J1  GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCCGGC GGCAGTGACC CACCATGTAC CATTACATCA TATGGCTTCC   | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGGCGTT TCCGCCTCCT TGCCCTGCTT TTCCCAAGTA TCTTGGTATG AACCCTTTT TAAAACCTTG   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GATGGGACCTT GATGGGACCTC GGGAGCCTTG GCTAGGGGAT   | 60<br>120<br>120<br>180<br>300<br>360<br>420<br>480   |
| 50<br>55<br>60<br>65             | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGCCTCT CCCCGGCGCA CAAGATGAGA GTCCTGCCATCG GGGCTGCCATCG GGGCTGCCATCG  | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec id Accession sence: 116  11   CCCTACCAG ACCGCCTGCT CCCTTCTCT ACTGGCTGCT ACAGGAGGTT TCTTGGTTCT CCCCCAAGGA  | CSFCKPKKFT  TUENCE  #: CAT cl  21  TCGCCATGGC TCGGCTCAA  TUENCE  #: FGENES  550  21  AATGTCTCGG GCACCTCGTG CTTCCTGCTC CTACATCACC GGGCACCTG GGACAACATG GGTGCACCTT TGACCTCTTC TGACCTCTTC TGACCTCTTC TGACCTCTTC TGACCTCTTC TGACCTCTTC TGACCTCTTC TGACCAAGTGG   | TMMVTLNCPE  J1   CGAGTTGCGC GCCCAAGGTG G  EH predicted  J1   GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TCCCGCCGGCA GGCATGTAC CACCATGTAC GATTACATCA TATGGCTTCC TAGGCTCCT TAGGCTTCC AGCCGGCACC  | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGGCTTT TCCGCCTGCT TCCGCTGCTTTTCCAAATGA TCTTGGTATG AACCCTTTT TAAAACCTTG GTCGCCTGCT   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGATATAC GCTGCGGTTC CCCCAGCCT GGCGGCCTT GATGGGACCT GGGAGCCTCA GCTAGGGACT GCTAGGGACT GACACCCGCC   | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540   |
| 50<br>55<br>60                   | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac: GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence I I ATGCCACCTC CCCATCACAG GCGGTACTAC CTGACGCTCT CCCCGCGCCA CAAGATAGAGA GTCCTGCCGC GCTGCCATCC GGGCTGCTGC GTTCCACTTTG GTTCCACTTTTG  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT GGCTGAGCG GAGAACGGGC  166 DNA sec dd Accession ience: 116  TGCCATCCAG ACCGCTGCT GCAGGAGGTT ACTAGCTTGCT TGTTGGTTCT CCCCCAAGGA TCAGCAAAGG ACATCCTGAA ACATCCTGAA  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCCTG CTTACATCACC GGGCCACCTG GGACAACATG GGACAACATG GGACACATC TGACACTCTTC TGACAGTGG GCCTTACATG GCCTTACATG   | TMMVTLNCPE  J1 GCGCCAAGGTG G H predicted J1 GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCCGGC GGCATGTACC CACCATGTAC CACCATGTAC AGCATGTAC   | 41  GTGGTTGTGG CGGCSGAAGC  41  TGGTGACAGG AGACSGCTT TCCGCCTGCT TCCTAATGA TCTTGGTATG ACCCCTTT TAAAACCTG GTCGCCTGCT ACCAGGAGGCSC  | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGCGTTC CCCCCAGCCT GGCGGCCTT GATGGGACCT GGGAGCCTCA GCTAGGGGAT GCTAGGGAT GCTAGGGGAT GCTAGCTTATG   | 60<br>120<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600   |
| 50<br>55<br>60<br>65             | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC  GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  I  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGGCGCA GTCCTCCCGGGCTGCTGC GTCCACTTGC GTCCACTTGC GCTTCCACTTGC CCATCACAG GCTGCCATCC GCGCTGCCATCC GCGCTGCTGC CATCACATG   | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGC GAGAACGGGC  166 DNA sec dd Accession ience: 11c  TGCCATCCAG ACCGCCTGCT CCCTTCTCCT GCAGGAGCTT ACTGGCTGCT AGAAGGTACT TGTTGGTTCT CCCCCAAGGA TCAGCAAAGG ACATCCTGA ACACCAGA GCAGCAACGA ACATCCTGA ACACCAGA ACATCCTGA ACACCAGA ACATCCTGAAAGG ACAGCAGAAAGG ACATCCTGAAAGG ACATCCTGAAAGG ACATCCTGAAAGG ACATCCTGAAAGG ACATCCTGAAAGG ACAGCAGC ACGCAGCACTCT   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCCTG CTTCCTGCTC CTACATCACC GGGCACCTG GGACAACATG GGGTGCACCTT TGACCATGTG TGACCATCAGT GGCCACTT TGACAATGTG GCCTTACATC   | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted  J1   GGGCCCTCCT GGGCTGAGA TTCTTCCTGT TGCCTCGGC GGCATGTAC CACCATGTAC CACCATGTAC TATGGCTTCC AGCAGCACC AGATCTTCA TATGGCTTCC AGCAGCACC AAGATCTTCA TCAGCGGTCT TCAGCGGTCT   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCGTT TCCGAATGA TCTTGGTATG TCTTGGTATG TAAAACCTTG GTCGCTGCT TAAAACCTG GTCGCTGCT ACCAGAGCGC CCCTTGATAT  | TRVKQCRCIS  51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GAGGGCTCA GCTAGGGCAT GATAGGGACT GCTAGGGGAT GACACCGCC TGACATTAT GTTTGAGCAT GTTTGAGCAT  | 60<br>120<br>120<br>180<br>240<br>360<br>420<br>540<br>600  |
| 50<br>55<br>60<br>65             | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGCGCAC CAAGATGAGA GTCTGCCCGC GCTGCCATCG GCGCTCTCCCCCGC GCTCCCATCAAT ATCAGCCTCA   | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 11c  11   TGCCATCCAG ACCGCCTGGT CCCTTCTCT GCAGGAGGTTT ACTAGGTACT ACAGGAGGTACT TGTTGGTTGT TCCCCCAAGGA TCAGCAAAGG ACATCCTGAA GGGGGCATCT TGACCCTGGA  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCCTG CTTCCTGCTC CTACATCACC GGACAACATG GGTGCACCTT TGACCACTCT TGACCACTCT TGACAAGTGG GCCTTACATG GCCTACATCACT CACACACACCT CACACACACCT CACACACCT CACACACCT CACACACCT CACACACCT CACACACCT CACACACCT CACACACT CACACACCT CACACACT CACACACCT CACACACC CACACACACC CACACACC CACACACC CACACACC CACACACC CACACACC CACACACC CACACACAC CACACACAC CACACACACAC CACACACACAC CACACACACAC CACACACACACACAC CACACACACACACAC CA | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted  THE PREDICTOR GGGCCCTCCT GGGCCTCCT GGGCTGAGA TTCTTCCTGT TGCCGCGC GGCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC AAGAGTCTCA AAGAGTCTCA AAATGTGTCT   | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGGCTT TCCGCCTGCT TGCCCTGCT TTCCAAATGA TCTTGGTATG AACCCTTTT GTAAAACCTTG GTCGCCTGCT ACAGAGGGCC CCCTTGATAT   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GATGGGACCTC GGAGGCTCA GCTAGGGACT GATGGGACT GATGGGACT GATGGGACT GATGGGACT GATGGGACT GATGAGCT GATGAGCT GATGAGCT GATGAGCT GATGAGCT GATGAGCT GATGAGCT CAGCAACT CA | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>6720  |
| 50<br>55<br>60<br>65             | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac: GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence ATGCCACCTC CCCATCCAGG GCGGTTCCA CTGAGGCTCT CCCCGCGCGA CAAGATGAGA GTCCTGCCGC GCTGCCATCG GGGCTGCCATCG GTGCCATCT CAGGCTGCT CAGGCTGC CTCCACTTTG CATGCTAAAT ATCAGCCTCA CAAGAAGAA   | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT GGCTGAGCG GAGAACGGGC  166 DNA sec dd Accession ience: 116  TGCCATCCAG ACCGCTGCT GCAGGAGGTT ACTAGCTGCT TGTTGGTTCT CCCCCAAGGA TCAGCAAAGG ACATCCTGAA GGCGGCATCT TGACCCTGGA TGAGCAATT TGACCCTGGA TGAGCGAATT TGACCCTGGA TGAGCGATT TGACCCTGGA TGAGTGATTA   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACGAAC TCTGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCCTG CTACATCACC GGGCAACATG GGACAACATG GGACAACATG GGACACATG GGACAACATG GGACACATG GGACACATG GGACACATG GGACACATG TGACACATG GCACACATG TGACACTCTTC TGACAAGTGG GCCTTACATG GCCAGAGGGC CAGTCTTCACATG TATCTCCGCT  | TMMVTLNCPE  J1 GCGAGTTGCGC GCGCAAGGTG G H predicted TCTCCTGT TCCCGCCGGC GGCATGTACC CACCATGTAC AAGATCTTCA TCAGCGGTCT AAAATGTGTCT AAAATGTGTCT ATCATGAAC   | 41  GTGGTTGTGG CGGCSGAAGC  41  TGGTCACAGG AGACSGCTTT TCCACCTGCT TCCTAATGA TCTTGGTATG TCTTGGTATG GTCCCCTGT TAAAACCTTG GTCCCCTGT TAAAACCTTG TCCCCTGT TAAAACCTTG TCCCCTGTT TAAAACCTTG TCCCCTGTT TAAAACCTTG TCACGTACAA  | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGAGCTG GCTGGGGTTC CCCCCAGCCT GGGAGCCTCA GCTAGGGACTC GGGAGCCTCA GCTAGGGACTC GGGAACCCGC CTAGCATTATG GTTTGAGCAT CAGCAACTGC GTTTGAGCAT CAGCAACTGC GTTTGTCCGG  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>6720  |
| 50<br>55<br>60<br>65<br>70       | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac: GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence ATGCCACCTC CCCATCCAGG GCGGTTCCA CTGAGGCTCT CCCCGCGCGA CAAGATGAGA GTCCTGCCGC GCTGCCATCG GGGCTGCCATCG GTGCCATCT CACAGGAGAAGA ATGCCACATA ATCACCTCA CAAGAGAAGA  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT GGCTGAGCG GAGAACGGGC  166 DNA sec dd Accession ience: 116  TGCCATCCAG ACCGCTGCT GCAGGAGGTT ACTAGCTGCT TGTTGGTTCT CCCCCAAGGA TCAGCAAAGG ACATCCTGAA GGCGGCATCT TGACCCTGGA TGAGCAATT TGACCCTGGA TGAGCGAATT TGACCCTGGA TGAGCGATT TGACCCTGGA TGAGTGATTA   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACGAAC TCTGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCCTG CTACATCACC GGGCAACATG GGACAACATG GGACAACATG GGACACATG GGACAACATG GGACACATG GGACACATG GGACACATG GGACACATG TGACACATG GCACACATG TGACACTCTTC TGACAAGTGG GCCTTACATG GCCAGAGGGC CAGTCTTCACATG TATCTCCGCT  | TMMVTLNCPE  J1 GCGAGTTGCGC GCGCAAGGTG G H predicted TCTCCTGT TCCCGCCGGC GGCATGTACC CACCATGTAC AAGATCTTCA TCAGCGGTCT AAAATGTGTCT AAAATGTGTCT ATCATGAAC   | 41  GTGGTTGTGG CGGCSGAAGC  41  TGGTCACAGG AGACSGCTTT TCCACCTGCT TCCTAATGA TCTTGGTATG TCTTGGTATG GTCCCCTGT TAAAACCTTG GTCCCTGCT TCACAGGCCC CCCTTGATAT TCAGCTACAA   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGAGCTG GCTGGGGTTC CCCCCAGCCT GGGAGCCTCA GCTAGGGACTC GGGAGCCTCA GCTAGGGACTC GGGAACCCGC CTAGCATTATG GTTTGAGCAT CAGCAACTGC GTTTGAGCAT CAGCAACTGC GTTTGTCCGG  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600<br>600<br>720<br>780   |
| 50<br>55<br>60<br>65<br>70       | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  I   ATGCCACCTC CCCATCACAG GCGGTGTCCA CCAGAGAGAGAGAGAGAGAAGAGA   | IRKEEGSFQS  165 DNA sec dd Accession  11   | CSFCKPKKFT  THENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  AATGTCTCGG GCACCTCTG CGACACCTG GGACACCTG TGACACTGTC TGACATCACC GGGCCACTT TGACATCACC GGCCACTT TGACATCACC TGACATCTC TCACATCACC TCACATCACC TCACATCTC TCACATCTC TCACATCTC TCACATCTC TCACCTCTC TCACCTCTC TCACCTCTC TCACCTCTC TCACCTCGAC TATCTCCGGT TCTACCTCGAC  | TMMVTLNCPE  J1  GCGAGTTGCGC GCGCAAGGTG G  H predicted  TCTCCTCT GGGCTGGAGA TTCTTCCTGT TGCCGCCGGC GGCATGTACC CACCATGTAC CACCATGTAC CACCATGTAC AGATACTCA TATGGCTTCC AGCAGCACC AGATATTCA TCAGCGGTCT AAATGTGTCT ATCATTGACT TTCATTTACT  | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCCTT TCCACATGA TCTTGGTATG TCTGCCTGCT TTCAAATGA TCTTGGTATG TCACAGAGGCC CCCTTGATAT TCAGCTACAA TCAGCGCTCT TCAGCTGCT TCAGCTCCAACAC ACCAGTACAA TCAGCTACAA TCAGCTACAA TCAGCTACAA   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGCTCT GCGCGGCCTT GATGGGACCT GGGAGCCTCA GCTAGGGACT GCTAGGGACT GCTAGGGACT GCTAGGGACT GCTAGGGACT GCTAGGGACT GCTAGGGACT GCTAGGGACT GCTAGGGACT GCTTGTCCGG GGGATGCGG  | 60<br>120<br>120<br>180<br>360<br>420<br>480<br>540<br>660<br>720<br>780  |
| 50<br>55<br>60<br>65             | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGGTTCCA CAAGATAGGA GTCCTCCCCTCC   | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 11c  17   TGCCATCCAG ACCGCTGCT CCCTTCTCT TGTTGGTTCT TGTTGGTTCT TGTTGGTTCT TGTTGGTTCT TGAGCAAAGG ACATCCTGAA ACGCCTGGA TCAGCAAAGG ACATCCTGGA TCAGCAAAGG ACATCCTGGA TCAGCAAAGG ACATCCTGGA TCAGCAAAGG ACATCCTGGA TGACCTGGA TGACCTGGA TGACCTGGA TGACCTGGA ACGCCTGTGA   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TGGACAACTG GCACCTCTGCTC CTTCCTGCTC CTACATCACC GGACAACATG GGTGACCCT TGACCTCTTC TGACAAGTGG GCCTACATG GCCTACATG TGCCTTTCAG TATCTCCGTC CATGCTCCCC CATGTGCAC  | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted  J1   GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCGC GGCATGTACC CACCATGTAC CATTACATCA TATGGCTTCC AGCGGCACC AAGATCTICA TCAGTGGTCT TCAGTGTCT TCATTTACT TCACTTCACCA  | 41   GTGGTTGTGG CGGCGGAAGC  41   TGGTGACAGG AGACGCGTT TCCGCCTGCTT TCCGCTGCTT TTCCAAATGA TCTTGGTATG AACCCTTTT TAAAACCTTG GTCGCTGCT TCAGGTACA TCAGCTACAA TCTGGTATA TCAGCTACAA TCAGCTACAA TCAGCTACAA TCAGCTACAA TCAGCTACAA TAGCGCTCTCGC CTGAAGTCAT   | TRVKQCRCIS  51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GATGGGACCTC GGGAGCCTCA GCTAGGGAT GACACCGCC TGACATTATG GTTTGACAT CAGCAACTGC GTCTGCCGG GGATCGCCGG CCCAGCACTGC GCAGCACTGC GCAGCACTGC GCAGCACTGC CCCCGCC CGACCTGC CCCCGCC CGACCTGC CCCCGCC CGACCTGC CCCCCC CCCCCCC CCCCCC CCCCCCC CCCCCCC   | 60<br>120<br>180<br>240<br>360<br>420<br>600<br>600<br>720<br>780<br>840<br>900   |
| 50<br>55<br>60<br>65<br>70       | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  1   ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGCGCGA CAGARAGAG GTCTGCCTC CTGCCTCCCTCCCTCCCTCCCCCCCCCC   | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGCT GGCCTGAGCG GAGAACGGGC  166 DNA sec ld Accession  160 Accession  17   TGCCATCCAG ACCGCCTGCT GCAGGAGCT ACTGGCTGCT TGCTCTCT TCCCCCAAGGA TCAGCAAAGG ACATCCTGAA GGCGGCATCT TGACAGGAAAGG ACATCCTGAA GGCGGCATCT TGACCCTGGA TCAGCAAAGG ACATCCTGAA GGCGCGCATCT TGACCCTGAA TGAGTGATTA GCTTGCACCA AGGCCTGGCA TGAGCCTGGA TGAGCCTGGA  | CSFCKPKKFT  Dience  #: CAT cl  TGGCCATGGC TGGACCGAAC TCTGGCTCAA  TH: FGENES  550  21  AATGTCTCGG GCACCTCCTG CTTCACTCAC GGGCAACTG GGACAACTG GGACAACTG GGACACTG TGACTCTTC TGACATGT GCCTTACATG GCTTACATG GCCTACATG GCCTTACATG GCCTTACATG GCCTTACATG GCCTTACATG GCCTTCAC TATCTCCGCT CATCTCCGCT CATCTCCGCT CATCTCCGCT CATCTCCGCT CATCTCCGCT CATCTCCGCT CATCTCCGCT CATCTCCGCT CATCTCGCAC CATGGTGCAC CATGGTGCAC GGGGGGCCGAC GGGGGGCCGAC  | TMMVTLNCPE  J1   GGGCCCTCCT GGGCCTCCT GGGCCTCCT TGCCGCGGC GGCATGTACC CACCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC TATGGCTCT AAATGTGTCT AAATGTGTCT ATCATTGAAC TTCATTTAAC TCACTTCACC CACCTTCACC ACCTTCACC ACCTTCACC ACCTTCACC ACCTTCACC ACCATTTACT ACATTTACT ACATTTACT CACTTCACCACT CACTTCACCACT ACATTTACT CACTTCACCACT ACATTTACT CACTTCACCACT ACATTCACCACT ACATTCACT ACATTCACT ACATTCACT ACATTCACACT ACATTCACT ACATTCACT ACATTCACT ACATTCACT ACATTCACT ACATTCACT ACAT | 41    GTGGTTGTGG CGGCSGAAGC  41    TGGTGACAGG AGACGGCTTGT TCCGCCTGCT TCTCGAATGA TCTTGGTATG AACCCTTTT TAAAACCTTG GTCGCCTGCT ACCAGAGGGC CCCTTGATAT TCAGCTACAA TCAGCTACAA AGGCCAGCC CTGAAGTCAT ACGGCTCGGC CTGAAGTCAT ACGGCTCGGC CTGAAGTCAT ACGGCTAGCAAG  | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCCCAGCCT GCGGGGTC CCCCAGCCT GATGGGACCT GATGGGACCT GATGGGACCT GATGGGACCT GCTAGGGAT CACACCGC GTAGCACT GATGCACT GATGGACT GATGGACT GATGGACT GACACCGC GTAGGAACT GTTTGAGCAT CAGCAGT GTTGCGG GGATGGCGG GGATGGCGG GGATGGCGG GGGAAGGACC GGGGAAGGACCC GGGGACGACC GGGGAAGGACCC GGGGAAGGACCC GGGGAAGGACC GGGGAAGGACC GGGGAAGGACC GGGGACCC GGGAAGGACC GGGAAGGACC GGGAAGGACC GGGAAGGACC GGGAAGGACC GGGAAGGACC GGGAAGGACC GGGGAAGGACC GGGGAAGGACC GGGGAAGGACC GGGGAAGGACC GGGGAAGGACC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGACC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGACGAC GGGGAAGGACC GGGGAAGGACC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGACGAC GGGGAAGGAC GGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGAAGGAC GGGGAAGGAC GGGGAAGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGGAC GGGGAAGAC GGGGAAGAC GGGAAGC GGGAAGC GGGAAGCC GGGAACGAC GGGAC GGGAAGC GGGAAGC GGGAACC GGGAC GGGAC GGGAC GGGAC GGGAC GGGAC GGG | 60<br>120<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>660<br>720<br>840<br>900  |
| 50<br>55<br>60<br>65<br>70       | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  I I ATGCCACCTC CCCATCACAG GCGGTGCCAC CAGATGAGA GTCCTGCCGCGCGC CAGATGAGA GTCCTGCCTC CCCGCGCGCA CAGATGAGA GTCCTGCCTC CATCACTTG CATGCTAAAT ATCACCTCA ATGAGAGAAGA CGCAGTATC ACGCTCACTTG CAGGTTCCGGC CTGCAGTATC ACGCTCACTTA ACGCCTCA ACGCTCACTTA ACGCCTCA ACGCTCACTTA ACGCCCCACTATC ACGCTCCACTTTA ACGCCCCCACTATC ACGCTCCACTTTA ACGCCCCCCC CTGCGACCTTTA | IRKEEGSFQS  165 DNA sec dd Accession  11   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  AATGTCTCGG GCACCTCTG GGACAACATG GGGCACCTT TGACATCACC GGGCACCTT TGACATCACC GGCTCTTCAGC GCAGAGGGC CATGTTCAG GCAGAGGGC CATGTTCAGC CATGTTCAGC CATGTTCAGC GGGGCCGAC GGGGCCCAA GGCCCAC GGGGCCCAC GGGGCCCAC GGGGCCCAC GGGGCCCAC GGCCCCAC GGGGCCCAC GGCTCTTCAGC  | IMMVTLNCPE  J1  GCGCAAGGTG  GH predicted  H predicted  TTCTTCTCT TTCCTGT TTCCTGT TTCCCGGGCAGAGA  AGATTACATCA AGGCATGTAC AGCCGGCT AAATGTCTC AAAATGTCTC AAAATGTCTC ATCATGAAC TTCATTACATC ATCATGAAC ATCATTACATC ATCATTACATC ATCATTACATC ATCATTACATC ACCTTCACCA AGGGTCTA AGGGATGAAG AGGGATGAAG   | 41    GTGGTGTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCCTT TCCACATGA TCTTGGTATG GTCGCTGCT TTCAAATGA TCTTGGTATG TCACCTTGTATAT AACCCTTT TAAAACCTTG GTCGCTGCT TCAGATGATAT ACAGGGGCC CCCTTGATAT TCAGCTACAA ACGCACCAGCA ACGCAAGCA AGGCAAGCA AGGCAAGCA  | 51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGCTT GCGGGTCCT GCGGGCCTT GGGAGCCTA GCTAGGGACT GCTAGGAACT GCTAGGAACT GCTCTCCG GGATGGCGG GCAGGAACG GCAGGAACG GCAGGAACG GCAGGAACG GCAGGAACG GCAGGAACG GCAGGAACG GCACGGAACG CCAGGAACG CCACGCACACACC CCACGACACAC CCACGCACACAC CCACGACACAC CCACCACACAC CCACCACAC CCACCACAC CCACCA  | 60<br>120<br>120<br>120<br>1300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>960<br>960   |
| 50<br>55<br>60<br>65<br>70       | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  I I ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGCGCGCA GTCCCATCACAG GCTGTCCACTC CATCACAG GCCTGCCATCACAG GCCTGCCATCACAG GCCTGCCATCACAG GCCTGCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCAGCATATC CATGCTAAAT ATCAGCCTCA CAAGAGAAGA AGCACAGATATCC CGGCCGGCACAC TCGACTTTA AGAGGATATCC                         | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec dd Accession lence: 11c   TGCCATCCAG ACCGCTGCT CCCTTCTCT ACTAGGTTCT ACTAGGTTCT TGTTGGTTCT CCCCCAAGGA TCAGCAAGGA TCAGCAAGGA TGAGCAGTACT TGACCCTGGA TGACCCTGGA TGACCTGGA TGAGCACA ACGCCTGTGA TGAGCACA ACGCCTGTGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCGAAGG  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACATCCTG CTTACATCACC GGACAACATG GGTGACCTT TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCAAGTGG GCCAAGTGG CCATGTCACC CATGTCACC CATGTCACC CATGTGCAC AGACACTTC  | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted  H predicted  GH predicted  GH predicted  GH predicted  GH predicted  GGGCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCCGC GGCATGTACC CACCATGTAC CACCATGTAC CACCATGTAC CATTACATCA TATGGCTTC AAGCGGTCT AAATGTGTCT AAATGTTGACG ACCTGGCTTA ACGGATGAAG ACGGATGAAG ATGTTTGAGG   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCGTT TCCACATGG TCCCCTCCT TTCCAAATGA TCTTGGTATG AACCCTTTT TCAGCAGCCCCCTCT ACCAGAGCGC CCCTTGATAT TCAGCTACAA TGAGGGCTCT ACCGCTGCT ACCAGAGCACA ATGAAACGA ATGAAACGA ATGAAACGA   | 51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG C3GAGTGCTG C3GAGGTTCC C3GCAGCTT GATGGGACTT GATGGGACTT GATGGGACTT GATAGGACTT GATAGCAT GACACTGC GTTTAGGGAT CAGCAACTGC GTTGTCCGG GCAGGACTGC GCAGGAACGG GCAGGAACGG GGGGAAGAC ACTGTCAGA   | 60<br>120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020  |
| 50<br>55<br>60<br>65<br>70<br>75 | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  I I ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCT CCCCGCGCGCA GTCCCATCACAG GCTGTCCACTC CATCACAG GCCTGCCATCACAG GCCTGCCATCACAG GCCTGCCATCACAG GCCTGCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCATCACAG GCCAGCATATC CATGCTAAAT ATCAGCCTCA CAAGAGAAGA AGCACAGATATCC CGGCCGGCACAC TCGACTTTA AGAGGATATCC                         | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGT COCCTGAGGG GAGAACGGGC  166 DNA sec dd Accession lence: 11c   TGCCATCCAG ACCGCTGCT CCCTTCTCT ACTAGGTTCT ACTAGGTTCT TGTTGGTTCT CCCCCAAGGA TCAGCAAGGA TCAGCAAGGA TGAGCAGTACT TGACCCTGGA TGACCCTGGA TGACCTGGA TGAGCACA ACGCCTGTGA TGAGCACA ACGCCTGTGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCTGGA TGATGTGTT TGACCCGAAGG  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACATCCTG CTTACATCACC GGACAACATG GGTGACCTT TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCTTTC TGACCAAGTGG GCCAAGTGG CCATGTCACC CATGTCACC CATGTCACC CATGTGCAC AGACACTTC  | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted  H predicted  GH predicted  GH predicted  GH predicted  GH predicted  GGGCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCCGC GGCATGTACC CACCATGTAC CACCATGTAC CACCATGTAC CATTACATCA TATGGCTTC AAGCGGTCT AAATGTGTCT AAATGTTGACG ACCTGGCTTA ACGGATGAAG ACGGATGAAG ATGTTTGAGG   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCGTT TCCACATGG TCCCCTCCT TTCCAAATGA TCTTGGTATG AACCCTTTT TCAGCAGCCCCCTCT ACCAGAGCGC CCCTTGATAT TCAGCTACAA TGAGGGCTCT ACCGCTGCT ACCAGAGCACA ATGAAACGA ATGAAACGA ATGAAACGA   | 51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG C3GAGTGCTG C3GAGGTTCC C3GCAGCTT GATGGGACTT GATGGGACTT GATGGGACTT GATAGGACTT GATAGCAT GACACTGC GTTTAGGGAT CAGCAACTGC GTTGTCCGG GCAGGACTGC GCAGGAACGG GCAGGAACGG GGGGAAGAC ACTGTCAGA   | 60<br>120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020  |
| 50<br>55<br>60<br>65<br>70       | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequitable ATGCCACCTC CCCATCACAG GCGTGTCCA CTGAGGCTCT CCCCGCCGC CAAGATGAGA GTCCTGCCATCA GGGTTCTAAAT ATCAGCTTA ACTGCTAAAT ATCAGCTCA CAAGAGAAGA CGCCAGTATC CAAGAGAAGA CGCCAGTATC AGGTTCCGC CGGCGGCAC TTGGACTTTT GAGGTTATC GGGATTTCTTTT GAGGTTATCC GGGATTCTCTTT  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGCT CGCCTGAGCG GAGAACGGGC  166 DNA sec ld Accession  11   TGCCATCCAG ACCGCTGCT CCCTCTCTCT GCAGGAGCT TGTTGGTTCT TGTTGGTTCT TGACCAGAAGG ACATCCTGAA GGCGCATCTA TGACCTGAA GGCGCATCT TGACCTGAA TGACTGATTA GCTTGCACCA ACGCCTGGA TGAGTGATTA GCTTGCACCA ACGCCTGGA TGAGTGATTA GCTTGCACCA ACGCCTGGA TGAGTGATTA GCTTGCACCA ACGCCTGGA TGCGTCAGCA TTGATGTGCT GACCCGAAGC GGCATCT GACCCGAAGC GGCATCAGCA GGCCGAAGC GGCCGAAGC GGCATCT GGCTGAT GGCTGAAGC GGCATCT GGCTGAT GGCTGAAGC GGCATCT GGCTGAT GGCTGAAGC GGCATCT GGCTGAT GGCTGAAGC GGCATCT GGCTGAAGC GGCATCT GGCTGAAGC GGCATCT GGCTGAAGC GGCATCT GGCTGAAGC GGCTGAAGC GGCATCT GGCTGAAC GCCTGAAC GGCTGAAC G | CSFCKPKKFT  Dience    #: CAT cl    TGSCCATGGC TGGACCGAAC TCTGGCTCAA    #: FGENES   AATGTCTCGG GCACCTCTG CTTCCTGCTC TACATCACC GGGCAACATG GGTGCACCT TGACAAGTGG GCACTACATG GCTTCTCAG TACTCTCCC TACATCACC CAGTCTTCAG TATCTCCGCT TATCTCCGCT CAATTCAGCC CATGGTGCAC CATGGTGCAC CATGGTGCAC CAGGGGCCGAG GCTCCTGGCC AGACACCTT CAATTTGGCA CATGTTGCC CATTTTGCCAC CAGGACACCTC CAATTTTGCCA  | TMMVTLNCPE  J1  GGGCCTCCT GGGCTGGGG GGCATGTGC GGGCTGGGT TCCTGT TGCCGCCGGC GGCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC CACCATGTAC TATGGCTCC AAGATCTCA TCAGGGGTC TAAATGTGTC AAATGTGTC AATTATGAAC TTCATTACT CACTTCACCA AGGGATGAAG ATGTTTTACT AGGGATGAAG ATGTTTTACT AGGGATGAAG ATGTTTTACGA AGGATGAAG ATGTTTTACGA AGGATGAAG ATGTTTTACGA AGGATGAAG ATGTTTTACGA AGGATGAAG ATGTTTTACGA AAGTATACCGA   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGGCTTT TCCGCCTGCT TCTCGAATGA AACCCTTT TAAAACCTTG GTCGCTGCT ACCGAGAGGC CCCTTGATTA TCAGCTACAA TCAGCTACAA ACGGCTCCGC CTGAAGTCAT ACGCCTAGGA   | TRVKQCRCIS  51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CCCCAGCCT GCGAGCCTCA GCTAGGGATC GCTAGGGAT GACACCCGC TGACATTATG GTTTGAGCAT CAGCAACTGC GCTAGGAACTGC GCAGGAACTGC GCAGGAACTGC GCAGGAACTGC ACTGTCAGA ACACCCAGC ACTGTCAGAC AACATCCAGT AGAATCCCAGT AGAATCCCAGT AGAATCCCAGT GAAATCCCAGT GAAATCCCCAGT GAAATCCCCAGT GAAATCCCCAGT GAAATCCCCAGT GAAATCCCAGT GAAATCCCCAGT GAAATCCCAGT GAAATCCAGT GAAATCAGT GAAATCCAGT GAAATCCAGT GAAATCCAGT GAAATCAGT GAAATCCAGT GAAATCAGT GAAATCCAGT GAAATCCAGT GAAATCCAGT GAAATCCAGT GAAATCCAGT GAAATCAGT GAAATCCAGT GAAATCCAGT GAAATCAGT GAAATCCAGT GAAATCCAGT GAAATCAGT GAAATCCAGT GAAATCCAGT GAAATCCAGT GAAATCCAGT GAAATCCAGT GAAAT | 60<br>120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140                                      |
| 50<br>55<br>60<br>65<br>70<br>75 | Seq ID NO: Nucleic Ac:  GAATTGCATC GGTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence I I I ATGCCACCTC CCCATCACAG CTGAGGCTCT CCCCGCGCGCA CAGATGAGA GTCCTGCCGCGCGCACACAGATGAGA ATCACCTTTG CATGCTACTTG CAGGATCTCCGGC CGGGGGCAC CTGGACTTTTA GAGGATTTCTT GAAGGATTTCTT GAAGGATTTCTT GAAGAGATTC   | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGC GGACAGAGGC GAGAACGGGC  166 DNA sec dd Accession ience: 11c  TGCCATCCAG ACCGCCTGCT ACAGGAGGCT ACAGGAGGCT AGAAGGTACT TCTTGGTTCT CCCCCAAGGA TCAGCAGAGG ACACCCTGGA GGCGCATCT AGACCCTGAA GGCGCATCT AGACCCTGAA TGACTCTGAA TGACTCTGAC TGACCCTGAA TGACTCTGCA TGACCCTGAA TGACTCTGCA TGACCCTGAA TGACTCTGCA TGACCCTGAA TGACTCTGCA TGACCCTGAA TGACTCTGCA TGACCCTGAA TGACTCTCT AGGAAGTCAT AGGAAGTCAT   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGGCCAAGC TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  AATGTCTCGG CATCCTGC CTTCATCACC GGGCCACCTT TGACAATCACC TGACAATCACC GGGCCACTT TGACAATCACC GGCTCTTCAG GCAGAAGGC CATGTTCAG GCAGAAGGC CATGTTCAG GCAGAAGGC CATGTTCAG CATGTTCAC CATGTTCAC GGGGCCAAC GGGGCCAAC GGGGCCAAC GGGGCCAAC AGACACCTTC CAATTTTGGC AGACACCTTC CAATTTTGGC AGAAAGGCCG AGAAAGGCCG AGAAAGGCCG AGAAAGGCCGC AGAAAGGCCGC AGAAAGGCCGC AGAAAGGCCGC  | TMMVTLNCPE  J1   CGAGTTGCGC GCGCAAGGTG G  H predicted TTCTCCTCT GGGCTGGAGA TTCTTCCTGT TTCCCGCGGC GGCATGACA TATGGCTTCC AGCCGGCTCA AGAGTTTCACA TATGGCTTC AAAATGTTCA TCATGAC TTCATTACAT ATCATGAC TCATTTACT ATCATTGAC ACCTTGCTTA AGGGATGAAG ATGTTTGAGG AAGTATCCGAC GGGGTGGGGGGGGGG   | 41    GTGGTGACAGG AGACGCCTTT TCCGCCTGCT TCCTAATGA TCTTGGTATG GTCGCTTGTT TAAAACCTTG GTCGCTTGTT TAAACCTTG ACCAGTACAA ACCAGTACAA AGACGCCTACAA AGACGCCTACAA AGACGCCAACAA AGACCACAACAA AGACCAGACAA AATACCAGGA  | 51   CACTAACACT CGGAGCTCAT  51   CAGGATGCTG CGCGCTT GCGGGTTC CCCCCAGCCT GGAGGCTCAT GCTAGGGACCT GCTAGGGACCT GCTAGGGACT GACACTGC GCAGAACGG GGAGACGG GAACGCCGA ACATCCAGT GAAATGCCGA GGACGACTCT GGACTCTCAGAC AACATCCAGT GAAATGCCGA GGACGACTCTG GGACGACTCTG GGACGACTCTG GGACGACTCTG GGACGACTCTG GAATGCCGA ACATCCAGT GAACTCCAGT GGACGACTCTG GCACTCTCTC GCACTCTCTC GCACTCTC GCACTCTC GCACTCTC GCACTCT GCACTC GCACT GCACTC GCACT GCACTC GCACT GCACTC GCACT GCACTC GCACTC GCACTC GCACTC GCACTC GCACTC GCACTC GC | 60<br>120<br>60<br>120<br>180<br>240<br>300<br>480<br>540<br>660<br>720<br>840<br>900<br>1020<br>1080<br>1140<br>1200                               |
| 50<br>55<br>60<br>65<br>70<br>75 | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  I  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGACTCT CCCCGCGCAC GCTGCCATC GGGTGCTGC CATCACAG GTCCTCCCCCCCCCC  | IRKEEGSFQS  165 DNA sec dd Accession  11   GGACAGAGGC GAGAACGGGC  166 DNA sec dd Accession ience: 11c  TGCCATCCAG ACCGCTGCT CCCTTCTCCT GCAGGAGCTT ACTGGCTGCT ACTAGCAAAGG ACATCCTGA ACACCTGCT TGTTGGTTCT CCCCAAGGA TCAGCAAAGG ACATCCTGA ACACCTGGA TGAGTACTT TGACCATGA TGAGTACTGA TGAGTGATT TGACCCTGGA TGAGTGATT TGACCCTGGA TGAGTGATT TGACCCTGGA TGAGTGATT TGACCCTGGA TGAGTGATGAT TGATGTGCT GAGCCGAAGC GGATGCTTT AGGAAGTCTT AGGAAGTCTT AGGAAGTCTT AGGAAGTCTT CCTTTACAAC  | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TCGCCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGGCTCAA  TCTGCTCTCTGCTC TCTACTCTGCTC TCTACTCTGCTC TCTACATCACC GGCCACCTG GGCCACCTG GGCTCTTCCTGCTC TCACCTCTTC TCACCTCTTC TCACCTCTTC TCACCTCTCC TCACCTCTCC TCACCTCTCC TCACCTCTC TCACCTCTCC CAGTCTTCAG CATGTTGCAC CATGGTGCAC CATGGTGCAC CATGGTGCAC CATGGTGCAC CATGGTCAC TCACCTTC CAATTTGCAC GAAAGGCCGG TATGTGCATT   | TMMVTLNCPE  J1  CGAGTTGCGC GCGCAAGGTG G  H predicted  H predicted  TCATCTCTCT GGGCTGGAGA TTCTTCCTCGT TGCCGCCGGC GGCATGTACC CACCATGTAC CACCATGTAC TATGGCTTCC AAGATCTTCA TATGGCTTC AATGTGTCT AAGGGATGAGA AGGATGAGG AAGGTGAGG AAGGTGAGG AAGGTGAGG AAGGTGAGG AAGGTGAGG   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGCGTT TCCGACTGCT TTCCAAATGA TCTTGGTATG AACCCTTTT TAAAACCTTG GTCGCTGCT ACCAGAGGGC CCCTTGATAT TCAGCTACAA TGAGGCCTCCT CTGAAGTCAC AGGCCAGGA AGCCAGGAAGGA GTCACGACAC AATACCAGGA ATCCAGGACAC AATACCAGGA TGGGCCAGTA TGGCCCAGTA TGGCCCAGTA TGGCCCAGTA TGGCCCAGTA TGCGCCAGTA TGCGCCAGTA  | 51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG C3GAGGTCAT  51   CAGGATGCTG C3GAGGATGCTG C3GAGGATGCTG G3GAGGCTCA G3GAGGCTCA G3GAGGCTCA G3GAGACTGC G3GAGGACTG G3GAGACTGC G3GAGACTGC G3GAGACTGC G3GAGACGG G3GAAGACC ACTGTCAGGA AACATCCAGT GAAATGCCGA G3ACGATCTG C3AACTCCAGT GAAATGCCGA C3AACTCCAC CCCACCTGTC   | 60<br>120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>960<br>1020<br>1080<br>1140<br>1260  |
| 50<br>55<br>60<br>65<br>70<br>75 | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCC CCAGCACG GCTGCCATCG GGCTGCCATCG GCTGCCATCG GGCTGCCATCG GGCTGCTCC CAAGAGAGAGA ATCAGCTCA CAAGAGAGAAGA CGCAGTATC CAGGTTCCGGC CGGCGGCAC TTGGACTTTG CAGGTTCCTTT GAAGAGATTC CACTCAGCTGC ACTCTAGCTGC ACTCTAGCTGC ACTCTTGTCT  | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT CGCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 11c  17   TGCCATCCAG ACCGCTGCT CCCTTCCTT TGTTGGTTCT TGTTGGTTCT TGCACCAAGGA TCAGCAAAGG ACATCCTGAA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCAAGCA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGCGTCAGCA TGACCCAAGCA TCAGCAAGC GGATGCTTT AGGAGGAGTCAT CCTTTACAAC CCTCGCCAATG   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCTG CTTCCTGCTC CTACATCACC GGACAACATG GGTGCACCCT TGACCAGATGG CCTTACATG GCCTACATG GCCTACATG GCCTACATG CGCAGAGGGC CAGTCTTCAG TATCTCCGT CTACCTCGAC CATGTGCAC GGGGGCCGAG GCTCCTGCAC GGAGAGGCC CATGTGCAC GGAGAGGCC CATGTGCAC CAATTTGGCA GAAAGGCCGG TATGTGCATT CACGGAGGAC  | IMMVTLNCPE  J1   CGAGTTGCGC GCCGAAGGTG G  H predicted  H predicted  GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCGCGCGCAC GAGTTACATC ACCATGTAC ACCATGAC ACCATGAAG AAGTATCCGG AAGTATCCGG AAGTATCCGG AAGTATCCGG AAGTATCCGG AAGTAGAGCC ATCAAGCTCC   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGGGTT TCCGCTGCTT TCCGAATGA TCTTGGTATG AACCCTTTT TAAAACCTTG GTCGCTGCT ACCAGAGGGC CCCTTGATAT ACCGTGAATGA TGAGGGCTC ACCAGAGGGC ATGAAGGA ATGACAGA ATGCAGACAC ATGCAGACAC ATGGAAGGA TGCCCAGTA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA CAGATGGCCAGTA AGCTGGAATGA CAGATGGCCAGTA AGCTGGAATGGCCAGTA AGCTGGAATGGCCAGTA AGCTGGAATGGCCAGTA AGCTGGAATGGCCAGTA | 51   CACTAACACT C3GAGCTCAT  51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GATGGGACCT GATGGGACCT GATGGGACTTATG GCTAGGGATTATG GCTAGGGACT GACACTGC GTATGAGCAT CAGCAACTGC GGGAAGACTGC GGGGAAGACTGC GGGGAAGACTGC GCAGGAAGACTGC AACATCCAGT GAAATCCCGA GGACGATCTG CCACCTGTT CAACACTCTC CCACCTGTTC CATCATCCCC CATCATCCCCC CATCATCCCCC   | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>660<br>6720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1210<br>1200<br>1320      |
| 50<br>55<br>60<br>65<br>70<br>75 | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac:  GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence  ATGCCACCTC CCCATCACAG GCGGTGTCCA CTGAGGCTCC CCAGCACG GCTGCCATCG GGCTGCCATCG GCTGCCATCG GGCTGCCATCG GGCTGCTCC CAAGAGAGAGA ATCAGCTCA CAAGAGAGAAGA CGCAGTATC CAGGTTCCGGC CGGCGGCAC TTGGACTTTG CAGGTTCCTTT GAAGAGATTC CACTCAGCTGC ACTCTAGCTGC ACTCTAGCTGC ACTCTTGTCT  | IRKEEGSFQS  165 DNA sec id Accession  11   GGACAGAGGT CGCTGAGGG GAGAACGGGC  166 DNA sec id Accession ience: 11c  17   TGCCATCCAG ACCGCTGCT CCCTTCCTT TGTTGGTTCT TGTTGGTTCT TGCACCAAGGA TCAGCAAAGG ACATCCTGAA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCAAGCA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGACCCTGGA TGCGTCAGCA TGACCCAAGCA TCAGCAAGC GGATGCTTT AGGAGGAGTCAT CCTTTACAAC CCTCGCCAATG   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCTG CTTCCTGCTC CTACATCACC GGACAACATG GGTGCACCCT TGACCAGATGG CCTTACATG GCCTACATG GCCTACATG GCCTACATG CGCAGAGGGC CAGTCTTCAG TATCTCCGT CTACCTCGAC CATGTGCAC GGGGGCCGAG GCTCCTGCAC GGAGAGGCC CATGTGCAC GGAGAGGCC CATGTGCAC CAATTTGGCA GAAAGGCCGG TATGTGCATT CACGGAGGAC  | IMMVTLNCPE  J1   CGAGTTGCGC GCCGAAGGTG G  H predicted  H predicted  GGGCCCTCCT GGGCTGGAGA TTCTTCCTGT TGCCGCGCGCGCAC GAGTTACATC ACCATGTAC ACCATGAC ACCATGAAG AAGTATCCGG AAGTATCCGG AAGTATCCGG AAGTATCCGG AAGTATCCGG AAGTAGAGCC ATCAAGCTCC   | 41    GTGGTTGTGG CGGCGGAAGC  41    TGGTGACAGG AGACGGGTT TCCGCTGCTT TCCGAATGA TCTTGGTATG AACCCTTTT TAAAACCTTG GTCGCTGCT ACCAGAGGGC CCCTTGATAT ACCGTGAATGA TGAGGGCTC ACCAGAGGGC ATGAAGGA ATGACAGA ATGCAGACAC ATGCAGACAC ATGGAAGGA TGCCCAGTA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA AGCTGGAATGA CAGATGGCCAGTA AGCTGGAATGA CAGATGGCCAGTA AGCTGGAATGGCCAGTA AGCTGGAATGGCCAGTA AGCTGGAATGGCCAGTA AGCTGGAATGGCCAGTA | 51   CACTAACACT C3GAGCTCAT  51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG CCGCATATAC GCTGCGGTTC CCCCCAGCCT GATGGGACCT GATGGGACCT GATGGGACTTATG GCTAGGGATTATG GCTAGGGACT GACACTGC GTATGAGCAT CAGCAACTGC GGGAAGACTGC GGGGAAGACTGC GGGGAAGACTGC GCAGGAAGACTGC AACATCCAGT GAAATCCCGA GGACGATCTG CCACCTGTT CAACACTCTC CCACCTGTTC CATCATCCCC CATCATCCCCC CATCATCCCCC   | 60<br>120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320                                     |
| 50<br>55<br>60<br>65<br>70<br>75 | QCNSPYIPRH IDLD  Seq ID NO: Nucleic Ac: GAATTGCATC GCTACGTTTC ACTGCGCACG  Seq ID NO: Nucleic Ac: Coding sequence ATGCCACCTC CCCATCACAG GCGTACTCC CCCATCACAG CTGACGCTCT CCCCGCCCAC CAAGARAGAG GTCCTGCCGC GGGTGCCTTC CAAGAGAAGA CGCAGTATC AGGTTCCGGC CGGCGGCAC TTGGACTTTT GAAGGATATCC GGGATCTCTT CATCACTTGC ACTCTACTGC ACTCTACTCACTTC ACTCACTTCT AAAGGAATCA  | IRKEEGSFQS  165 DNA sec dd Accession  11   | CSFCKPKKFT  TUENCE  1 #: CAT cl  21    TCGCCATGGC TGGACCGAAC TCTGGCTCAA  TUENCE 1 #: FGENES 550  21    AATGTCTCGG GCACCTCCTG CTACATCACC GGGCCACCTG GGACACACTG TGACCTCTTC TGACATCACC TGACATCTCC TGACATCTCC TGACATCTCC TGACATCTCC TGACATCTCC TGACATCTCC CATGTTCCAC GCGCGCCCAG GCTCTTCACAT GCGAGACGCC CATGTTCCAC CATGTTCCAC CATGTTCAC GGGGGCCAC GCTCCTGCC AGACACCTTC CACTGCC AGAAGGCCG TATTTGGCA TATTTGCAT TCACGGAGGAC CAGCATCTAT CACGGAGGAC CAGCATCTAT  | TMMVTLNCPE  J1  GCGAGTTGCGC GCGCAAGGTG G  H predicted  TCCTCCT GGGCCCTCCT GGGCTGGAGA TTCTCCTGT TCCCCCGGC CACCATGTAC CACCATGTAC TATCGTTCA TATCGTTCA TATCATTCA TATCATTCA TATCATTGAAC TTCATTTACT ACGAGTAGA ACGTTTAAGAC ATGTTTTAGAG AGGAGAGAGC ATCAAGCTCC AGGAACCCACC  | 41    GTGGTTGTGG CGGCSGAAGC  41    TGGTGACAGG AGACSGCTTT TCCACCTGCT TCCTAATGA TCTTGGTATG ACCCCTTT TAAAACCTTG GTCGCCTGCT ACCGCTGATAT ACCGCTACAA ACCACAAGAAGCA ATGAAGCAC ATGGAAGCA ATGGAAGCA ATGGAAGCA ATGGAAGCA ATGGAAGCA AGCAGAAGCA AGCAGAAGCA AGCAGAAGCA ATGGAAGCA ATGGAAGCA AGCAGAACA AATACCAGGA AGCTGGAGTG TGCCCAGTA ACAACCCAC ACAACACCAACA AACAACCCCAC ACAACCCCAC ACCACC  | 51   CACTAACACT C3GAGCTCAT  51   CAGGATGCTG C3GAGGTCAT  51   CAGGATGCTG C3GAGGATGCTG C3GAGGATGCTG G3GAGGCTCA G3GAGGCTCA G3GAGGCTCA G3GAGACTGC G3GAGGACTG G3GAGACTGC G3GAGACTGC G3GAGACTGC G3GAGACGG G3GAAGACC ACTGTCAGGA AACATCCAGT GAAATGCCGA G3ACGATCTG C3AACTCCAGT GAAATGCCGA C3AACTCCAC CCCACCTGTC   | 60<br>120<br>120<br>120<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>900<br>900<br>900<br>1020<br>1080<br>1120<br>1260<br>1380 |

| 5           | ACGCGCAAGG                             | GCGTGGTTGT  | TGCAGGACCC<br>GGCACTAACA<br>GCCGGAGCTC<br>GCGGGCCTGA               | CTGCTACGTT                             | TCCGCCTGAG                             | CGTGGACCGA                             | 1500<br>1560<br>1620            |
|-------------|--|---|--|--|--|--|---------------------------------|
| _           | Seq ID NO:<br>Protein Acc              | 167 Protein<br>cession #:                         |  | predicted                              |  |  |                                 |
| 10          | 1                                      | 11  | 21   | 31                                     | 41                                     | 51                                     |                                 |
| 10          | LRLCRSFYIT<br>VLPLLVLVHP               | CRRLRCFPQP<br>DYIKPLLGAS                          | PITDRLLHLL<br>PRRNWLLGHL<br>AAIAPKDDLF                             | GMYLPNEAGL<br>YGFLKPWLGD               | QDEKKVLDNM<br>GLLLSKGDKW               | HHVLLVWMGP<br>SRHRRLLTPA               | 60<br>120<br>180                |
| 15          | QEKMSDYISA<br>RRALRQQGAE<br>GISWMLFNLA | IIELSALSVR<br>AWLKAKQGKT<br>KYPBYQEKCR            | HAKWRHLAEG<br>RQYRLHHYLD<br>LDFIDVLLLA<br>EEIQEVMKGR<br>KGIICLVSIY | FIYYRSADGR<br>RDEDGKELSD<br>ELEELEWDDL | RFRQACDMVH<br>EDIRAEADTF<br>TQLPFTTMCI | HFTTEVIQER<br>MFEGHDTTSS<br>KESLROYPPV | 240<br>300<br>360<br>420<br>480 |
| 20          | Layvpfsagp<br>Kveplppra                | RNCIGQSFAM  | AELRVVVALT   | LLRFRLSVDR                             | TRKVRRKPEL                             | ILRTENGLWL                             | 540                             |
| 25          | Nucleic Act                            | 168 <u>DNA sec</u><br>id Accession<br>Lence: 252. | #: AK05808   | 8.1                                    |  |  |                                 |
|             | 1                                      | 11  | 21   | 31                                     | 41                                     | 51                                     |                                 |
|             | ]                                      | 1   |  | 1                                      | 1                                      | 1                                      |                                 |
|             | GCCCCAGATG                             | TGATGAGCTCC                                       | CCCTGTCAAA<br>TTCCAGGCTT   | GCACCTTGGC                             | CCATAAGAAG                             | AAAAGGGGGA                             | 60                              |
| 30          | TAACTCAGAG                             | GCCAGTGTGA  | TGGGAGTTCC   | TCCACTCAGC                             | ACACTTCCCC                             | TGTAAACACG                             | 120<br>180                      |
|             | CCTGTGGTGG                             | GCAAAAGGGC  | TTTGGAACGG   | TTGCTTGTCT                             | TTTCTCTCCT                             | GCGTAATTTC                             | 240                             |
|             | CACTTTCATT                             | CATGATAATG  | TOGAACACGC   | ACAAAGCTCG                             | GCTGGAACGC                             | CGGGTCACTG                             | 300                             |
|             | CCCAGATGTG                             | CAAGGCTCTG  | TTGCCCAAAC<br>AGCATAGACT   | TTCACCAACC                             | TEGGGACCTG                             | CCCCACTCT                              | 360                             |
| 35          | TATGCATTTC                             | ACAAATCCAG  | AAGTTTTTCT   | TTGAGAATTT                             | CAAGAACAAG                             | GACATCCAAA                             | 420<br>480                      |
|             | GTGGGGAAGC                             | AGATGTGATT  | CTCGAGTGCC   | TGGGCTTCAA                             | ATGGGAGCTC                             | CATCAGCCCC                             | 540                             |
|             | CACACCCCCT                             | GAGGGAGCTG  | TTGGCCAAGC<br>GAGGAGCTTC   | TCTACCTGAA                             | AGCCCTGGCG                             | CAGGGCACCA                             | 600                             |
| 40          | AAAAATCCCC                             | TGCAAAGAGG  | ATCATCATTT   | CCTTGAAGAT                             | CAATGACCCA                             | CTGGTCACTA                             | 660<br>720                      |
| 40          | AAGTCGCCTT                             | CGCCACGGCC  | CTGAAGAACC   | TCTACATGAG                             | TGAGGTGGAG                             | ATTAACTTCC                             | 780                             |
|             | AAGACCTACT                             | GGGAGTGCTG  | GCTTCCGCCC   | ACATCCTCCA                             | GTTCAGTGGC                             | CTGTTTCAAA                             | 840                             |
|             | CCGGCTGCAA                             | GTACAAGGAA  | GCCAGACTCA<br>GAGCAGCTCA   | AGCCAAGCAC                             | CATCAAGAAA                             | TTCTACGAGG                             | 900                             |
| 4.5         | ACTTGGTTCC                             | TCTAGGGGGG  | ACGCAGATCC   | ACCTCCACAA                             | AATCCCACAG                             | GACCTGCTCC                             | 960<br>1020                     |
| 45          | ACAAAGTGCT                             | GAAGTCCCCC  | AGGITATITA   | CCTTTAGTGA                             | ATTCCATCTT                             | CTGAAAACAA                             | 1080                            |
|             | TGCTTTTGTG                             | GGTCTTCTTG  | CAACTGAACT   | ACAAGATTCA                             | GGCAATTCCG                             | ACTTATGAAA                             | 1140                            |
|             | GACGGAGCTT                             | GAGGCCGCTC  | AGCTTTCCTG<br>TTCCTCTGCT   | TGCGTCTGCA                             | CTTTCTGGAC                             | CGGGACATAG                             | 1200<br>1260                    |
| 50          | ATCTGGAGGT                             | GCTGCGGCAC  | CTTAACTTCT   | TCCCAGAGTC                             | ATGGCTCGAC                             | CAGGTTACAG                             | 1320                            |
| 50          | TCAACCATTA                             | CCACGCACTG  | GAGAATGGGG   | GCGACATGGT                             | CCACCTGAAA                             | GATCTTAACA                             | 1380                            |
|             | TTGCTCTATA                             | TEGATTTEGG  | CTGCTCTTTA<br>TTTAAGATAA   | ACCAGGAGAA                             | TACAACTTAT                             | TCGAAAACGA                             | 1440                            |
|             | GTTTTTACAT                             | GCAGAGAATA  | AAGCACACAG   | ACCTGGAATC                             | TCCCTCTGCG                             | GTCTACGAGC                             | 1500<br>1560                    |
| 55          | ACAACCACGT                             | CAGCCTGCGA  | GCGGCACGCC   | TGGTGAAGTA                             | TGAGATCAGA                             | GCAGAGGCCC                             | 1620                            |
| <i>JJ</i> . | TGGTTGACGG                             | CAAGTGGCAG  | GAGTTCAGGA<br>CATACCTTGA   | CAAACCAGAT                             | CAAGCAGAAG                             | TTTGGGTTGA                             | 1680                            |
|             | TAAGTTTTGC                             | ATTCATCTTC  | CCAGCATCTT   | GACAGTTTCC                             | AGAAGAATCT                             | ATCCCATTTT                             | 1740<br>1800                    |
|             | CCCCCCACTG                             | GTCTGCATAA  | AAGAAAATAA   | AATGACATAA                             | AAGGGAGC                               |  | 2000                            |
| 60          |  | 169 Protein                                       |  |  |  |  |                                 |
|             | 1                                      | 11  | 21   | 31                                     | 41                                     | 51                                     |                                 |
| 65          |  |   |  | <u></u>                                | 1                                      | 1                                      |                                 |
| 05          | OIOKFFFENF                             | KNKDIOSGEA  | RWRLPKOPFS<br>DVILECLGFK   | GDLLSLSQMC                             | KALSIDPERA                             | LRNPDRLCIS                             | 60<br>120                       |
|             | RELECTIVAC                             | SPKKTKEKSP  | AKRIIISLKI   | NDPLVTKVAF                             | ATALKNLYMS                             | EVEINLEDLL                             | 180                             |
|             | GVLASAHILQ                             | FSGLFQRCVD  | VMIARLKPST   | IKKFYRAGCK                             | YKEEOLTTGC                             | EKWLEMNIJVP                            | 240                             |
| 70          | LGGTQ1HLHK                             | IPODLLHKVL  | KSPRLFTFSE   | FHLLKTMLLW                             | VFLQLNYKIQ                             | AIPTYETVMT                             | 300                             |
|             | HALENGGDMV                             | HLKDLNTOAV  | RPLFLCLRLH<br>RFGLLFNOEN   | TTYSKTIALY                             | CPPPKIKCLK                             | HDTTSYSFYM                             | 360<br>420                      |
|             | QRIKHTDLES                             | PSAVYEHNHV  | SLRAARLVKY   | EIRAEALVDG                             | KWQEFRTNQI                             | KOKFGLTTSS                             | 480                             |
|             | CKSHTLKIQT                             | VGIPIYVSFA  | FIFPAS   |  | -                                      |  |                                 |
| 75          | Seg ID NO:                             | 170 DNA sec                                       | TIETCO   |  |  |  |                                 |
| -           | Nucleic Aci                            | id Accession                                      | 1 #: NM 007  | 000.1                                  |  |  |                                 |
| 90          | 1                                      | 11  | 21   | 31                                     | 41                                     | 51                                     |                                 |
| 80          | \<br>\<br>\                            |   | 1  |  | 1                                      | 1                                      |                                 |
|             | GTTGTGGGGC                             | ATATCATTAT  | GGAGGCCGAG<br>TCTGCTGTCA   | AAGGGATCTC                             | CAGTTGTGGT                             | GGGCCTGCTA                             | 60                              |
|             | GTGACAGCCG                             | ACCAGTACCG  | TGTATACCCA   | CTGATGGGAG                             | TCTCAGGCAA                             | GGATGACGTC                             | 120<br>180                      |
|             | TTCGCTGGTG                             | CCTGGATTGC  | CATCTTCTGC   | GGCTTCTCCT                             | TCTTCATGGT                             | AGCCAGTTTT                             | 240                             |

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GGTGTGGGTG CCGCACTCTG CCGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG
                                                                                                300
         CTCATCGTCT ACATCTTCGA GTGCGCCTCC TGCATCACGT CCTACACCCA CCGTGACTAC
                                                                                                 360
         ATGGTGTCCA ACCCATCCCT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC
         GACCAGGGCC AGGAGCTGAC CCGCCTCTGG GACCGCGTCA TGATTGAGCA AGAATGCTGT
                                                                                                 480
         GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACGTCAG CCTTCCGGGC GGCCACTCCG
                                                                                                540
         GAGGTGGTGT TCCCCTGGCC CCCACTGTGC TGTCGCCGGA CGGGAAACTT CATCCCCCTC AACGAGGAGG GCTGCCGCCT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA
                                                                                                600
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|    |  | 2040         |
|----|--|--------------|
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|    | ATTACANANT CONTROLARC ACCACCTAGA TTCCTGGTTT CCAGGGTCTC CAGGAAGGGA  | 2160<br>2220 |
| -  |  | 2280         |
| 5  | CATCATACCA CAACTITUIG AATATAATAA AATCATIGAA TIGIAGAAT  | 2340         |
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| 10 | COMPANIED ANATOTARA TTACRARCT GCCATTTARA ATGGCCCGTC TGTTTCART  | 2580         |
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|    | AAACATACCT GAGACTGGCA AGAAAAAGAG GTTTAATTGG GCTTAGAGTT CCACGTGATT  | 2760         |
|    | GGGGAGGCCT CAGAATCACA GTAGGAGGCA AAAGTTATTC TTACATGGTG GCTGCAAGAG<br>AAGATGAGGA AGAAGCAAAA GAAGAAACCC CTGATAAACC CATCGGATCT CCTGAGGCTT   | 2820         |
| 15 | ATTAR OTRACE ATTENDED THE CACABGAAG ACCEGCCCC ATGATTCAAT TACCICTACC  | 2880         |
| 13 | TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TRANSPORT AGAIN TOTAL TO | 2940         |
|    | CCCARCACA CCARACCATA TCACTCAGCA AGGCAGATAA CTTTCTCACT GAGCCTATGC   | 3000         |
|    | ANDRONANC CATCTCCCAT CCTTCTAACG GGCACAGGAA GTGACTGGTA GGATCACTGC   | 3060<br>3120 |
| 20 | CAAAGCTGAG CACTCAGGAG AAGGCAATAG AATCCTATTC TCCATAGTAT GCTATAAGAT  | 3180         |
| 20 | ACTGARGTAC ACTTCTTCAC TATCTCTTTG GACTTAGAAT TAGGACTACA TTCCTTGTTA TACAGAAAAA TTACTAAGGA AATTCATAGG ATGACAAAAA CTTTCAGAAC TGAAAAACAG  | 3240         |
|    | CARACCTARC CTTTTAGTT CTTTGGTATT CGAAGTATGC CTAAAAGACA ATGCAAAATC   | 3300         |
|    | CARCARAGO AGGOTOGOCT TTTTGTTTGT TTGGTTTTGT TTTTGTTTTA CAGCIGGAGI   | 3360         |
|    | AGRAMACARA COCATOCACT TORRACORAT GAGAGGARAT TGGARTICIA ARCITATICI  | 3420         |
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| 50 | TATELLA CONTROL TATELLA CATCATE CATT CIGICIGATI ATAITITACI   | 3840         |
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|    | COMMANANT ANGAGARAR CTTTRANTCT CARACTCTCA CARCCCAGAT ATATCATIC   | 4260         |
| 40 | TOTAL AND THE TOTAL AND  | 4320<br>4380 |
| 40 | TGATGCTTTT CCAGGAGTTC CAGATCACAT CGAGTTCACC ATGAATTCAC TCAGTGAAGC  | 4440         |
|    | CACACCARG TICATETTCC ATCIGITCCA ACAGITCAGA AAATCAAAAG AGAACAACAT<br>CTICTATTCC CCTATCAGCA TCACATCAGC ATTAGGGATG GTCCTCTTAG GAGCCAAAGA  | 4500         |
|    | CARCACTOR CARCARATTA GUARGETAGO TATCAGCATO ATTACGITGI CUIGIIGOAG   | 4560         |
|    | THE PROPERTY OF THE CATCOLOGICAL CATCOLOGICAL TOTAL CONTROL OF THE CATCOLOGICAL CATCOLOGICA CATCOLOGICAL CATCOLOGICA CATCOLOGICA CATCOLOGICA CATCOLOGICA CATCOLOGICA CATCOLOGI | 4020         |
| 45 | ACCRUMENCE CONCRETE ANTICCONTA ACTOTGAGAC CACIGACTIA AACAGAICII  | 4000         |
|    | THE PROPERTY OF THE PROPERTY O | 4/40         |
|    | CACAGAGAAC ACCACAGAAA AAGCTGCAAC ATATCATGTG AGTCACAGAG CACTCTGATT  | 4860         |
|    | CAGCITTAGA TCCCTGAACA GGTCATAGTT TAAACCTGGA ACTTCACAAA AACTAAGAAA AGGCCAGTTT TAGGGAAAAT CTTGGACACA AAGATTGAGA CATACAGAGT GGGTTGGCAT  | 4920         |
| 50 | THE PROPERTY OF A PARTY OF A PROPERTY OF A CONTRACT CAGCACIGIA   | 4900         |
| 20 | CONCROR TRECTORIES TORGESTICS CTGGGTTCAG ACTCCAGCTT TGCTC11CAC   | . 5040       |
|    | ANAMONDON TANDROCKES ACACANCES TOGGAGTECE AGTGACCTEA TECCAGAMA   | 2700         |
|    |  | . 3100       |
|    | GCCTTGCCCA TAAAAGTCAT AATAAATGTT ATTATTATTA TAAAGTAGCT ATAATTATAA  | 5220<br>5280 |
| 55 | TARICATRAT ARTGTGARAR TRATTIRATI TICATTGAGT CATTRATGAG ATTCAGAGG/<br>ATRAGCACAR GTCCARGTRI ATTTTGGARA ATGATTGCTA TGGARTATAT TGGTTTAGAC   | 5340         |
|    | COMPANDATION CONNATION TECTIONAL GRACAGET CTAGATTAA ACAGGITAL  | 3 5400       |
|    | COMPANDE DECEMBER ANTERNATE TOTATABACA GGGTTTTTT CCCCATICA   | _ 3460       |
|    | MONGOTOR TOTATO TOTATO TARACTA GAGTTACCA TOTAGAGIC   | 3520         |
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|    | CCTGGCATAA TCTATTTAAA ATATCCAACC ITCAACATAC TCAACCTGGGA AGCTAAACC AGAAGTGAAA TATGGTCCTT GCCCATAAGG AGCTGAGAGT TTAACTGGGA AGCTAAACC   | r 5760       |
|    | ACCOMPANA ACCORCAGO ACABATCTA CTGGTAGACA GCGCTGCATC TITAGTTCA  | G 5820       |
| 65 | ANGENERAL REPORTS CONTROL OFFICE CONTROL CARACTATA   | A 5880       |
|    | CONCOMPTER CARCECTATE TEACETGAAA TACACCAATT ATCAGGGAAT AACATCAAA   | G 3340       |
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| 70 | AGGAAATGIT CATCACCAGT TICAAAAGCI ICIGACIGAA ACGTATCAAT TITTACAGG ATATGAGCTG AAGATCGCCA ACAAGCTCTT CGGAGAAAAG ACGTATCAAT TITTACAGG  | T 6180       |
| 70 | ADDRESS OF COOTROOCA CATTTOATT COATCOTGAT GTCTGTGTCT CIGAGIGGC   | C 6240       |
|    | PARTICIA DE PARCINACION CATGACOCTO GOOGACOCAG GTGGAGAGCA TITACTUAU   | A 6300       |
|    | OFFICE AND A STREET OF A ACTOTOCO CONTIGGRAT GICCOAGACE COACGRIA   | C 6360       |
|    | AMON CONTROL DETECTION OF COCKETANTET TETEGATARA GAGGAGUTTU TUTARIAGA  | 6 6440       |
| 75 | TGAGTAAGAG TAATAAGTAA TAAGATACCA TCGATAAACT GGCACTGACT CAGTCACAT<br>CGATACATCT TGGTGGGAAA TGTATGACTA ATGGGATATT ATTGGAATGG GCAGGCTTC   | A 6460       |
|    | COCACONACO CACAATACTT CACCAACTAC CAGGAAATAT TGAATGCACA GGATGAAAG   | A GOOD       |
|    | GREEN CARCACAAC ATCATCCTTA AAATTACTGG AGAGAAGTCT GAGAAGUA  | 77 G000      |
|    | CARROCCER CACCGAAGCC TGCTCTGCAG TTTGCAAACC ACAGCCTCTT CTGCTTCTC  | SC 6720      |
| 80 | COMMISSION AND PARTY ACCTORED ACCTOTTET TOTOCCAGE CACATION   | JC 6/60      |
|    | THE PROPERTY OF THE PROPERTY AND ANATATOCAT GGACAGGAGA TACTGCAT  | 7 6040       |
|    | ATTCAGGGTC TGGATTCAGC TTACTGTTGT TACAAATAAG TAAGTTTGGT AATATATAG<br>TACATAAATT ACTCCTAATT CCTACTTCTT CCTTCATATC TCAAAGGAAT ATTTAGAT  | 3C 6960      |
|    | TACATAAATT ACTCCTAATT CCTACTTCTT CCTTCATATC TCAAAGGAAT ATTTAGAACCCATCAAGAAA TTTTACCAGA CCAGTGTGGA ATCTACTGAT TTTGCAAATG CTCCAGAAC  | GA 7020      |
|    | CATCAMORAN IIIINCCAON CONSTOLOGO   |              |

|      | AAGTCGAAAG        | AAGATTAACT                   | CCTGGGTGGA                 | AAGTCAAACG  | AATGGTAGGA                   | GAGCCACCCA   | 7080         |
|------|-------------------|------------------------------|----------------------------|-------------|------------------------------|--------------|--------------|
|      | TTATAGAAAC        | ACCTTTGAGA                   | AACCTATGCC .               | AGTGAGCCTT  | GTGCTTGACA                   | CTGCATGGGG   | 7140<br>7200 |
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| 5    | GCCAATTAGA        | TGGAAACACA                   | TCTGGAGAAT                 | TATTTGCTTA  | TGGCCCTGCA                   | TGACAATAGC   | 7320         |
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|      | CTAAAATGCA        | ATCAGGGCCT                   | CCTTCCTCTG                 | AATGGGGACC  | CCGTAGTTAA                   | AAAAAAATAA   | 7800         |
| 15   | AAGTAGGAAG        | AGGAGGGAGG                   | GAGAAAGGAA                 | AGACACATGT  | TGGAAGAGTA                   | GACAAAATCA   | 7860<br>7920 |
| 15   | GTTTATCAGT        | ATTCCAAATC<br>CAAGAAGTGA     | AGATGATIGG                 | AGACATTCAT  | TTATACCACAC                  | GGAGCCTTGA   | 7980         |
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| 20   | GAAAAAATTA        | AAAACCTATT                   | TCCTGATGGG                 | ACTATTGGCA  | ATGATACGAC                   | ACTGGTTCTT   | 8220<br>8280 |
|      | GTGAACGCAA        | TCTATTTCAA<br>TTTGGCCAAA     | AGGGCAGTGG                 | TOTATATET   | DATATATT                     | TGTAATATGT   | 8340         |
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|      | AGTGATACA'        | r ACAGTTCATT                 | GTGTACAAAA                 | TAATGTAATC  | ATATTTTACA                   | TGTGTATCAT   | 9540         |
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| 50   | አጥር ተለል አስርም      | C CTACACAAGG                 | COTTTGTGG                  | GGTCACTGAG  | G GAGGGAGTGG                 | AAGCTGCAGC   | 10080        |
|      | TECCO             | ጥ ርጥኦርጥኦርጥኦር                 | TOTALTAR                   | ATCTCCTTC   | A ACTAATGAAG                 | AGTTCTGTTG   | 10140        |
|      | TAATCACCC         | T TTCCTATTCT                 | TCATAAGGC                  | AAATAAGAC   | C AACAGCATCO                 | : TCTTCTATGG | 10200        |
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|      |                   |                              |                            |             |                              |              |              |

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| 5   | GATGACATGC<br>GCTGAGGACA                             | ACAAGAACAA<br>CCAGCGGCTC<br>CAGTGTTGCG                             | GGGCTTCTTC<br>CTCCGCGCTG<br>GCAGGTACGC<br>AAATCCTGAG<br>GCTATTCGAA | GTGGATGAGT<br>AGCAGGAACG<br>CTGGACCCCT<br>GAGCTGCGGG<br>ATTATTGGAG | CGGAGCCCT<br>GTTCCTTTAT<br>GTGACTTGCA<br>TGATTGAAGA<br>TCAAGAGCCA | TCTCCGCTGT<br>TACCAAAGAA<br>GCCTATCTTT<br>GATTCCCCAG | 1620<br>1680<br>1740<br>1800<br>1860<br>1920 |
|-----|--|--|--|--|---|--|--|
| 10  |  | 191 <u>Protein</u><br>ession #: N                                  |  |  |   |  |  |
|     | 1  | 11   | 21   | 31   | 41  | 51   |  |
| 15  | TGQVLTCDKC<br>LPCAALTDRE<br>SSVMKCKAYT<br>VPSSTYVPKG | LASCSRIARR PAGTYVSEHC CTCPPGMFQS DCLSQNLVVI MNSTESNSSA             | TNTSLRVCSS<br>NATCAPHTVC<br>KPGTKETDNV<br>SVRPKVLSSI               | CPVGTFTRHE<br>PVGWGVRKKG<br>CGTLPSFSSS<br>QEGTVPDNTS               | NGIEKCHDCS<br>TETEDVRCKQ<br>TSPSPGTAIF<br>SARGKEDVNK              | QPCPWPMIEK<br>CARGTFSDVP<br>PRPEHMETHE<br>TLPNLQVVNH | 60<br>120<br>180<br>240<br>300               |
| 20  | VLVVIVVCSI<br>LVAAQVGSQW<br>ALRQHRRNDV<br>SPQDKNKGFF | KLLPSMEATG<br>RKSSRTLKKG<br>KDIYQFLCNA<br>VEKIRGLMED<br>VDESEPLLRC | PRODPSAIVE<br>SEREVAAFSN<br>TTOLETDKLA<br>DSTSSGSSAL               | KAGLKKSMTP<br>GYTADHERAY<br>LPMSPSPLSP<br>SRNGSPITKE               | TQNREKWIYY<br>AALQHWTIRG<br>SPIPSPNAKL<br>KKDTVLRQVR              | CNGHGIDILK<br>PEASLAQLIS<br>ENSALLTVEP<br>LDPCDLQPIF | 360<br>420<br>480<br>540<br>600              |
| 25  | DOMERATIONE  | ELRVIEBIPQ   | AEDKLDKLFS   | TIGANSONAS   | OTT TO SA 124   | DEDUB  |  |
| 20  | Nucleic Ac   | 192 <u>DNA sec</u><br>id Accession<br>uence: 238.                  | 1 #: XM_044  | 1533   |   |  |  |
| 30  | 1<br>i   | 11   | 21   | 31<br>1  | 41  | 51<br>   |  |
| 0.5 | AGGGGCTGAG<br>GGAGGCGGGG                             | AGCCGAGGCT<br>TTTGCCAGGG<br>GCCCCCGGGG                             | CCCACTTGAC<br>CGACTCGGGG   | CCTGTTTCCC<br>GCGGACCGCG   | ACCTCCCGCC<br>GGGCGGAGCT  | CCCCAGGTCC<br>GCCGCCCGTG                             | 60<br>120<br>180                             |
| 35  | CTGCGCACCG<br>CGGCCACCGC                             |  | GAGGAGCTGG<br>CCTGCTGCTG   | CTCGCCGCCC   | CATGGGGCGC<br>TGCAGCCGCC  | GCTGCCGACC<br>GCCTCCGACC<br>ATTCCTCAGA               | 240<br>300<br>360<br>420                     |
| 40  | TTCGAAGCTG<br>CTGTACGTGG<br>GGCGGGGAGT               | AACACATCTC<br>GTGCTCGAGA<br>ACCAGGAGCT                             | CAACTACACA<br>GGCCCTCTTT<br>GCTTTGGGGT                             | GCCCTTCTGC<br>GCACTCAGTA<br>GCAGACGCAG                             | TGAGCAGGGA<br>GCAACCTCAG<br>AGAAGAAACA                            | TGGCAGGACC CTTCCTGCCA GCAGTGCAGC CCTGCCGCTC          | 480<br>540<br>600<br>660                     |
|     | AGCGGCAGTC   | ACCTGTTCAC   | CTGTGGCACA   | GCAGCCTTCA   | GCCCCATGTG  | TACCTACATC   | 720<br>780                                   |
| 45  | AAGGGCCGTT   | GTCCCTTCGA   | CCCGAATTTC   | AAGTCCACTG   | CCCTGGTGGT  | GGAAGATGGC<br>TGATGGCGAG                             | 840  |
|     | AGCCTTCGCC<br>GCCTCAGCCT                             | CCACCAAGAC<br>ACATTCCTGA   | GAGCCTGGGC   | CTCAACTGGC<br>AGCTTGCAAG   | TGCAAGACCC<br>GCGATGATGA  | GCGGAGCCAA<br>AGCTTTTGTG<br>CAAGATCTAC               | 900<br>960<br>1020                           |
| 50  |  |  |  |  |   | TGTGTCCCGC<br>GCGCTGGACC                             | 1080<br>1140                                 |
|     | TCCTTCCTC  | AGGCCCAGCT   | GCTGTGCTCA   | CGGCCCGACG   | ATGGCTTCCC  | CTTCAACGTG   | 1200<br>1260                                 |
|     | GGGGTCTTC  | CTTCCCAGTC   | GCACAGGGG  | ACTACAGAAG   | GCTCTGCCGT  | CTTTTCTAT<br>CTGTGTCTTC                              | 1320   |
| 55  | ACAATGAAGO   | ATGTGCAGAC   | AGTCTTCAGO CCACCCGGT   | GGCCTCTACA   | AGGAGGTGAA<br>GGCCTGGAGG  | CCGTGAGACA<br>CGTGCATCACC                            | 1380<br>1440                                 |
|     | AACAGTGCCC   | GGGAAAGGA  | GATCAACTC  | TCCCTGCAGC   | TCCCAGACCC  | CGTGCTGAAC CGTGCTGCAG                                | 1500<br>1560                                 |
|     | CCCCAGGCT  | GCTACCAGC  | CGTGGCTGTA   | CACCGCGTCC   | CTGGCCTGC   | CCACACCTAC   | 1620   |
| 60  |  |  |  |  |   | GCAGAATCTG   | 1680<br>1740                                 |
|     |  |  |  |  |   | AGTCCAGGTG   | 1800<br>1860                                 |
|     | TACTGTGCT  | r GGAGCGGCTY   | CAGCTGCAA  | CACGTCAGC  | TCTACCAGC   | CCGGGACCCC<br>CTCAGCTGGCC                            | 1920   |
| 65  |  |  |  |  |   | G CAGCGCGTCT<br>A AGTCCAGTTC                         | 1980<br>2040                                 |
|     | CAGCCCAAC  | A CAGTGAACA  | TTTGGCCTG  | COGCTCCTC  | CCAACCTGG   | C GACCCGACTC   |  |
|     |  |  |  |  |   | r acccactggg<br>c actagaggag                         |  |
| 70  |  |  |  |  |   | G GGTGGCAGAC   |  |
| 10  | GCTGGTGGC  | A AGGCCAGCT  | G GGGTGCAGA  | C AGGTCCTAC  | r ggaaggagt   | r gagtgcacca<br>r cctggtgatg                         | 2400   |
|     | TGCACGCTC  | T TTGTGCTGG  | C CGTGCTGCT  | C CCAGTTTTA  | r TCTTGCTCT.  | A COGGCACOGG<br>C CAAGACOTGC                         | 2460   |
| -   | CCTGTGGTG  | C TGCCCCCTG  | A GACCCGCCC  | A CTCAACGGC  | C TAGGGCCCC   | C TAGCACCCCG   | 2580   |
| 75  |  |  |  |  |   | g agtetteact<br>c cecagtgtge                         |  |
|     | CCCCGGCCC  | C GGGTCCGCC  | T TGGCTCGGA  | G ATCCGTGAC  | T CTGTGGTGT   | g agagetgaet   | 2760   |
|     | TCCAGAGGA  | C GCTGCCCTG  | G CTTCAGGGG  | C TGTGAATGC<br>G ACCCTGGTG   | T CGGAGAGGG<br>C CCGGCCCTT  | T CAACTGGACC<br>G GGAGCCTTGG                         | 2820<br>2880                                 |
| 80  | GGCCAGCTG  | G CCTGCTGCT  | C TCCAGTCAA  | G TAGCGAAGC  | T CCTACCACC   | C AGACACCCAA   | 2940   |
|     | ACAGCCGTG  | G CCCCAGAGG  | T CCTGGCCAA  | A TATGGGGGC  | C TGCCTAGGT   | T GGTGGAACAG<br>G AAACTAGAAT                         | 3000<br>3060                                 |
|     | GAGAGGGAA  | G AGATAGCAT  | G GCATGCAGO  | A CACACGGCT  | G CTCCAGTTC   | A TGGCCTCCCA   | 3120   |
|     | GGGGTGCTG  | G GGATGCATC  | C AAAGTGGTT  | G TCTGAGACA  | g agttggaaa   | C CCTCACCAAC   | 3180   |

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                                                                                  1920
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         TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCCTGGC CCGGCCGCGG CGCGACGCCG
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                                                                                  2340
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Coding sequence: 222..1898
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                                                                                       1200
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PLGPECSRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI
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                                                                                          240
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```

|   |  | PSGTLEKLVS<br>DGLANQINNP   |   |  |  |  | 420<br>480   |
|---|--|--|---|--|--|--|--|
| 5   | Nucleic Aci  | 249 DNA seg<br>d Accession<br>lence: 818   | #: NM_0014  | 92.3   |  |  |  |
| 10  | 1  | 11   | 21  | 31   | 41   | 51   |  |
| 10  | CATTTTCCTC<br>GCCGGGTCCA   | GTCTCCCCAC<br>CCCCAGACAC<br>GGCCCTGGGG<br>GTCTGCCTGA   | CCCCCCCTCC  | CCCCTGCAGC   | CTGCAGATCC<br>GCCCGGCTCC   | ACTCTTTCGG<br>CCTGCCGCCT   | 60<br>120<br>180<br>240  |
| 15  | CCTGGGCGCG<br>GCCTGATCTC<br>CACCTTCTCT<br>CGCCTGGAGC   | GCGCTGAGTG<br>CCACTGCCCG<br>TTCATCATCG<br>CTGCTGGCGC   | CGCGCGGACC<br>ACGGGCTCTT<br>AAACCTGGAG<br>GCGTGGCTGG  | GGTCTACACC<br>GCAGGTGCCC<br>AGAGGAGTTA<br>CAGGCGGCGC   | GAGCAGCCCG<br>TTCCGGGACG<br>GGAGACCAGA<br>TTGGCAGCCG   | GAGCGCCCGC<br>CCTGGCCTGG<br>TTGGAGGGCC<br>GAGGCCCGTG   | 300<br>360<br>420<br>480   |
| 20  | CGAGCCGCCT<br>GCGGTGCGGT<br>GGTGTGCCGA<br>ATGCCTAGAG   | ATTCAGCGCG<br>GCCGTCGGGA<br>CCGGGACTGC<br>GCAGGCTGCA<br>GGCTGGACTG                             | CCGCGTGCAC<br>GCCCTGCGC<br>GCCCTGAGCA<br>GACCCCTCTG   | GCGCCTCTGC<br>ACCGCTCGAG<br>TGGCTTCTGT<br>CACGGTCCCT   | CGTCCGCGCA<br>GACGAATGTG<br>GAACAGCCCG<br>GTCTCCACCA   | GCGCCCCTC<br>AGGCGCCGCT<br>GTGAATGCCG<br>GCAGCTGCCT  | 540<br>600<br>660<br>720<br>780  |
| 25  | TGACGGGAAC<br>CACCTGCCCG<br>TGGACCCTGC<br>CTGCCACTGC   | GGCCCGTCCT<br>CCGTGTGCCA<br>CGTGGGTTCT<br>TTCAACGGCG<br>CCACCTGGTT                             | ATGGAGGCAG<br>ACGGGCTGCG<br>GCTTGTGTGT<br>TCCAAGGCTC  | CTGTAGTGAG<br>GTGTGAGGTG<br>CGGGGGTGCA<br>CAACTGTGAG   | ACACCCAGGT<br>AGCGGGGTGA<br>GACCCTGACT<br>AAGAGGGTGG   | CCTTTGAATG<br>CATGTGCAGA<br>CTGCCTACAT<br>ACCGGTGCAG   | 840<br>900<br>960<br>1020<br>1080  |
| 30  | CTGCCGCGCC<br>CGCCTGCGCT<br>GCTGGGCTTC<br>TGCTCACGGC   | GGCTTCGCGG<br>AACGGCGGCA<br>GGCGGCCGCG<br>GGCCGCTGCT   | GTCCTCGCTG<br>CGTGTGTGGA<br>ACTGCCGCGA<br>ACGCCCACTT  | CGAGCACGAC<br>GGGCGGCGGC<br>GCGCGCGGAC<br>CTCCGGCCTC   | CTGGACGACT<br>GCGCACCGCT<br>CCGTGCGCCG<br>GTCTGCGCTT   | TGCGCTGCCG<br>GCGCGGGCCG<br>GCTCCTGCGC<br>CGCGCCCCTG<br>GCGCTCCCGG   | 1140<br>1200<br>1260<br>1320<br>1380   |
| 35  | GGCCCCGCCG<br>ACTGCTCGTG<br>TGGCCACTCC<br>CGCACTCCCG   | GGCCTCAGGC<br>GCCGCGGGCG<br>CAGGATGCTG<br>GATGCACTCA   | CCGGGGACCC<br>TGGCCGGCGC<br>GGTCTCGCTT<br>ACAACCTAAG  | TCAGCGCTAC<br>TGCGCTCTTG<br>GCTGGCTGGG<br>GACGCAGGAG   | CTTTTGCCTC<br>CTGGTCCACG<br>ACCCCGGAGC<br>GGTTCCGGGG   | CCTTGCCGC<br>CGGCTCTGGG<br>TGCGCCGCCG<br>CGTCAGTCCA<br>ATGGTCCGAG  | 1440<br>1500<br>1560<br>1620<br>1680   |
| 40  | TGCTCCTTCC   | ATCTACGCTC<br>CAGAGGCAGC   | GGGAGGTAGC<br>ACCTGCTTTT  | GACGCCCCTT<br>TCCCTACCCT   | TCCCCCCGC  | ATGTCATATC<br>TACACACTGG<br>TGTCCGTGAA<br>CTTACTTTCA   | 1740<br>1800<br>1860   |
|   |  |  |   |  |  |  |  |
| 45  |  | 250 Proteincession #:  |   |  |  |  |  |
| 45<br>50  | Protein Ac  1     MVSPRMSGLI  RVCLKPGLSE   | cession #: 11<br> <br>  SQTVILALIF<br>  EAAESPCALG   | NP_058637.1<br>21<br> <br>  LPQTRPAGVP<br>  AALSARGPVY  | TEQPGAPAPD   | LPLPDGLLQV   | 51<br> <br>  SARLPCRLFF<br>  PFRDAWPGTF<br>  RPSYRANCEP  | 60<br>120<br>180   |
|   | Protein Ac  I   mvsprmsgli Rvclkpglse sfiletwree PAVGTACTRI EGWTGPLCTL PRGFYGLRCE PCRNGGLCLI   | 11     SQTVILALIF   SARESPCALG   LGDQIGGPAW   CRPRSAPSRC   PVSTSSCLS   VSGVTCADGP   LGHALRCRCR | NP_058637.1  21  LPQTRPAGVF AALSARGPVY SLLARVAGRR GPGLRPCAPL RGPSSATTGC CFNGGLCVGG AGFAGPRCEH   | ELQIHSFGPG<br>TEQPGAPAPD<br>RLAAGGFWAR<br>EDECEAPLVC<br>LVPGPGPCDG<br>ADPDSAYICH<br>DLDDCAGRAC   | PGPGAPRSPC<br>LPLPDGLLQV<br>DIQRAGAWEL<br>RAGCSPEHGF<br>NPCANGGSCS<br>CPPGFQGSNC   | SARLPCRLFF PFRDAWPGTF RFSYRARCEP CEOPGECRL ETPRSFECTC EKRVDRCSLQ GAHRCSCALG  | 120<br>180<br>240<br>300<br>360<br>420   |
| 50  | Protein Ac  I  | 11   | 21  | ELQIHSFGPG TEQPGAPAPD RLAAGSPWAR EDECEAPLVC LVPGPGPCDC ADPDSAYICH DLDDCAGRAC LVCACAPGYM LLVHVRRRGH   | PGPGAPRSPC LPLPDGLLQV DIQRAGAWEL RAGCSPEHG NPCANGGSCS CPPGFQGSNC ANGGTCVEGG GARCEPPVHE SQDAGSRLLP  | SARLPCRLFF PFRDAWPGTF RFSYRARCEP CEQPGECRCL ETPRSFECTC EKRVDRCSLQ  | 120<br>180<br>240<br>300<br>360  |
| 50<br>55  | Protein Ac  I     MVSPRMSGLI RVCLKPGLSE SFIIBTMREE PAVGTACTRI EGWTGPLCTV PRGFYGLRCE PCRNGGLCLI FGGRDCREER PGLRPGDPOR PDALNNLRTC GQRQHLLFPY Seq ID NO:  | 11   | 21  | <br>ELQIHSFGPG<br>TEQPGAPAPD<br>RLAAGGPWAR<br>EDECEAPLVC<br>LVPGFGPCDG<br>ADPDSAYICH<br>DLDDCAGRAC<br>LVCACAPGYM<br>LLVHYRRGH<br>PQGIYVISAF  | PGPGAPRSPC<br>LPLPDGLLQV<br>DIQRAGAWEI<br>RAGCSPEHGF<br>NPCANGGSCS<br>CPPGFQGSNC<br>ANGGTCVEGG<br>GARCEPVHE<br>SQDAGSRLLE<br>SIYAREVATE  | SARLPCRLFF SPRIDAWPGTF RFSYRACCEP CEQPGECRCL ETPRSFECTC EKRVDRCSLQ GAIRCSCALG DGASALPAAP AGTPEPSVHAL LFPPLHTGRA  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540   |
| 50<br>55  | Protein Ac  I     MVSPRMSGLI RVCLKPGLSE SFIIETWREE PAVGTACTRI EGWTGPLCTV PRGFYGLRCE PCRNGGLCLI FGGRDCRERA FGLRPGDPQE PDALNNLRYC GQRQHLLFPY Seq ID NO: Nucleic Ac  I       GAAATATAAC AGATTATTGJ  | 11   | NP_058637.1  21    LPQTRPAGVF AALSARGPVY SLLARVAGRR GPGLRPCAPL RGPSSATTGC CFNGGLCVGG AGFAGPRCPH GGRCYAHFSG VAAGVAGAAL VDWNRPEDVD  CQUENCE II #: CAT cl.  21    AGAAAATATC   | ELQIHSFGPG ELQIHSFGPGPAPPD RLAAGGFWAR EDECAPLIVE LVPGFGPCDG ADFDSAYICH DLDDCAGRAC LVCACAPGYM ELWHYRRGH PQGIYVISAF USEET 31   CAAAATAGCC TTCTTTAAAF   | PGPGAPRSPC LPLPDGLLQV DIQRAGAWEI RAGCSPEHGE RPCANGGSC CPPGFGGSNC ANGGTCVEGG GARCEPPVHE SQDAGSRLLE SIYAREVATE  41   CTGTTATCTTT GTAGTACAA   | SARLPCRLFF PFRDAWPGTF RFSYRARCEP CEOPGECRCL ETPRSFECTC EKRYDRCSLQ GGHRCSCALG DGASALPAAP GTPEPSVHAL   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600  |
| 50<br>55<br>60  | Protein Ac  I    MVSPRMSGLI RVCLKPGLSE SFIIBTWREE PAVGTACTRI EGWTGPLCTV PRGFYGLRCE PCRNGGLCLI FGGRDCREER PGLRPCDPOF PDALNNLRTC GQRQHLLFPY  Seq ID NO: Nucleic Ac  I  GAAATATAAA AGATTATTAG GGTTCAATTY TTAGAAAGTY AGTTTTACTA  | 11   | NP_058637.1  21    LPOTRPAGVF AALSARGPVY SILLARVAGRR GPGLRPCAPL RGPSSATTGC CFNGGLCVGG AGFAGPRCEH GGRCYAHFSG VAAGVAGAAL VOWNRPEDVD  21    AGAAAATATC TTTCAGACTGG TATTACATAAF C CGTTGAGAAG C TGTTAAGTGG C TGTTAAGTGG C CATTGTCTAA   | ELQIHSFGPG ELQIHSFGPG RLAAGGPWAR EDECEAPLVC LVPGPGPCDG ADPDSAYICH DLDDCAGRAC LVCACAPGYM LLVHVRRCH PQGIYVISAF CAAAATAGCC TTCTTAAAA AGAAGCCTGTT TTCTCAATTTAAC CCTGTATTCC TACAATTAAC TACAATTAACAATTAAC TACAATTAAC TACAATTAAC TACAATTAAC TACAATTAAC TACAATTAAC TACAATTAAC TACAATTAACAATTAACAATTAACAATAATTAACAATTAAATTAAATTAAATTAA | PGPGAPRSPC LPLPDGLLQU DIQRAGAWEL RAGCSPEHGE NPCANGGSCS CPPGFGGSN ANGGTCVEGG GARCEPVHI SQDAGSRLLE SIYAREVATE  41   CTGTTATCTTT GTAGTACACT TARACCACT GGCTGCTGT ATTTACATT: TTCATTTACATT:  | SARLPCRLFF PFRDAWPGTF RFSYRARCEP CEOPGECRCL EKRVDRCSLQ GAHRCSCALG ODGASALPAAP AGTPEPSVHAL LFPPLHTGRA  51   CACGTGGCCT TTCCTTTGTA   | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>600   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | Protein Ac  I    MVSPRMSGLI RVCLKPGLSE SFI IBTWREE PAVGTACTRI EGWTGPLCTV PRGFYGLRCE PCRNGGLCLI FGGRDCREFR PDALINILRY GQRQHLLFPY  Seq ID NO: Nucleic Ac  I    GAAATATAAA AGATTATAGI GCTTCAATY TTAGAAAGTY AGTTTTACTAAT GGGTGCTATT GGTTTACTGAAT TTACTGAAAT TGCCAATGTT TTACTAAAT TGCCAATGTT TTACTAAAT TGCCAATGTT TGCCAATGTT TGCCAATGTT TGCCAATGTT TGCCAATGTT TGCCAATGTT TGCCAATGTT TGCCAATGTT TGCCAATGTT | 11   | NP_058637.1  21    LPOTRPAGUF AALSARGPVY SILLARVAGRR GPGLRPCAPL RGPSSATTGC CFNGGLCUGG AGFAGPRCEH GGRCYAHPSG VAAGVAGAAL VDWNRPEDVD  21    TATACAATTC TATACAATTC TATACAATTGC TATACAATTGC TATACAATTGC TATACAATTAAC TTGTTAAGTGC CATTGTCTAAC TTCAATTAAC TTCAATTAAC TTCAATTAAC TTGAATTAAC                                  | ELQIHSFGPG ELQIHSFGPG RLAAGGPWAR EDECAPLVC LVPGGPCDG ADPDSAYICH DLDDCAGRAC LVCACAPGWM LLVHVRRGCH PQGIYVISAF CAAAATAGCC TTCTCAATT ACGAATTATCC TACAATTAAC GCAATAAACA CATACTAATC ACATACTAATC CATACTAATC ACATACTAATC ACATACTAATCAATC   | PEGPGAPRSPC LPLPDGLLQV DIQRAGAWEL RAGCSPEHGE NPCANGGSCS: ANGGTCVEGG GARCEPFVHE SUPAREVATE  41  | SARLPCRLFF SARLPCRLFF PFRDAWPGTF RFSYRACCEP CEOPGECRCL EKRYDRCSLQ GAHRCSCALG GAHRCSCALG GAHRCSCALG CTPPPLHTGRA  51   CACGTGGGCCT TTCCTTTGTA TTAGTTTCAG ACACGTGCCAG TGAAGCACTGT TCATGTCCAG ACAAGTGTGT   | 120<br>180<br>240<br>300<br>360<br>420<br>600<br>600<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Protein Ac  I    MVSPRMSGLI RVCLKPGLSE SFIIBTWREE PAVGTACTRI EGWTGPLCTV PRGFYGLRCE PCRNGGLCLI FGGRDCREER PGLRPCDPOF PDALINLRTC GQRQHLLFPY  Seq ID NO: Nucleic Ac  I  GAAATATAAA AGATTATTACT TTAGAAAGT TTAGAAAGT TTAGTAAA TGCCATTGT TAAAAATAC Seq ID NO  Seq ID NO  | 11   | NP 058637.1  21    LPOTRPAGVF AALSARGPVY SILLARVAGRR GEGLRPCAPL RGPSSATTGC CFNGGLCVGG AGFAGPRCEH GGRCYAHFSG VAAGVAGAAL VOWNRPEDVD  21    AGAAAATATC TTCAATAAA TTCAATTAAA TTACAATTA TTCAATTAAA TTACAATTA TTCAATTAAAA TTACAATTA   | ELQIHSFGPG ELQIHSFGPG RLAAGGPWAR EDECEAPLVC LVPGPGPCDG ADPDSAYICH DLDDCAGRAC LVCACAPGYM LLVHVRRCEH PQGIYVISAF CAAAATAGCC TTCTCAATT ACAATTAAG GCAAATTAAG GCAAATTAAG GGAAAATAAG CATACTAATT AAAAAAAAAA  | PEGPGAPRSPC LPLPDGLLQV DIQRAGAWEL RAGCSPEHGE NPCANGGSCS: ANGGTCVEGG GARCEPFVHE SUPAREVATE  41  | SARLPCRLFF PPHDAWPGTF RFSYRARCEP CEOPGECRCL EKRYDRCSLQ GAHRCSCALG GAHRCSCALG CTPESYWAL FIFPLHTGRA  51   CACGTGGCCT TTCCTTTGTA ACACGTCCAG GAAACCACTGT TACATTCCAG ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACTTGTCT ACTTGTCT ACTTGTCT ACTTGTCTT ACTTGTCT ACTTGTC ACTTGT ACTTGTC ACTTGT | 120<br>180<br>240<br>300<br>360<br>420<br>600<br>600<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | Protein Ac  I     MVSPRMSGLI RVCLKPGLSE SFIIETWREE PAVGTACTRI EGWTGPLCTV PRGFYGLRCE PCRNGGLCLI FGGRDCRERP PDALMNLRTX GQRQHLLFPY  Seq ID NO: Nucleic Ac  I     GARATATAGA AGATTATTGG GCTTCAATTT TTAGAAAGTM TAGAAAGTM TTAGTAAAG GGGTGCTAT TTATGTAAAA TGCCATTGT TTAAAAATAC Seq ID NO Nucleic A  | 11   | NP_058637.1  21    LPQTRPAGVF   AALSARGPVY   SLLARVAGRR   GPGLRPCAPL   RGPSSATTGC   CFNGGLCVGG   AGFAGPRCPH   GGRCYAHFSG   VAAGVAGAAL   VDWNRPEDVD    CTATACAATTI   TACAATTACAATTI   TACAATTACAATTACACACACACACACACACACACACAC | ELQIHSFGPG ELQIHSFGPG RLAAGGPWAR EDECAPLIVE LIVPGFGPCDG ADFDSAYICH DLDDCAGRAC LIVCACAPGYME ELGIPTE E | PGPGAPRSPC LPLPDGLLQV DIQRAGAWEI RAGCSPEHGE RPCANGSCS CPPGFGGSNC ANGGTCVEGG GARCEPPVHE SQDAGSRLLE SIYAREVATE TGTATCTTT GTAGTACATT TTCATTTACATTT TTCATTTACATTT TTCATTTACATTT TTTCATTTACATTT TTTCATTACATTT TTTCATTACATTACATTT TTTCATTACATACATACATTACATTACATTACATTACATTACATTACATTACATTACATACATTACAT | SARLPCRLFF PPHDAWPGTF RFSYRARCEP CEOPGECRCL EKRYDRCSLQ GAHRCSCALG GAHRCSCALG CTPESYWAL FIFPLHTGRA  51   CACGTGGCCT TTCCTTTGTA ACACGTCCAG GAAACCACTGT TACATTCCAG ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACAAGTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACATTGTCT ACTTGTCT ACTTGTCT ACTTGTCT ACTTGTCTT ACTTGTCT ACTTGTC ACTTGT ACTTGTC ACTTGT | 120<br>180<br>240<br>300<br>360<br>420<br>600<br>600<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600 |

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| 10        |            |                          |            |               |             | GGGTTGCTAC                | 2460         |
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|           |            |                          |            |               |             | CCACCTTGAG                | 2580         |
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| 20        |            | CTGGGCATAG<br>TGGGAGGAGG |            |               |             |                           | 2940<br>3000 |
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|           |            |                          |            |               |             | GACACTGTGG                |              |
| 75        |            |                          |            |               |             | AAAAAAAA A                |              |
|           | АААААААА   |                          |            |               |             |                           |              |
|           |            |                          |            |               |             |                           |              |
|           |            | 262 Protei               |            |               |             |                           |              |
| 80        | Protein Ac | cession #:               | NP_004377. | L             |             |                           |              |
| 00        |            |                          |            |               |             |                           |              |
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|           | Ī          | 1                        | Ĩ          | 1             | 1           | 1                         |              |
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|           |            |                          |            |               |             |                           |              |

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Seq ID NO: 264 Protein sequence
Protein Accession #: Eos sequence

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| 10  | DECAMPAGE   | KSPGPSRRSQ         | TENUCOCCCN 1 | INCOPPI.DEC       | TODECVNEND  | CSESSTLLEK   | 360          |
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|     |             |                    |              |                   |             | A TAATTTTGGT |              |
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| ~~  |             |                    |              |                   |             | T CCTTGTATGA |              |
| 75  | ATTTTTGTT   | T CTTAGAAGT        | C AATTTGTGTG | AAATGAGAT         | CTTCAAAAO   | G ATGAAACCTC | 3060         |
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| 20 | <br>PLVINTLKRP<br>ACFYVAVIFI                         | LNGLMMALFF  | 21<br> <br>  WYRIYTKIMD<br>  IYGTYLSGSR<br>  LYRGSLIALC   | LGGLVTVLCF   | FFNHGECTRV   | MWTPPLRESF  | 60<br>120<br>180   |
| 25 | ELSLWVIQGC<br>DFMEKETPLR<br>LQLLAYTALG               | FWLFGTVILK<br>YTKTLLLPVV<br>ILIMRLKLFL  | LCFVLMFGNS<br>YLTSKIFGIA<br>LVVFVAIVRK<br>TPHMCVMASL<br>EELIEWIKYS  | DDAHIGNLLT<br>IISDMWGVLA<br>ICSRQLFGWL   | SKFFSYKDFD<br>KQQTHVRKHQ<br>FCKVHPGAIV   | TLLYTCAAEF<br>PDHGELVYHA<br>PAILAAMSIQ  | 240<br>300<br>360<br>420<br>480  |
| 30 | YEDAGLRART<br>EDPANAGKTP                             | KIVYSMYSRK<br>LCNLLVKDSK  | AAEEVKRELI<br>PHFTTVFQNS  | KLKVNYYILE   |  |   | 540  |
| 35 | Nucleic Aci  | 267 DNA second Accession tence: 59  | #: U26744   | .1   |  |   |  |
|    |  |   | 21<br> <br>TTTGAAAAGT   |  |  |   | 60   |
| 40 | GATGAGGGCT<br>TAGGTTTGTT<br>ATTGCGGGAA<br>AGAGGCTGTG | CAAGATCTGG<br>CAGAAGAAAT<br>AATGCTCTGA<br>CTCTCCACTA  | GAGGAAATAC<br>ATCGCATCCG<br>GCAATTTGCA<br>ACAACCTGGA<br>TTTTTTACCA  | ACTOTOCACO<br>CCTGGTGGAC<br>CCCAAACACT<br>GCTCAACAAA   | TACAGAACAG<br>ATATGGAATG<br>GAACTCAACG<br>CGGATGCCAA   | CATGCAAGCT<br>TCATAGAAGC<br>TGTCCCGCTT<br>CCACTCACCA  | 120<br>180<br>240<br>300<br>360  |
| 45 | GGAAGGCCAT<br>AGGGAAGATC<br>GATGGTTTAT<br>TTTGGAGGGT | GGTAAAATTT<br>ATGGACAAAT<br>GGACGATATG<br>CCTTCATTTG  | TCAGCCTCCT<br>CAGTATTTGC<br>TAAGATATAT<br>ACCAATTCCT<br>GTTACACAGA  | TGTCAAAATG<br>TTTCTCAATG<br>TCGGGAAGTT<br>ACAGTCAGCC   | GCTTTAGCCA<br>ATTTCTGACT<br>CTCAAACTAC<br>AGATCCTGTT   | CATTGTGTGG<br>CCAGTGGGGT<br>CCACGGAAGT<br>TCTCCCAACA  | 420<br>480<br>540<br>600<br>660  |
| 50 | TCTGGTCTGG<br>TGAGTGTTCC<br>TCACAATTAC<br>CAACCAGCAC | TTGCCTCTTC<br>TACTGCCACA<br>CAGCTCTGTC<br>CAAATGAAAG  | GTTTCTTGGA<br>TGCATCGACT<br>GTGAGAGTAT<br>AGGACTGCTT<br>AGTACACGTC  | AGCAAATGTG<br>GATGGGATTT<br>CTGGAGGGGA<br>ATGGAAATCA   | GAAAATGTCT<br>CGCTACCGAT<br>CATGCCGGTG<br>CCTGCTAAGA   | TCCATCCGGT<br>GCCAACAGTG<br>GTTCTCATAG<br>AGCTGACTAA  | 720<br>780<br>840<br>900<br>960  |
| 55 | AGATCAGCCT<br>TGTAACCAGC<br>TATTACCAGG<br>CAGGTATGCG | GAGAAGCCAC<br>ATGAACGACA<br>AGCATGCTTG<br>GCAAGGCTGG  |   | TCACATCGTT<br>CCACTCTGTT<br>CCGGCTTGAT<br>CTCTTCGTCT   | GATACTTGGC<br>CCCTCCTCAG<br>GAAGAACACA<br>CAGCCACCTC   | CTCCCAGACC<br>GAAGTCCTTT  | 1020<br>1080<br>1140<br>1200<br>1260<br>1320   |
| 60 | GCTAGAAAAC<br>ACAAGCTTCT<br>CCGGCTCCTC<br>CCGGAGAGAG | AAGAACAGAG<br>CAGCCCACGC<br>AGACAGCGCA<br>CTAATGGTCC  | AAATCTTACA<br>CAGAGAAGGC<br>AAGATGAGCT<br>AGTTGGAGGG  | GGAGATCCAG<br>ACAGCAAAAC<br>GGAACAGAGA<br>TCTCATGAAG   | AGACTTCGGC<br>CCCACCCTGC<br>ATGTCTGCTC<br>CTACTAAAGG   | TAGAGCATGA<br>TGGCAGAACT  | 1380<br>1440<br>1500<br>1560<br>1620   |
| 65 | CGACCTGCGG<br>AGAAAAAAGT<br>ATTTAGCATT<br>TTAGAAAAGG | TTTTCTCATT<br>CATACTAATT<br>TTTTATAACT<br>GAACGAATTG  | GCTTTTGCTC<br>TGCTTCTTTT<br>ATCACTACTA<br>TCATTTATTG  | TAATGTATGT<br>TCAATGTAGT<br>TCCACATCAA<br>GAAACATTTT   | TCATGCTTCA<br>GCTTGAATTG<br>AAGAAGAACT<br>AGATCCCCAG   | GTTTGGAAAG<br>AGATATATAA<br>ATGACATCTT<br>AGGTATAAGT  | 1680<br>1740<br>1800<br>1860   |
| 70 | CACAGTCACT<br>TAACCTCTAC<br>GTGAAACCTC<br>GCCTTGTTCC | AGAGATACCO<br>ACCCACTCAC<br>TTTTTATAAA<br>CCATGGCTCA  | TGAGGTTCAT ACTGTGAGTA AATCAGGCAA CCAAAATGTG   | GTCATCCCAA<br>TTCAGTTCGG<br>TTAAATCCCT<br>CTCAATTTG  | AACCCACAGO<br>TTTCATTTTA<br>TTTCATCACA<br>TGAGAGAAAG   | AGAGAGATAC ACTCAGAAGC CTGAAAACCT CAATTATTGA ACTGTACTCC  | 1920<br>1980<br>2040<br>2100<br>2160   |
| 75 | GGTTGACAGT<br>TTCGGCTCCG<br>ATTGTGACTT               | AATCTCTTTT<br>GGAGACGAGA  | TAAAAAGTAA<br>GGGTCATTAC  | CTCTCAGCTT<br>ATACTTTTTT   | TTTCCTTAGC<br>TTTTTTCTGG   | CCTTACTGTT<br>ACCAGAGCCT<br>AAATAGGGGC<br>CAAGAGCCAG  | 2220<br>2280<br>2340<br>2400   |
| 80 |  | 268 <u>Protei</u><br>cession #:   |   |  |  |   |  |
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|     | ACCGAGGCCT | ACTITGGGGC (                 | CAAAGAGCCG        | GAGCCGGCGC   | CGCCGTACCA  | CAGCCCGGAA   | 1980         |
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| 5   | TCCACGGGCC | GGCAGCCACA                   | TO COCCUCCO       | CCCCAGGGCC   | ACGGCACCTC  | CCCCGTGGGG   | 2160         |
| -   | GACCACGGCT | CCCTGGTGCG                   | CATCCCGCCG        | CCGCCTGCCC . | ACGAGCGGTC  | GCTGTCCGCC   | 2220         |
|     | TACCGCCGGG | GCAACCGCGC                   | CAGCATGGAG        | TTCCTGCGGC   | AGGAGGACAC  | CCCGGGCTGC   | 2280         |
|     | AGGCCCCCCG | AGGGGACCCT                   | GCGGGACAGC        | GACACGTCCA   | TCTCCATCCC  | GTCCGTGGAC   | 2340<br>2400 |
| 10  | CACGAGGAGC | TGGAGCGTTC<br>ACAGCTGCTA     | CTTCAGCGGC        | CCCCTTGTG    | CCCAGTCCAA  | GCCCTACATT   | 2460         |
| 10  | GCGGAGGGAG | AGTCAGACAC                   | CGACTCCGAC        | CTCTGTACCC   | CGTGCGGGCC  | CCCGCCACGC   | 2520         |
|     | TCGGCCACCG | GCGAGGGTCC                   | CTTTGGTGAC        | GTGGGCTGGG   | CCGGGCCCAG  | GAAGTGAGGC   | 2580         |
|     | GGCGCTGGGC | CAGTGGACCC                   | GCCCGCGGCC        | CTCCTCAGCA   | CGGTGCCTCC  | GAGGTTTTGA   | 2640         |
| 15  | GGCGGGAACC | CTCTGGGGCC                   | CTTTTCTTAC        | AGTAACTGAG   | TGTGGCGGGA  | AGGGTGGGCC   | 2700<br>2760 |
| 13  | CTGGAGGGGC | CCATGTGGGC<br>CAGGGCACTC     | TGAAGGATGG        | TOCOCATTOA   | CAGIGACCII  | CTGGGCTGTC   | 2820         |
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|     | AGCCACTGTC | CAGGCTCCCA                   | CTGCCTGTCT        | GCTCTGTTCC   | CAAAGGCAGC  | GTGTGTGGCC   | 2940         |
| 00  | TCGGGCCCTG | CGGTGGCATG                   | AAGCATCCCT        | TCTGGTGTGG   | GCATCGCTAC  | GTGTTTTGGG   | 3000         |
| 20  | GGCAGCGTTT | CACGGCGGTG                   | CCCTTGCTGT        | CTCCCTTGGG   | CTGGCTCGAG  | CCTGGGGTCC   | 3060<br>3120 |
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|     | TATGAGIGGG | CTACCTGGAC                   | TCCAGGACCC        | TGGAGAAGGG   | AGACCTGGCA  | GTGGAGGGAG   | 3240         |
|     | GCTGTGCTGT | GTGTCCCCCT                   | <b>GCAGGTGTGA</b> | CCCCGCCTGC   | TCTTTCCTCC  | CCCGCCAGGT   | 3300         |
| 25  | GTGGCCCCGC | CTGCTCTTTC                   | CTCCCCCACC        | AGTATGGCCC   | CACCTGCTCT  | TTCCTNCCCC   | 3360         |
|     | CCCAAGGTGT | GCCCCACCT                    | GTTCTTTCCT        | CCCCTGCCGA   | GGTGTGACCC  | CACCIGCICI   | 3420<br>3480 |
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|     | ACCATGAGGA | AGACAGGCCA                   | ATCCCTTCCC        | TCCCAGAAGC   | TGGCCGCCCA  | GCAGGAGGGA   | 3600         |
| 30  | CTGAGGCCAG | ACTCATGTCC                   | AGCAAGGAAC        | GTGTGGTGTG   | TCCCCTGGGA  | AGTCTCTGGG   | 3660         |
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| 35  | CCACTCTTTC | TTAGAGTGCA                   | CATCCTACGT        | GCCCACTGGC   | ACACACACGT  | GCTCACATAC   | 3960         |
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|     | CCTGCATACA | GGCATACACA                   | TGCACGCTTA        | CATGTACACG   | TGCACAGATC  | ACACACATGC   | 4140<br>4200 |
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| 50  | CACCACGGC  | r GGGACACGCT                 | GGGGGAGGG         | TCCTCCCATG   | CCTCCTGCAC  | ACAGCOGTCT   | 4860<br>4920 |
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| 55  | CTCAGTGTT  | T CTAGATTCC                  | GACCCTGCT         | G CCAGAGAGA  | CIGCIGCCG   | AGAGAAGGGG   | 5160         |
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| 60  | ATTGACACA  | A ACCCTCAAAC                 | CAGACGTGA         | G AGGGACGGT  | CACAAAGCT   | CONTROL OF THE CONTRO | 5460         |
|     | TGGAGGGTG  | C CCGGCAGAC                  | TGGCGTGAG         | A GGGACGGCT  | ACGAGGCTT   | GACCTGCTGT   | 5520         |
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| 65  | GCTCACGAG  | G CTTGGACCT                  | GTGGAGGGT         | G CCCGGCAGA  | C GTGTGAGAG | 3 GACGGTTCAC   | 5760         |
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| 70  | CCCATGCAG  | A ACTOCOAGG                  | GGGCTGCAG         | G ACGGAATGG  | C CACCTGGGG | A GCCTGTGTGG   | 6060         |
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| 5  | TAGGGAAAAT<br>ACTGCATAGA<br>TTTGTGGTAT<br>TCTATGTACA<br>TCATTGATTA<br>TGTTTTATGC | TGGAAAATAT<br>AATAACAAGC<br>ATGTATATAT<br>GTTTTGTATT<br>TTCTACAAAA<br>ATTATTTAAG | AGGAAACTTT<br>GTTAACATTT<br>GTACCTATAT<br>ATACTTTTTA<br>ACATGATTTT<br>CCTGTCTCTA | TTTTTCTAAA AAACGAGAAA TCATATTTTT GTATTTGCAT AATCTTGAAC AAACAGCTGT TTGTTGGAAT AAAAAAAAAA | ATGAAACCTC<br>TTCTTTCAGT<br>TTGAAATTTT<br>TTTATAAACA<br>AAAATATTCT<br>TTCAGGTCAT    | TCATAATCCC CATTTTTCTA GGAATCCTGC TTTTCTGAAA ATGATATGAA  | 1020<br>1080<br>1140<br>1200<br>1260<br>1320 |
|----|--|--|--|---|---|---|--|
| 10 |  | 292 <u>Proteir</u><br>ession #: E  | sequence   | :   |   |   |  |
|    | 1  | 11   | 21   | 31  | 41  | 51  |  |
| 15 | EGGHLATYKQ<br>ERWDAYCYNP<br>DLEDDPGCLA   | LEAARKIGFH<br>HAKECGGVFT<br>DYVEIYDSYD   | VCAAGWMAKG<br>DPKQIFKSPG   | LERAAGVYHR<br>RVGYPIVKPG<br>FPNEYEDNQI<br>GDELPDDIIS                                    | PNCGFGKTGI<br>CYWHIRLKYG  | IDYGIRLNRS<br>QRIHLSFLDF  | 60<br>120<br>180<br>240                      |
| 20 | Seq ID NO:<br>Nucleic Ac   | 293 DNA sec  | quence<br>1 #: NM_007  |   |   |   |  |
| 25 | 1  | 11   | 21   | 31  | 41  | 51  |  |
|    | <br>GAATTCGCAC<br>CTGACGATAT   | <br>TGCTCTGAGA<br>GATCATCTTA   | <br>ATTTGTGAGC<br>ATTTACTTAT   | AGCCCCTAAC<br>TTCTCTTGCT<br>CCATATGGCT  | ATGGGAAGAC  | ACTCAAGGAT  | 60<br>120<br>180                             |
| 30 | ACCACAGAGA<br>GTGAATTTGA<br>GATTTCATGT<br>AGCCAGGGCC                             | AGCACGGTCT<br>AGGCGGCCAT<br>CTGTGCTGCT<br>CAACTGATGA                             | GGCAAATACA<br>CTCGCAACTT<br>GGATGGATGG<br>TTTGGAAAAA                             | AGCTCACCTA<br>ACAAGCAGCT<br>CTAAGGGCAG<br>CTGGCATTAT<br>ACAACCCACA                      | CGCAGAAGCT<br>AGAGGCAGCC<br>AGTTGGATAC<br>TGATTATGGA                                | AAGGCGGTGT<br>AGAAAAATTG<br>CCCATTGTGA<br>ATCCGTCTCA  | 240<br>300<br>360<br>420<br>480              |
| 35 | TCTTTACAGA<br>ACCAAATCTG<br>TAGATTTTGA<br>GTTACGATGA                             | TCCAAGCGA<br>CTACTGGCAC<br>CCTTGAAGAT<br>TGTCCATGGC                              | ATTTTTAAAT<br>ATTAGACTCA<br>GACCCAGGTT<br>TTTGTGGGAA                             | CTCCAGGCTT<br>AGTATGGTCA<br>GCTTGGCTGA<br>GATACTGTGG                                    | CCCAAATGAG<br>GCGTATTCAC<br>TTATGTTGAA<br>AGATGAGCTT                                | TACGAAGATA<br>CTGAGTTTTT<br>ATATATGACA  | 540<br>600<br>660<br>720<br>780              |
| 40 | GAGGTTTCCA<br>ATACAAGTAC<br>AAAAAAAAA<br>TTGATCTCAC                              | AATCAAATAT<br>TACTTCTACT<br>AAGGATGATC<br>TGTTATTATT                             | GTTGCAATGG<br>GGAAATAAAA<br>AAAACACACA<br>AACATTTATT                             | ATCCTGTATC<br>ACTTTTTAGC<br>GTGTTTATGT<br>TATTATTTTT                                    | CAAATCCAGT<br>TGGAAGATTT<br>TGGAATCTTT<br>CTAAATGTGA                                | CAAGGAAAAA<br>AGCCACTTAT<br>TGGAACTCCT<br>AAGAAATACA  | 940<br>900<br>960<br>1020                    |
| 45 | ATCCCACTGC<br>TTGTATTTGT<br>CCTGCTCTAT<br>TGAAATCATT                             | ATAGAAATAA<br>GGTATATGTA<br>GTACAGTTTT<br>GATTATTCTA                             | CAAGOGTTAA<br>TATATGTACO<br>GTATTATACT<br>CAAAAACATG                             | CATTTTCATA<br>TATATGTATT<br>TTTTAAATCT<br>ATTTTAAACA                                    | TTTTTTTCTT<br>TGCATTTGAA<br>TGAACTTTAT<br>GCTGTAAAAT                                | ACCTCTCATA<br>TCAGTCATTT<br>ATTTTGGAAT<br>GAACATTTTC<br>ATTCTATGAT  | 1080<br>1140<br>1200<br>1260<br>1320         |
| 50 | Seq ID NO:   | TGCAATAAAT   | n sequence   | ATTC  | GGAATTCAG   | GTCATTTTCA  | 1380   |
|    | Protein Ac   | cession #:   | NP_009046.1  | •   |   |   |  |
| 55 | 1<br> <br>  MIILIYLFLI<br>  EGGHLATYKO   | 11<br> <br>  LWEDTQGWGY  | 21<br> <br>  KDGIFHNSIV  | 31<br> <br>  LERAAGVYHE<br>  RVGYPIVKPO   | 41<br> <br>  EARSGKYKL/<br>  PNXXFGKTG  | 51<br> <br>  YAEAKAVCEF<br>  IDYGIRLNRS   | 60<br>120                                    |
| 60 | ERWDAYCYNI<br>DLEDDPGCL  | HAKECGGVFT   | DPKRIFKSPO   | FPNEYEDNQI<br>GDELPDDIIS  | CYWHIRLKY   | QRIHLSFLDF<br>G SDASVTAGGF  | 180<br>240                                   |
| 65 | Nucleic A  | : 295 <u>DNA se</u><br>cid Accessio<br>quence: 116                               | on #: NM_001   | 218.2   |   |   |  |
| 70 | CCGGCGCAG  | GAGCCCCCG<br>C CTGCACGCG   | G CACAGCCCG<br>G CGGCCGTGC   | CCTGCTGGT   | G CAGGAGCCO<br>G ATCTTAAAG  | 51<br> <br>T GGAGAGCGAG<br>G CGAAGATGCC<br>G AACAGCCTTC<br>G GGGAGAATAG                                     | 180  |
| 75 | CTGGTCCAA<br>TGACATCCT<br>TGCCAACAA<br>GGACATGCA                                 | G AAGTACCCG<br>C CAGTATGAC<br>G CAGTTTCTC<br>C ATCCAGGGC                         | T CGTGTGGGG<br>G CCAGCCTCA<br>C TGACCAACA<br>C TCCAGTCTO                         | G CCTGCTGCA<br>C GCCCCTCGA<br>A TGGCCATTC<br>G CTACAGTGC                                | S TCCCCATA<br>S TTCCAAGGC<br>A GTGAAGCTG<br>C ACGCAGCTG                             | S ACCTGCACAG T ACAATCTGTC A ACCTGCCCTC C ACCTGCACTG   | 300<br>360<br>420<br>480                     |
| 80 | GGGGAACCC<br>CGAGCTGCA<br>CAAGTCAGA<br>CTATGACAA<br>CCCGGGATT<br>GGGGTCCCT       | G AATGACCCG C ATTGTCCAT A GGCCTCGCT G ATCTTCAGT C AACATTGAA G ACCACACCC          | C ACGGCTCTG T ATAACTCAG G TCCTGGCTG C ACCTTCAAC G AGCTGCTTC C CTTGCAACC          | A GCACACCGT A CCTTTATCC T TCTCATTGA A TGTAAAGTA C GGAGAGGAC C CACTGTGCT                 | C AGCGGACAG T GACGCCAGC G ATGGGCTCC C AAAGGCCAG C GCTGAATAT C TGGACAGTT A GCCCTGTAC | C ACTTOGOGG<br>A CTGCCAGCAA<br>T TCAATCCGTC<br>G AAGCATTCGT<br>T ACCGCTACCG<br>T TCCGAAACCC<br>T GCACACACAT | 540<br>600<br>660<br>720<br>780<br>840       |

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|     |               |              |               |              |              | •            |        |
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|     | GTTCGAACGA    | GCACCACTGT ' | TCCAACGACA    | ACGACTGTTC ( | CAACGACAAC   | TGTTCCAACA   | 540    |
| -   | ACAATGAGCA    | TTCCAACGAC   | AACGACTGTT    | CCGACGACAA   | TGACTGTTTC . | AACGACAACG   | 600    |
| 5   | AGCGTTCCAA    | CGACAACGAG   | CATTCCAACA    | ACAACAAGTG   | TTCCAGTGAC . | AACAACGGTC   | 660    |
|     | TCTACCTTTG '  | ITCCTCCAAT   | GCCTTTGCCC    | AGGCAGAACC   | ATGAACCAGT   | AGCCACTICA   | 720    |
|     | CCATCTTCAC    | CTCAGCCAGC . | AGAAACCCAC    | CCTACGACAC   | TGCAGGGAGC   | AATAAGGAGA   | 780    |
|     | GAACCCACCA    | GCTCACCATT   | GTACTCTTAC    | ACAACAGATG   | GGAATGACAC   | CGTGACAGAG   | 840    |
| 10  | TCTTCAGATG    | GCCTTTGGAA   | TAACAATCAA    | ACTCAACTGT   | TCCTAGAACA   | TAGTCTACTG   | 900    |
| 10  | ACGGCCAATA    | CCACTAAAGG   | AATCTATGCT    | GGAGTCTGTA   | TTTCTGTCTT   | GGTGCTTCTT   | 960    |
|     | GCTCTTTTGG    | GTGTCATCAT   | TGCCAAAAAG    | TATTTCTTCA   | AAAAGGAGGT   | TCAACAACTA   | 1020   |
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|     | CAAGCAGAAG    | ACAATATCTA   | CATTGAGAAT    | AGTCTTTATG   | CCACGGACTA   | AGACCCAGTG   | 1140   |
| 1.5 | GTGCTCTTTG    | AGAGTTTACG   | CCCATGACTG    | CAGAAGACTG   | AACAGGTATC   | AGCACATCAG   | 1200   |
| 15  | ATGTCTTTTA    | GACTCCAAGA   | CAATTTTTCT    | GTTTCAGTTT   | CATCTGGCAT   | TCCAACATGT   | 1260   |
|     | CAGTGATACT    | GGGTAGAGTA   | ACTCTCCCAC    | TCCAAACTGT   | GTATAGTCAA   | CCTCATCATT   | 1320   |
|     | AATGTAGTCC    | TAATTTGTTT   | TGCTAAAACT    | GGCTCAATCC   | TTCTGATCAT   | TGCAGAGTTT   | 1380   |
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| 20  |               | 302 Protein  |               |              |              |              |        |
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|     | SPEIALL       | TOWNSTOWN    | ATTAKTOTTA    | DI.DDONUEDU  | ATCDCCCODA   | ETHPTTLQGA   | 240    |
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| 30  | ULLALICUTT    | VARABBRREAL  | OOLSVSESSI.   | QIKALQNAVE   | KEVOAEDNIY   | IENSLYATD    | • • •  |
| 50  | ADDIVIDUOATI  | ARRITERADO   | QQDSVSESSB    | Ø1100DØ11110 |              |              |        |
|     | Sec ID NO.    | 303 DNA sec  | mience        |              |              |              |        |
|     |               | d Accession  |               | 044.1        |              |              |        |
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|     | î             | i.           | î^            | ĭ -          | 1            | ī            |        |
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|     | ACCGCTCCGG    | CCCCCCCCCCC  | CAGACCAAGA    | GGGAAGAAGC   | ACAGAATTCC   | TCAACTCCCA   | 120    |
| 40  | COCOCCOCA TO  | CACTARGACC   | AAATCCTCC     | TGGGACTCAT   | GTCTTCCGTG   | GIGGCCCCGG   | 180    |
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|     |               |              |               |              |              | GTGGAGGCCC   | 300    |
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|     | TOGACCTGGC    | CAACGTCTGG   | CGGTTCCCCT    | ACCTGTGCTA   | CAAAAATGGT   | GGCGGTGCCT   | 420    |
| 45  | TOCTCGTCCC    | CTACCTCCTC   | TTCATGGTCA    | TTGCTGGGAT   | GCCACTTTTC   | TACATGGAGC   | 480    |
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|     | TGAAAGGTGT    | GGGCTTCACG   | GTCATCCTCA    | TCTCACTGTA   | TGTCGGCTTC   | TTCTACAACG   | 600    |
|     | TCATCATCSC    | CTGGGCGCTG   | CACTATCTCT    | TCTCCTCCTT   | CACCACGGAG   | CTCCCCTGGA   | 660    |
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| 80  | GATGCGTGG     | C TCCCAGCAG  | A GGCCGTAAA   | T TGAGCGTTC  | A GITGACACA  | T TGCACACACA | 2580   |
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Seq ID NO: 307 DNA sequence

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| 5   | QLNHTGPQQD               | RRRPYGCVLR<br>PRLYWQGGPA<br>GICSPASRSI<br>VPP | LGRSPLHGPE | LDKGQLRIHR        | DGIYMVHIQV | TLAICSSTTA               | 60<br>120<br>180 |
| 10  | Seq ID NO:<br>Nucleic Ac | 311 DNA sec<br>id Accession<br>mence: 135     | #: Eos se  | quence            |            |                          |                  |
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|     | 1                        | 11  | 21<br>     | 31<br>            | 41<br>     | 51<br>                   |                  |
| 15  |                          | AAGGACCCTA                                    |            | GATCTGGACC        |            |                          | 60               |
| 13  |                          | GATATGACCC<br>ACCCGGTGGA                      |            |                   |            |                          | 120<br>180       |
|     |                          | TGGTGAAAGG                                    |            |                   |            |                          | 240              |
|     |                          | ACTCATCTGA                                    |            |                   |            |                          | 300              |
| 20  |                          | TGGGTCCTGA<br>TGATGGACAT                      |            |                   |            |                          | 360<br>420       |
|     | CCGACAGTTC               | TCATTCACCA                                    | AATCCTCCAG | CAGACTGAGA        | GGACCTCTGG | GAAAGTCTGG               | 480              |
|     |                          | GACTGTGCAT<br>GGGCCATCAA                      |            |                   |            |                          | 540              |
| 0.5 |                          | AAAACCTAGT                                    |            |                   |            |                          | 600<br>660       |
| 25  | CTCAATATAC               | TGTCAAGTGA                                    | TAGCTATTCT | TTGTTTGAAG        | CTGCCTTGTT | TTGTCCTTTG               | 720              |
|     | CCAGCCACCA               | TCCCGATCCT<br>TCATCGGGAT                      | AATGGTCTTT | TGTGCGGCGT        | ACGCCTTTTT | CATTCTGGGG               | 780<br>840       |
|     | GCCAAGCTCA               | ATTCAGCTTT                                    | CCGAAGGTCA | <b>GCAATTTTGG</b> | TGACAGACAA | GCGAGTTCAG               | 900              |
| 30  |                          | AGTTTCTGAC                                    |            |                   |            |                          | 960              |
| 50  |                          |   |            |                   |            | AAAAGCTGGA<br>CATCGTGCTG | 1020<br>1080     |
|     | ACATTATCCT               | GCCACATCCT                                    | CCTGAGACGC | AAACTCACCG        | CACCCGTGGC | ATTTAGTGTG               | 1140             |
|     |                          | TTAATGTAAT<br>CGAATGTCTC                      |            |                   |            | CATCAAAGCA               | 1200             |
| 35  |                          | TCACCCAACC                                    |            |                   |            |                          | 1260<br>1320     |
|     |                          |   |            |                   |            | GAACCAGAAA               | 1380             |
|     |                          |   |            |                   |            | ACCAGCCAAG<br>CAGCATAAGC | 1440<br>1500     |
| 40  | TTTGTGGTGA               | GAAAGTTATG                                    | TCGTTATCCC | GAAGCCCAGC        | TCCTGGCTTG | GAGGTGGCCA               | 1560             |
| 40  |                          |   |            |                   |            | TGCTAAAGAC               | 1620             |
|     |                          |   |            |                   |            | TCAAAGGGCA<br>AAAGAGCTCC | 1680<br>1740     |
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| 45  |                          |   |            |                   |            | AGAAAACATA<br>CTGTGGCCTC | 1860             |
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|     | AACCTCTCTG               | GGGGGCAGAG                                    | GCAGAGGATT | AGCCTGGCCC        | GCGCTGTCTA | CTCCGACCGT               | 2040             |
|     |                          |   |            |                   |            | GAAGCACGTC<br>GACCCACCAG | 2100<br>2160     |
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| •   | AAGGGAACCC               | ACAAGGAGTT                                    | AATGGAGGAG | AGAGGGCGCT        | ATGCAAAACT | GATTCACAAC               | 2280             |
|     |                          |   |            |                   |            | GGTGGAAGCC               | 2340<br>2400     |
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| 55  |                          |   |            |                   |            | CAACAGGACC               | 2520<br>2580     |
|     |                          |   |            |                   |            | CTTCACCAAG               | 2640             |
|     |                          |   |            |                   |            | CTTAAAGAGC               | 2700             |
| 60  | ATGGACGAGO               | TGGATGTGAG                                    | GACTECCACT | CACGCAGAGA        | ACTITCTGCA | TTCCAAGGAT<br>GCAGTTTTTT | 2760<br>2820     |
|     | ATGGTGGTGT               | TTATTCTCGT                                    | GATCTTGGCT | GCTGTGTTTC        | CTGCTGTCCT | TTTAGTCGTG               | 2880             |
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|     | CAGGGCCTGG               | GCATCATTCA                                    | CGCCTATGGC | AAGAAGGAGA        | GCTGCATCAC | CTATACTICA               | 3000<br>3060     |
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| 70  |                          |   |            |                   |            | GATTGTTGGA               | 3360             |
| 70  | AGAACAGGTI               | CCGGAAAGTC                                    | ATCGTTAGGA | ATGGCTTTGT        | TTCGTCTGGT | GGAGCCAGCC<br>AGACCTCAGA | 3420<br>3480     |
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|     | TTGGATCCCI               | TTGAGAGTCA                                    | CACCGATGAG | ATGCTCTGGC        | AGGTTCTGGA | GAGAACATTC               | 3600             |
| 75  |                          |   |            |                   |            | AGAAAATGGA<br>TCTCCGTAAT | 3660<br>3720     |
|     | TCAAAGATCA               | TTCTCCTTGA                                    | TGAAGCCACC | GCCTCTATGG        | ACTCCAAGAC | TGACACCCTG               | 3780             |
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| 80  | GCAGAAGTCA               |   |            |                   |            |                          |                  |
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Seq ID NO: 312 <u>Protein sequence</u> Protein Accession #: Eos sequence

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PCT/US02/36810 WO 03/042661

120

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1077

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|    | CACAAAAGGA AACAGACACA GAAA                              | GAGGTT ACTGTGCTGC                          | TAGAACATCA GA                    | AGAAGGTA 420                       |
| 10 | TCGAAGACAA GACACACTAG AGA                               | ACTOTT CTCAGGCGTG                          | CCAAGAGGAG ATC                   | GGGCACCT 480<br>AACAAGTT 540       |
| 10 | ATTCCTTGCT CTATGCAAGA GAA'GAATCTGATG CAGCACAGAA CTA'    | PACTETE GGCCCTTTCC                         | TAAGTGGACG TG                    | GAGTTGAT 600                       |
|    | AAAGAACCTT TAAATTTGTT TTA                               | PATAGAA AGAGACACTG                         | GAAATCTATT TI                    | GCACTCGG 660                       |
|    | CCTCTCCATC GTGAAGAATA TGA                               | GTTTTT GATTTGATTG                          | CTTATGCGTC AA                    | CTGCAGAT 720                       |
| 15 | GGATATTCAG CAGATCTGCC CCT                               | CCACTA CCCATCAGGG                          | TAGAGGATGA AA                    | ATGACAAC 780<br>GACCTGGT 840       |
| 15 | CACCCTGTTT TCACAGAAGC AAT<br>ACTACAGTGG GGGTGGTTTG TGC  | PTATAAT TITGAAGITT                         | CGGACACAAT GC                    | ATACGCGC 900                       |
|    | CTCABATACA CCATTTTCCA CCA                               | BACACCA AGGTCACCTG                         | GGCTCTTTTC TG                    | TGCATCCC 960                       |
|    | AGCACAGGGG TAATCACCAC AGT                               | CTCTCAT TATTTGGACA                         | GAGAGGTTGT AG                    | ACAAGTAC 1020                      |
| 20 | TCATTGATAA TGAAAGTACA AGA<br>ACTTGTATCA TAACAGTAAC AGA  | CATGGAT GGCCAGTTTT                         | TTGGATTGAT AG                    | GCACATCA 1080<br>AAAATGCT 1140     |
| 20 | ACTTGTATCA TAACAGTAAC AGA<br>TATGAAGCAT TTGTAGAGGA AAA  | TCAAAT GATAATGCAC                          | TCTTACGAAT AC                    | CTATAGAA 1200                      |
|    | CATABCCATT TAATTAACAC TGC                               | CAATIGG AGAGICAATI                         | TTACCATTTT AA                    | AGGGAAAT 1260                      |
|    | CARATTCARC ATTTCARATT CAG                               | CACAGAC AAAGAAACTA                         | ATGAAGGTGT TO                    | TITCIGIT 1320                      |
| 25 | GTAAAGCCAC TGAATTATGA AGA<br>GAAGCGCCAT TTGCTAGAGA TAT  | AAACCGT CAAGTGAACC                         | TGBACAGAGC CT                    | TAAACAAT 1380<br>TGGTTACA 1440     |
| 23 | CTTCATGTGA GGGATCTGGA TGA                               | GGGGCCT GAATGCACTC                         | CTGCAGCCCA AT                    | ATGTGCGG 1500                      |
|    | ATTABAÇADA ACTTACCACT CCC                               | GTCAAAG ATCAACGGCT                         | ATAAGGCATA TG                    | ACCCCGAA 1560                      |
|    | ANTEGAANG GCAATGGTTT AAG                                | GTACAAA AAATTGCATG                         | ATCCTAAAGG TI                    | GGATCACC 1620                      |
| 30 | ATTGATGAAA TTTCAGGGTC AAT<br>CCCAAAAATG AGTTGTATAA TAT  | TATAACT TOUAAAATUU                         | ACAAAGATGA TA                    | AGATCATGT 1740                     |
| 30 | ACTEGNACAC TIGCTETERA CAT                               | TGAAGAT GTAAATGATA                         | ATCCACCAGA AF                    | ATACTTCAA 1800                     |
|    | CANTATCIBE TOATTICEAN ACC                               | AAAAATG GGGTATACCG                         | ACATTTTAGC TO                    | STTGATCCT 1860                     |
|    | GATGAACCTG TCCATGGAGC TCC<br>AGTAGACTGT GGAGCCTCAC CAP  | ATTTTAT TTCAGTTTGC                         | CCAATACTTC TO                    | CAGAAATC 1920<br>FATCAGAAA 1980    |
| 35 | AGTAGACTGT GGAGCCTCAC CAP<br>AATGCTGGAT TTCAAGAATA TAG  | CATTCCT ATTACTGTAA                         | AAGACAGGGC CO                    | GCCAAGCT 2040                      |
| 55 | GCAACAAAAT TATTGAGAGT TA                                | TCTGTGT GAATGTACTC                         | ATCCAACTCA G                     | rgrcgrgcg 2100                     |
|    | ACTTCAAGGA GTACAGGAGT AAT                               | ACTTGGA AAATGGGCAA                         | TCCTTGCAAT AT                    | TTACTGGGT 2160                     |
|    | ATAGCACTGC TCTTTTCTGT ATGGGGAAACGTT TTCCTGAAGA TT       | GCTAACT TTAGTATGTG                         | GAGTTTTIGG IV                    | GCAACTAAA 2220<br>ACAGAAGCA 2280   |
| 40 | CCTGGAGACG ATAGAGTGTG CT                                | TIGCCAAT GGATTTATGA                        | CCCAAACTAC C                     | AACAACTCT 2340                     |
|    | አርርሮአአርርምም ምምርምርናቸልሮ ቸል                                 | NGGGATCA GGAATGAAAA                        | ATGGAGGGCA G                     | GAAACCATT 2400                     |
|    | CARATGATGA AAGGAGGAAA CC                                | AGACCTTG GAATCCTGCC                        | : GGGGGGCTGG G                   | CATCATCAT 2460                     |
|    | ACCCTGGACT CCTGCAGGGG AGGAGTGGCACA GTTTTACTCA AC        | SACACACG GAGGTGGACA                        | ACTGCAGATA C                     | CACACTGGT 2580                     |
| 45 | талалаттал асаталалда аа                                | PTGCATCG ATGTAATCAC                        | B AATGAAGACC G                   | CATGCCATC 2640                     |
|    | CCARGATTAT GTCCTCACTT AT                                | AACTATGA GGGAAGAGG                         | L TCTCCAGCTG G                   | TTCTGTGGG 2700                     |
|    | CTGCTGCAGT GAAAAGCAGG AA                                | GAAGATGG CCTTGACTT                         | T TTAATAAATT T                   | GGAACCCAA 2760<br>AATTAGGTC 2820   |
|    | ATTTATTACA TTAGCAGAAG CA<br>TTTGTCAGAC ATTCTGGAGG TT    | TGCACAAA GAGATAATG<br>TCCAAAAA TAATATTGT   | A AAGTTCAATT T                   | CAACATGTA 2880                     |
| 50 | TGTATATGAT GATTTTTTTC TC                                | AATTTTGA ATTATGCTAG                        | C TCACCAATTT A                   | TATTTTTAA 2940                     |
|    | AGCCAGTTGT TGCTTATCTT TT                                | CCAAAAAG TGAAAAATG:                        | r taaaacagac a                   | ACTGGTAAA 3000                     |
|    | TCTCAAACTC CAGCACTGGA AT<br>GATATTTTAG TAATAAATAT GC    | TAAGGTCT CTAAAGCAT                         | C TGCTCTTTT T                    | TTTTTTACG 3060<br>GTTATGCTA 3120   |
|    | ATATCACATT ATTATGTATT CA                                | CTTTAAGT GATAGTTTA                         | а алалталаса а                   | GAAATATTG 3180                     |
| 55 | AGTATCACTA TGTGAAGAAA GI                                | TTTGGAAA AGAAACAAT                         | 3 AAGACTGAAT T                   | AAATTAAAA 3240                     |
|    | ATGTTGCAGC TCATAAAGAA TI                                | GGGACTCA CCCCTACTG                         | C ACTACCAAAT T                   | CATTTGACT 3300                     |
|    | TTGGAGGCAA AATGTGTTGA AG<br>GGAAATAAAT GTGTGTGTGT AT    | TGCCCTAT GAAGTAGCA                         | A TITICIATAG G<br>C AATATTTAAA A | SAATATAGIT 3360<br>ATGAAATGAG 3420 |
|    | AACAAAGAGG AAAATGGTAA AA                                | ACTTGAAA TGAGGCTGG                         | G GTATAGTTTG I                   | CCTACAATA 3480                     |
| 60 | GAAAAAAGAG AGAGCTTCCT AG                                | GCCTGGGC TCTTAAATG                         | C TGCATTATAA C                   | TGAGTCTAT 3540                     |
|    | GAGGAAATAG TTCCTGTCCA AT                                | TTGTGTAA TTTGTTTAA                         | A ATTGTAAATA A                   | AATTAAACTT 3600<br>SCTTTGCAGT 3660 |
|    | TTCTGGTTTC TGTGGGAAGG AF                                | ACAAGTTA GTAGCAAAC                         | T GGGGAATACT (                   | GCTGCAGCT 3720                     |
|    | GGGGTTCCCT GCTTTTTGGT AC                                | CAAGGGTC CAGAGATGA                         | G GTGTTTTTT (                    | CGGGGAGCTA 3780                    |
| 65 | атаасааааа саттттаааа ст                                | TACCITIA CIGAAGITA                         | A ATCCTCTATT O                   | CTGTTTCTA 3840                     |
|    | TTCTCTCTTA TAGTGACCAA CA<br>AGTTTAGAGG CTAGAGGGAG C     | ATCTTTTTA ATTTAGATO                        | C AAATAACCAT (                   | GGGAGATTG 3960                     |
|    | ATTICTCCTTA AACCTAAGCC CO                               | CACAAACTT GACACCTGA                        | T CAGGTCTGGG 1                   | AGCTACAAAA 4020                    |
|    | THE CATTER CICCICACIG C                                 | CTTCTTCT GAGTGGCAT                         | T GGCCTGAATC A                   | AAGGAAAGCC 4080                    |
| 70 | AGGCCTTGTG GGCCCCCTTC T                                 | PROGGETTT CTGCTAAAG                        | C AACACCTCCA (                   | SCAGAGATTC 4140                    |
|    | CCTTAAGTGA CTCCAGGTTT TO<br>CTTTCTCCAG AGAAATTTTA A     | CACCATCC TTCAGCGIG                         | A ATTAATTTT I                    | TATAAAAGAA 4260                    |
|    | ANACATCARG TEGTCATETT A                                 | RAACAGAGG GAACTTTGG                        | G AGAAAGCAGC (                   | CCAAGTAGGT 4320                    |
| ~- | TATTTCTACA CTCAGAGGGC A                                 | ACAGGAAGA TGCAGGCCT                        | T CAAGGGCAAG                     | GAGAGGCCAC 4380                    |
| 75 | ANGGANTATG GGTGGGAGTA A                                 | AAGCAACAT CGTCTGCTT                        | C ATACTTTTTC                     | CTAGGCTTGG 4440                    |
|    | CACTGCCTTT TCCTTTCTCA G<br>CCAACCTCTT CTCTATGGCT C      | ACCARIGGC AACIGCCAT<br>ACCTTATTT GGAGTGAGI | A ATCAAGGAGA                     | CAGAGCTGAC 4560                    |
|    | TOCATOATGA GTCTGAAGGC A                                 | TTTGCAGGA TGAGCCTG                         | VA CTGGTTGTGC .                  | AGAACAAACA 4620                    |
| 00 | AGGCATTCAT GGGAATTGTT G                                 | TATTCCTTC TGCAGCCC                         | C CTTCTGGGCA                     | CTAAGAAGGT 4680                    |
| 80 | CTATGAATTA AATGCCTATC T<br>TGACCCTAAA ATCTATGTGT T      | AAAATTCTG ATTTATTC                         | T ACATTTCTG                      | TITICIAATT 4740                    |
|    | THENCACEGA GTCTCGCTCT G                                 | ACCCACAGG CTGGAGTG                         | CA GTGGCTCCGA                    | TCTCTGCTCA 4860                    |
|    | CTGARAGCTC CGCCTCCCGG G                                 | TTCATGCCA TTCTCCTG                         | CC TCAGCCTCCT                    | GAGTAGCTGG 4920                    |
|    | GACTACAGGC GCCCACCACC A                                 | CGCCCGGCT AATTTTTT                         | ST ATTTTTAATA                    | GAGACGGGGT 4980                    |
|    |   |  |                                  | 70                                 |

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TTCACTGTGT TAGCCAGGAT GGTCTCGATC TCCTGACCTC GTGATCCGCC TGCCTCGGCC 5040
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                                                                                    5220
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TGTAACCAGA AGCCAGTTTT ATCTAACGGC TACTGAAACA CCCACTGTGT TTTGCTCACT
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                                                                                    5280
                                                                                    5340
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                                                                                     5400
        TCAAAGAGCA ACCAGTATCA CTTCCCTGTT TATAAAACCT CTAACCATCT CTTTGTTCTT
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        TGAACATGCT GAAAACCACC TGGTCTGCAT GTATGCCCGA ATTTGTAATT CTTTTCTCTC
                                                                                    5520
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        AAATGAAAAT TTAATTTTAG GGATTCATTT CTATATTTTC ACATATGTAG TATTATTATT
                                                                                     5580
        TCCTTATATG TGTAAGGTGA AATTTATGGT ATTTGAGTGT GCAAGAAAAT ATATTTTTAA
        AGCTTTCATT TTTCCCCCAG TGAATGATTT AGAATTTTTT ATGTAAATAT ACAGAATGTT
                                                                                     5700
        TTTTCTTACT TTTATAAGGA AGCAGCTGTC TAAAATGCAG TGGGGTTTGT TTTGCAATGT
TTTAAACAGA GTTTTAGTAT TGCTATTAAA AGAAGTTACT TTGCTTTTAA AGAAACTTGG
                                                                                    5760
                                                                                     5820
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        CTGCTTAAAA TAAGCAAAAA TTGGATGCAT AAAGTAATAT TTACAGATGT GGGGAGATGT
                                                                                     5880
        AATAAAACAA TATTAACTTG GCTGCTTAAA ATAAGCAAAA ATTGGATGCA TAAAGTAATA
                                                                                     5940
                                                                                     6000
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GTATTAAAAG TATTAGAAGG TGGTTATAAT TGCAGAGTAT TCCATGAATA GTACACTGAC
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                                                                                     6300
        6360
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                                                                                     6420
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                                                                                     6480
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        AAAGCCTTAC ATTTTAATAT AGGTTGAACC AAAATTTCAA TTCCAGTAAC TTCTATTGTA
                                                                                     6600
        ACCATTATIT TIGIGIATGI CIICAAGAAI GIICATIGGA TITTIGITIG TAATAGIAAA
                                                                                     6660
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        GTTGAGAAGC ATGGACACTA GAGCCAGAAT GCTTGGATAT GAATCCTGGA TCTGTCACTT
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        ACTICIGIGI GACCITIGAA AGGCIACITA TITCCICICI TAGCITICIC ATTAAAATCA
                                                                                     6840
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        ADLIRSSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS
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        KTRHTRETYL RRAKRRWAPI PCSMOENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVDK
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                                                                                       240
        PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDTMHTRL KYSILQQTPR SPGLFSVHPS
                                                                                       300
        TGVITTVSHY LDREVVDKYS LIMKVQDMDG QFFGLIGTST CIITVTDSND NAPTFRQNAY
EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKGNE NGHPKISTDK ETNEGVLSVV
KPLNYEENRQ VNLEIGVNNE APPARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI
                                                                                       360
                                                                                       420
                                                                                       480
50
         KENLAVGSKI NGYKAYDPEN RNGNGLRYKK LHDPKGWITI DEISGSIITS KILDREVETP
                                                                                       540
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Coding sequence: 64..2754
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                                                                                       120
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         CTGACCCTCG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG
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         TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCAGTG
                                                                                       300
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                                                                                       360
                                                                                       420
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         ATTCCTTGCT CTATGCAAGA GAATTCCTTG GGCCCTTTCC CATTGTTTCT TCAACAAGTT
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CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTTGATTG CTTATGCGTC AACTGCAGAT
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         GGATATTCAG CAGATCTGCC CCTCCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC
                                                                                        780
         CACCCTGTTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT
ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC
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                                                                                        900
         CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACCTG GGCTCTTTTC TGTGCATCCC
         AGCACAGGCG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC
                                                                                      1020
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         TCATTGATAA TGAAAGTACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA
                                                                                      1080
         ACTTGTATCA TAACAGTAAC AGATTCAAAT GATAATGCAC CCACTTTCAG ACAAAATGCT
                                                                                      1140
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                                                                                      1200
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         GAAAATGGAC ATTTCAAAAT CAGCACAGAC AAAGAAACTA ATGAAGGTGT TCTTTCTGTT
                                                                                      1320
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|    | GTAAAGCCAC   | TGAATTATGA               | AGAAAACCGT   | CAAGTGAACC              | TGGAAATTGG               | AGTAAACAAT                     | 1380         |
|----|--|--------------------------|--------------|-------------------------|--------------------------|--------------------------------|--------------|
|    | GAAGCGCCAT   | TTGCTAGAGA               | TATTCCCAGA   | GTGACAGCCT              | TGAACAGAGC               | CTTGGTTACA                     | 1440         |
|    | GTTCATGTGA   | GGGATCTGGA<br>ACTTAGCAGT | TGAGGGGCCT   | GAATGCACTC              | CTGCAGCCCA<br>ATARCCCATA | TGACCCCGAA                     | 1500<br>1560 |
| 5  | ATTAAAGAAA   | GCAATGGTTT               | AAGGTACAAA   | ARATTGCATG              | ATCCTAAAGG               | TTGGATCACC                     | 1620         |
| 3  | ATTCATCAAA   | TTTCAGGGTC               | AATCATAACT   | TCCAAAATCC              | TGGATAGGGA               | GGTTGAAACT                     | 1680         |
|    | CCCAAAAATG   | AGTTGTATAA               | TATTACAGTC   | CTGGCAATAG              | ACAAAGATGA               | TAGATCATGT                     | 1740         |
|    | ACTGGAACAC   | TTGCTGTGAA               | CATTGAAGAT   | GTAAATGATA              | ATCCACCAGA               | AATACTTCAA                     | 1800         |
| 10 | GAATATGTAG   | TCATTTGCAA               | ACCAAAAATG   | GGGTATACCG              | ACATTTTAGC               | TGTTGATCCT                     | 1860<br>1920 |
| 10 | GATGAACCTG   | TCCATGGAGC<br>GGAGCCTCAC | CAARTITAL    | GATACAGCTG              | CCCGTCTTTC               | ATATCAGAAA                     | 1980         |
|    | AATGCTGGAT   | TTCAAGAATA               | TACCATTCCT   | ATTACTGTAA              | AAGACAGGGC               | CGGCCAAGCT                     | 2040         |
|    | GCAACAAAAT   | TATTGAGAGT               | TAATCTGTGT   | GAATGTACTC              | ATCCAACTCA               | GTGTCGTGCG                     | 2100         |
| 15 | ACTTCAAGGA   | GTACAGGAGT               | AATACTTGGA   | AAATGGGCAA              | TCCTTGCAAT               | ATTACTGGGT                     | 2160         |
| 15 | ATAGCACTGC   | TCTTTTCTGT<br>TTCCTGAAGA | ATTGCTAACT   | CARRACTER               | GAGTTTTTGG               | CACCAACTAAA                    | 2220<br>2280 |
|    | CCTCCACACGIT   | ATAGAGTGTG               | CTCTGCCAAT   | GGATTTATGA              | CCCAAACTAC               | CAACAACTCT                     | 2340         |
|    | AGCCAAGGTT   | TTTGTGGTAC               | TATGGGATCA   | GGAATGAAAA              | ATGGAGGGCA               | GGAAACCATT                     | 2400         |
| 00 | GAAATGATGA   | AAGGAGGAAA               | CCAGACCTTG   | GAATCCTGCC              | GGGGGGCTGG               | GCATCATCAT                     | 2460         |
| 20 | ACCCTGGACT   | CCTGCAGGGG               | AGGACACACG   | GAGGTGGACA              | ACTGCAGATA               | CACTTACTCG                     | 2520<br>2580 |
|    | GAGTGGCACA   | GTTTTACTCA<br>TGCCATCCCA | ACCCCGTCTC   | CTCACTTATA              | ACTATGAGGG               | AAGAGGATCT                     | 2640         |
|    | CCAGCTGGTT   | CTGTGGGCTG               | CTGCAGTGAA   | AAGCAGGAAG              | AAGATGGCCT               | TGACTTTTTA                     | 2700         |
|    | AATAATTIGG   | AACCCAAATT               | TATTACATTA   | GCAGAAGCAT              | GCACAAAGAG               | ATAATGTCAC                     | 2760         |
| 25 | AGTGCTACAA   | TTAGGTCTTT               | GTCAGACATT   | CTGGAGGTTT              | CCAAAAATAA               | TATTGTAAAG                     | 2820         |
|    | TTCAATTTCA   | ACATGTATGT               | ATATGATGAT   | TTTTTTCTCA              | CANADACTCA               | ATGCTACTCA<br>AAAATGTTAA       | 2880<br>2940 |
|    | BACAGACAAC   | TITTTAAAGC               | CAGTIGITGC   | CACTGGAATT              | AAGGTCTCTA               | AAGCATCTGC                     | 3000         |
|    | ար <del>ագրագրարի անհերի անհեր</del> | TTTTACGGAT               | ATTTTAGTAA   | TAAATATGCT              | GGATAAATAT               | TAGTCCAACA                     | 3060         |
| 30 | ATAGCTAAGT   | TATGCTAATA               | TCACATTATT   | ATGTATTCAC              | TTTAAGTGAT               | AGTTTAAAAA                     | 3120         |
|    | ATAAACAAGA   | AATATTGAGT               | ATCACTATGT   | GAAGAAAGTT              | TTGGAAAAGA               | AACAATGAAG                     | 3180<br>3240 |
|    | ACTGAATTAA   | ATTAAAAATG               | CACCCABAAT   | CTCTTGAAGT              | GCCCTATGAA               | CTACTGCACT                     | 3300         |
|    | TCTATAGGAZ   | TATAGTTGGA               | AATAAATGTG   | TGTGTGTATA              | TTATTATTAA               | TCAATGCAAT                     | 3360         |
| 35 | ATTTAAAATT   | AAATGAGAAC               | AAAGAGGAAA   | ATGGTAAAAA              | CTTGAAATGA               | GCTGGGGTA                      | 3420         |
|    | TAGTTTGTCC   | : TACAATAGAA             | AAAAGAGAGA   | GCTTCCTAGG              | CCTGGGCTCT               | TAAATGCTGC                     | 3480         |
|    | ATTATAACTO   | AGTCTATGAG               | GAAATAGTTC   | CTGTCCAATT              | TOTGTAATT                | GTTTAAAATT<br>AATGGAACAG       | 3540<br>3600 |
|    | TAGGETTE   | TAMACTITIC               | TTTCAAGATT   | TCTGCATCCA              | CAAGTTAGT                | GCAAACTGGG                     | 3660         |
| 40 | GAATACTCG  | TGCAGCTGGG               | GTTCCCTGCT   | TTTTGGTAGC              | AAGGGTCCAG               | AGATGAGGTG                     | 3720         |
|    | TETETETETETCCCC  | GGAGCTAATA               | ACAAAAACAT   | TTTAAAAACTT             | ACCTTTACTO               | BAAGTTAAATC                    | 3780         |
|    | CTCTATTGC  | GTTTCTATTC               | TCTCTTATAC   | TGACCAACAT              | CTTTTTAAT                | AAADOTADAT T                   | 3840<br>3900 |
|    | TAACCATGT  | CTCCTAGAGI               | TTAGAGGCTA   | CTARCCCCA               | CAAACTTGA                | CTTACTGAAA<br>C ACCTGATCAG     | 3960         |
| 45 | GTCTGGGAG  | C TACAAAATTI             | CATTTTTCTC   | CTCACTGCCC              | TTCTTCTGAC               | TGGCATTGGC                     | 4020         |
|    | CTGAATCAA  | G GAAAGCCAGG             | CCTTGTGGG    | CCCCTTCTT               | CGGCTTTCTC               | G CTAAAGCAAC                   | 4080         |
|    | ACCTCCAGC  | A GAGATTCCCT             | TAAGTGACT    | CAGGTTTTCC              | ACCATCCTT                | CAGCGTGAATT                    | 4140<br>4200 |
|    | AATTTTTAA  | r cagrirgeri             | CATCAGAG     | AAATTTTAAAA             | ACAGAGGGA                | A AATAGAAATT<br>A CTTTGGGAGA   | 4260         |
| 50 | AAGCAGCCC  | A AGTAGGTTAT             | TTGTACAGT    | CAGAGGGCAAC             | : AGGAAGATG              | C AGGCCTTCAA                   | 4320         |
|    | GGGCAAGGA  | G AGGCCACAAG             | GAATATGGG    | r gggagtaaaf            | GCAACATCG                | I CTGCTTCATA                   | 4380         |
|    | CTTTTTCCT  | A GCCTTGGCA              | TGCCTTTTC    | C TTTCTCAGGC            | CAATGGCAA                | C TGCCATTTGA                   | 4440<br>4500 |
|    | AACCACACA  | G GGATCAGCCA             | TACCICITCION | TAIGGCICAC              | TGCAGGATG                | A GTGAGAAATC<br>A GCCTGAACTG   | 4560         |
| 55 | GTTGTGCAG  | A ACAAACAAG              | CATTCATGG    | 3 AATTGTTGTA            | A TTCCTTCTG              | C AGCCCTCCTT                   | 4620         |
|    | CTGGGCACT  | A AGAAGGTCT              | A TGAATTAAA' | r GCCTATCTA             | TADTOTTAA A              | T TATTCCTACA                   | 4680         |
|    | TTTTCTGTT  | T TCTAATTTG              | CCCTAAAAT    | C TATGTGTTT             | r AGACTTAGA              | C TTTTTATTGC                   | 4740<br>4800 |
|    | CCCCCCCCC  | T CTGCTCACT              | AGACGGAGI    | c receeding             | CATGCCATT                | G GAGTGCAGTG<br>C TCCTGCCTCA   | 4860         |
| 60 | GCCTCCTGA  | G TAGCTGGGA              | CTACAGGCGC   | C CACCACCAC             | 3 CCCGGCTAA              | T TTTTTGTATT                   | 4920         |
|    | TTTAATAGA  | G ACGGGGTTT              | C ACTGTGTTA  | G CCAGGATGG             | r crcgarcrc              | C TGACCTCGTG                   | 4980         |
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|    | CAGA 1GA   | ic concentar             | a. Gargerer  |                         |                          |                                |              |

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| 25 | CGGTCCTTGC<br>TGCTGCCCTT                             | TGCACCTGTG<br>CCCCTTCCCA                             | CCGTCCCCAG<br>CACTGTCCAT<br>TTTCCAATAA                             | AGCTACAGGC<br>TCTTCCTCCC                             | CCCATCTGGT   | CCTAAGTCCC   | 540<br>600                      |
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| 25 | MRASSFLIVV<br>AQEPVKGPVS                             | VFLIAGTLVL<br>TKPGSCPIIL                             | EAAVTGVPVK<br>IRCAMLNPPN   | GQDTVKGRVP<br>RCLKDTDCPG                             | FNGQDPVKGQ<br>IKKCCEGSCG                             | VSVKGQDKVK<br>MACFVPQ                                | 60                              |
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| 45 | CTTGGAGGCG   | GGAGGCGCGG   | AGCAGGAGCC   | CGGCCAGGCG   | CTGGGGAAAG   | TATTCATGGG   | 240                             |
|    | CTGCCCTGGG   | CAAGAGCCAG   | CTCTGTTTAG   | CACTGATAAT   | GATGACTTCA   | CTGTGCGGAA   | 300                             |
|    | TGGCGAGACA   | GTCCAGGAAA   | GAAGGTCACI   | GAAGGAAAGG   | AATCCATIGA   | AGATETTECE   | 360<br>420                      |
|    |  |  |  |  |  | ATAAAGATAG   | 480                             |
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|    | CTTCGCTGTA   | GAGAAGGAGA   | CAGGCTGGTT   | GTTGTTGAAT   | AAGCCACTGG   | ACCGGGAGGA   | 600                             |
|    | GATIGCCAAG   | TATGAGCTCI   | TOGCCACGO  | CORGANICACIO   | CACAAGCCCA   | CAGTGGAGGA<br>AGTTTACCCA                             | 660<br>720                      |
|    | GGACACCTTC   | CGAGGGAGTG   | TCTTAGAGGG   | AGTCCTACCA   | GGTACTTCTC   | TGATGCAGGT   | 780                             |
| 55 |  |  |  |  |  | CTTACTCCAT   | 840                             |
|    | CCATAGCCAA   | GAACCAAAGG   | ACCCACACG  | CCCCATGITC   | CTCCCTGAG  | GGAGCACAGG<br>CACACTGAC                              | 900<br>960                      |
|    | CATCCAGGCC   | ACAGACATGO   | ATGGGGACG  | CTCCACCAC  | ACGCAGTG   | CAGTAGTGGA   | 1020                            |
| 60 | GATCCTTGAT   | GCCAATGACA   | ATGCTCCCAT   | GTTTGACCCC   | CAGAAGTAC  | AGGCCCATGT   | 1080                            |
| 00 | GCCTGAGAAT   | GCAGTGGGC  | ATGAGGTGC  | A GAGGCIGACO<br>TATCATGGGG                           | GICACIGAIC   | TGGACGCCCC<br>GGGACCATTT                             | 1140                            |
|    | TACCATCACO   | ACCCACCCTO   | 3 AGAGCAACC  | GGGCATCCTC   | ACAACCAGG/   | AGGGTTTGGA   | 1260                            |
|    | TTTTGAGGCC   | : AAAAACCAGG   | ACACCCTGT  | CGTTGAAGT  | ACCAACGAGG   | CCCCTTTTGT   | 1320                            |
| 65 | GCTGAAGCTC   | CCAACCTCC  | A CAGCCACCA  | P AGIGGICCAC   | C GTGGAGGATC   | TGAATGAGGC<br>CCACTGGGGA                             | 1440                            |
| 05 | GCCTGTGTGT   | GICCLACCE  | CAGAAGACC  | TGACAAGGA  | AATCAAAAG  | TCAGCTACCG   | 1500                            |
|    | CATCCTGAGA   | GACCCAGCAG   | GGTGGCTAG  | CATGGACCC  | A GACAGTGGG  | AGGTCACAGC   | 1560                            |
|    | TGTGGGCACC   | CICGACOGT  | AGGATGAGC  | A GTTTGTGAGG   | AACAACATC  | r ATGAAGTCAT<br>C TTCTGCTAAC                         | 1620<br>1680                    |
| 70 | ACTGATTGAT   | GTCAATGAC  | C ATGGCCCAG  | CCCTGAGCC  | CCTCAGATC  | A CCATCTGCAA   | 1740                            |
| =  | CCAAAGCCCT   | GTGCGCCAG  | G TGCTGAACA  | r cacggacaa  | G GACCTGTCT  | C CCCACACCTC   | 1800                            |
|    | CCCTTTCCAC   | GCCCAGCTC  | A CAGATGACT  | C AGACATOTA  | C TGGACGGCA  | A CATATGACGA   | 1860<br>1920                    |
|    | GCACCTTTC  | CTGTCTGAC  | C ATGGCAACA  | A AGAGCAGCT  | G ACGGTGATC  | A GGGCCACTGT   | 1980                            |
| 75 | GTGCGACTG  | CATGGCCAT  | G TCGAAACCT  | G CCCTGGACC  | C TGGAAGGGA  | G GTTTCATCCT   | 2040                            |
|    | CCCTGTGCTC   | GGGGCTGTC  | C TEGETETEC  | T GTTCCTCCT  | G CTGGTGCTG  | C TTTTGTTGGT   | 2100<br>2160                    |
|    | GAGAAAGAA(   | CGGAAGATC  | A AGGAGCCCC  | G CGAAGAGGA  | n GANGATGAC<br>C CAGGACTAT                           | A CCCGTGACAA<br>G ACATCACCCA                         | 2220                            |
| 00 | GCTCCACCG  | A GGTCTGGAG  | G CCAGGCCGG  | A GGTGGTTCT  | C CGCAATGAC  | G TGGCACCAAC   | 2280                            |
| 80 | CATCATCCC  | G ACACCCATG  | T ACCGTCCTC  | G GCCAGCCAA  | C CCAGATGAA  | A TOGGCAACTT   | 2340                            |
|    | TATAATTGA  | G AACCTGAAG  | G CGGCTAACA  | C CGACCCCAC  | A GUUUUGUCU  | T ACGACACCCT<br>T CCCTCACCTC                         | 2400<br>2460                    |
|    | CTCCGCCTC  | C GACCAAGAC  | C AAGATTACG  | A TTATCTGAA  | C GAGTGGGGC  | A GCCGCTTCAA   | 2520                            |
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           GGCACGAGGG TITCGTTTC ATGCTTTACC AGAAAATCCA CITCCCTGCC GACCTTAGTT
  70
           TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG
                                                                                                        120
            GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA
                                                                                                        180
            CCCACGCCTC AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC
                                                                                                        240
                                                                                                        300
            CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC
                                                                                                        360
  75
            AATGAATTIG ACACAATTGT CITGCCGGTG CITTATCTCA TTATATTTGT GGCAAGCATC
                                                                                                        420
            TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA
TTCTATCTCA AAAACATAGT GGTTGCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA
                                                                                                        480
                                                                                                        540
            ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT
                                                                                                        600
            TRAGITTIGI TITATGCAAA CATGIATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT
GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC
ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC
                                                                                                        660
  80
                                                                                                        720
                                                                                                        780
            ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAGT
                                                                                                        840
            CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC
                                                                                                        900
            GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC
```

| 5        | AGGCAATTCA COTGGCTGTGT CATTACACTTAG ATTACACTTT COTAGGTCAT CATTACAGATCAC COTGTAGGCCT TTCATTATCC | ITTTTACCTG ACAGGCTTTT ICTTGTCTGC ITTCAAGAAG IGCAAAGTGT ITTATTGTTT | CTTTCTACCA<br>AGATGAATCT<br>GTGTAATGTT<br>GCTGTTCAAA<br>GAGAAGATCG<br>GTTGGAATCG | TATCACTTGT<br>GCACAAAAA<br>TGCCTGGATC<br>AAATCAAATA<br>GAAGTTCGCA                | GCAGAATTCC<br>TCCTATATTA<br>CAATAATTTA<br>TCAGAACCAG<br>TATATTATGA | TTTTACTTTT<br>CTGCAAAGAA<br>CTTTTTCATG<br>GAGTGAAAGC<br>TTACACTGAT               | 1020<br>1080<br>1140<br>1200<br>1260<br>1320<br>1380 |
|----------|--|---|--|--|--|--|--|
| 10       | Seg ID NO:<br>Protein Acc  |   | n sequence<br>P_076404   |  |  |  |  |
| 15<br>20 | MGFNLTLAKL<br>GLAVWIFFHI<br>FYANMYTSIV<br>NGQPTEDNIH<br>ISQSSRKRKH                             | RNKTSFIFYL<br>FLGLISIDRY<br>DCSKLKSPLG<br>NQSIRVVVAV              | KNIVVADLIM<br>LKVVKPFGDS<br>VKWHTAVTYV<br>FFTCFLPYHL                             | TLTFPFRIVH<br>RMYSITFTKV   | DAGFGPWYFK<br>LSVCVWVIMA<br>ILIGCYIAIS<br>DRLLDESAQK               | FILCRYTSVL<br>VLSLPNIILT<br>RYIHKSSRQF<br>ILYYCKEITL                             | 60<br>120<br>180<br>240<br>300                       |
| -        | Seq ID NO:   | 365 <u>DNA se</u><br>d Accession                                  | equence  |  | DQJVKKSSVK   | ********   |  |
| 25       | 1 '  | 11  | 21   | 31   | 41   | 51   |  |
| 30       | GAGGACTTGG<br>TCCTCTGACA<br>CCTCAGGGAG<br>GAGGGCTCCA   | GCCTGATGGG<br>GCAAGGAGGA<br>GCGCTTCCTC<br>GCAGTCAAGA              | TGCACAGGAA<br>GGAGGTGTCT<br>CTCCATTTCC<br>AGAGGAAGAG                             | AAGCCTGATG<br>CCCACAGGCG<br>GCTGCTGGGT<br>GTCTACTACA<br>CCAAGCTCCT<br>AAGGTGGCTG | AGGAGGAGGA<br>CATCAAGTCC<br>CTTTATGGAG<br>CGGTCGACCC               | GACTACCTCC<br>TCCCCAGAGT<br>CCAATTCGAT<br>AGCTCAGCTG                             | 60<br>120<br>180<br>240<br>300<br>360                |
| 35       | CACAAATATC<br>AATTACAAGC<br>TTTGGCACTG<br>CTTGGCCTCT   | GAGTCAAGGA<br>GCTACTTTCC<br>ATGTGAAGGA<br>CGTGCGATAG              | GCCGGTCACA<br>TGTGATCTTC<br>GGTGGACCCC<br>CATGCTGGGT                             | AAGGCAGAAA<br>GGCAAAGCCT<br>GCCGGCCACT<br>GATGGTCATA                             | TGCTGGAGAG<br>CCGAGTTCAT<br>CCTACATCCT<br>GCATGCCCAA               | CGTCATCAAA<br>GCAGGTGATC   | 420<br>480<br>540<br>600<br>660                      |
| 40       | TGGGAAGCGT<br>CCCAGGAAGC<br>CCCGGCAGTG<br>AGCTATGAGA   | TGAGTGTGAT<br>TGCTCACCCA<br>ATCCTGCGCA<br>AGGTCATAAA              | GGGGGTGTAT<br>AGATTGGGTG<br>CTACGAGTTC<br>TTATTTGGTG                             | GTTGGGAAGG<br>CAGGAAAACT<br>CTGTGGGGTT   | AGCACATGTT ACCTGGAGTA CCAAGGCCCA CAAGAGAGCCC                       | CTACGGGGAG<br>CCGGCAGGTG<br>CGCTGAAACC<br>CATCTGCTAC                             | 720<br>780<br>840<br>900                             |
| 45       | Seq ID NO:   | 366 Prote   | in sequence  | 1  | , chorerer   |  |  |
|          | 1  | 11  | 21   | 31   | 41   | 51   |  |
| 50       | PQGGASSSIS<br>HKYRVKEPVT<br>LGLSCDSMLG   | VYYTLWSQFI<br>KAEMLESVII<br>DGHSMPKAAI                            | D EGSSSQEEE!<br>C NYKRYFPVII<br>L LIIVLGVIL                                      | e psssvdpaqi<br>F GKASEFMQVI<br>F KDNCAPEEVI                                     | EFMFQEALKI<br>FGTDVKEVDI<br>WEALSVMGV                              | AAGSSSPPQS<br>KVAELVHPLL<br>AGHSYILVTA<br>VGKEHMFYGE                             | 60<br>120<br>180<br>240                              |
| 55       | PRKLLTQDWV<br>PSLYEEVLGE   |   | / PGSDPAHYE  | F LWGSKAHAE  | L SIRKAINID  | / MLNAREPICY   | 300  |
| 60       | Nucleic Ac   | 367 <u>DNA s</u><br>id Accessionuence: 86.                        | on #: NM_01  | 4400   |  |  |  |
| 00       | 1  | 11  | 21   | 31   | 41   | 51   |  |
| 65       | GACGCCAAGG<br>GATCTGGACT<br>GTGCTACAGG   | GAGCAGGAC<br>GCAGGCTGG<br>TGCGTGCAG                               | G GAGCCATGG<br>C TGCTGCTGC<br>A AAGCAGATG  | A CCCCGCCAGG<br>T GCTGCTTCG<br>A CGGATGCTC                                       | g aaagcaggt<br>C ggaggagcg<br>C CCGAACAAG                          | <br>C ACCCAGGGGG<br>G CCCAGGCCAT<br>C AGGCCCTGGA<br>A TGAAGACAGT                 | 120<br>180<br>240                                    |
| 70       | GAAGTGCGCC<br>CGGACAATTC   | CCGGGCGTG<br>CTCGCTGGCA   | G ACGTCTGCA<br>G TGCSGGGTT<br>C TTCTGGCGT  | C CGAGGCCGT<br>G CGGTTCGGG<br>T CATCCAGCT  | G GGGGCGGTG<br>A CTCCCCGGC<br>G CAGCAATGC                          | G AGACCATCCA<br>A AGAATGACCG<br>G CTCAGGATCG<br>A ATGAGAGTGC                     | 300<br>360<br>420                                    |
|          | ATACCCGCCC<br>GGGTACATCC<br>CTTCGACGGC   | C AACGGCGTG G CCGCCGGTC C AACGTCACC                               | G AGTGCTACA G TGAGCTGCT T TGACGGCAG T GCACTCGG                                   | G CTGTGTGGG A CAACGCCAG C TAATGTGAC A TGGAGTAAC                                  | C CTGAGCCGG<br>C GATCATGTC<br>T GTGTCCTTG                          | G AGGCGTGCCA T ACAAGGGCTG C CTGTCCGGGG T TCACGCTCAG                              | 540<br>600<br>660                                    |
| 75       | TGGCTCCTG'<br>CCCTCGAATC<br>CACATCTGTC<br>GCCAGCGCC  | TGCCAGGGGCCCTTCCCCCTTCTAAACCAGTCAG                                | T CCCGCTGTA G TCCGGCTGC A CCTCGGCCC A CTCCGAGAC                                  | A CTCTGACCT<br>C CCCTCCAGA<br>C AGTGAGACC<br>A GGGAGTAGA                         | C CGCAACAAG<br>G CCCACGACT<br>C ACATCCACC<br>A CACGAGGCC           | A CCTACTTCTC G TGGCCTCAAC A CCAAACCCAT T CCCGGGATGA                              | 780<br>840<br>900<br>960                             |
| 80       | GGAGCCCAGA<br>TCCTGCAAAA<br>ATTGGCAGCA<br>AAATTTCCCC<br>CCCACCACTA                             | G TTGACTGGA A GGGGGGCCC C CTTCTGTTG T CTCACCTAC G GACTGGGCT       | G GCGCCGCTG C AGCAGCCCC G CCGTGGCTG T TCTCTGGCC                                  | G CCACCAGGA CA TAATAAAGG CC TGGTGTCCT CC TGGGTACCC CC TGTTTTTCC                  | C CGCAGCAAT C TGTGTGGCT C CTGTGAGCT C TCTTCTCAT CA ACATTCCCC       | T CAGGGCAGTA C CCACAGCTGG T CTCCACCTGGT C ACTTCCTGTT IA GTATCCCCAG IT ATTCTGGCAG | 1020<br>1080<br>1140<br>1200                         |

| 5  | GGGTGTTCTA<br>TCCTCTTGTG<br>AGGATGCTAA<br>GGTGGGACAA<br>ATCGGTTCCC<br>CTTATGTCTG<br>TTGTATAGTG | ATGTTAGGAC GCTTCCTACT TGGCTCCCCA CATATGTCTT TGTGTGATCA                                      | AGAGTGAGAG<br>CACTTTCTCC<br>CTCTAAGCAC<br>CCTTACTAGA               | AAGTCAGCTG TAGCCAGCCT TGCCTCCCCT CTGTGAGCTC                        | TCACGGGGAA (<br>GGACTTTGGA (<br>ACTCCCCGCA (<br>CTCGAGGGCA (               | EGTGAGAGAG<br>ECGTGGGGTG<br>FCFTTGGGGA<br>EGGACCGTGC   | 1380<br>1440<br>1500<br>1560<br>1620<br>1680         |
|----|--|---|--|--|--|--|--|
| 10 | Seq ID NO:<br>Protein Acc  | 368 <u>Protei</u><br>ession #: N  |  |  |  |  |  |
| 15 | CTEAVGAVET<br>SRALDPAGNE<br>AANVTVSLPV<br>LPPPEPTTVA   | 11<br> <br>AMIWTAGWLL<br>IHGQFSLAVX<br>SAYPPNGVEC<br>RGCVQDEFCT<br>STTSVTTSTS<br>QYPAKGGPQQ | LLLLRGGAQA<br>GCGSGLPGKN<br>YSCVGLSREA<br>RDGVTGPGFT<br>APVRPTSTTK | LECYSCVQKA<br>DRGLDLHGLL<br>CQGTSPPVVS<br>LSGSCCQGSR<br>PMPAPTSQTP | DDGCSPNKMK<br>AFIQLQQCAQ<br>CYNASDHVYK<br>CNSDLRNKTY<br>RQGVEHEASR         | DRCNAKLNLT<br>GCFDGNVTLT<br>FSPRIPPLVR   | 60<br>120<br>180<br>240<br>300                       |
| 20 | Seq ID NO:<br>Nucleic Ac:  | 369 DNA seld Accession  | equence  |  |  |  |  |
| 25 | 1  | 11  | 21   | 31   | 41   | 51   |  |
| 25 | ATGCCGGTGC   | AGCTGACGAC<br>GCATCCTGGC<br>CCTTCGGCCT  | AGCCCTGCGT<br>AGCCTATGTG   | GTGGTGGGCA<br>ACGGGCTACC   | CCAGCCTGTT<br>AGTTCATCCA   | TGCCCTGGCA<br>CACGGAAAAG   | 60<br>120<br>180                                     |
| 30 | CTTTTTGCCT<br>TCCCCGCGGC<br>TTGCGCAAGT<br>GTGGTGGATG   | TCCTGGAGCA GGGGCTCGGT GCCTGCGCTC GCAACCGCCA AGCAGGCCGG                                      | CCGGCGCATG<br>GGCACTGTGC<br>GGCCCAGCGC<br>GGAGGACGCC               | CGACGTGCCG<br>ATTGCCGCAT<br>ATCTCCTTCC<br>TACATGCTGG               | GCCAGGCCCT<br>ACCAGGAGGA<br>CTGACCTCAA<br>ACATCTTCCA                       | GAAGCTGCCC<br>CCCTGACTAC<br>GGTGGTCATG<br>CGAGGTGCTG   | 240<br>300<br>360<br>420<br>480                      |
| 35 | GGTGAGACGG AGCACCTTCT TTCAAGGCCC GATCCAGCCT GTCGGGGGAG   | AGGCCAGCCT CGTGCATCAT TCGGCGATTC GCACCATCGA ATGTCCAGAT                                      | GCAGAGGGC<br>GCAGAAGTGG<br>GGTGGACTAC<br>GATGCTTCGA<br>CCTCAACAAG  | ATGGACCGTG GGAGGCAAGC ATCCAGGTGT GTCCTGGAGG TACGACTCAT             | TGCGGGATGT GCGAGGTCAT GCGACTCTGA AGGATCCCCA GGATTTCCTT                     | GGTGCGGGCC<br>GTACACGGCC<br>CACTGTGCTG<br>AGTAGGGGGA<br>CCTGAGCAGC   | 540<br>600<br>660<br>720<br>780                      |
| 40 | GTGCGGTACT<br>CAGTGTATTA<br>GACTGGTACC   | GGATGGCCTT GTGGGCCCTT ATCAGAAGTT TCCTGAGCCT CCACTAAGTA                                      | CAACGTGGAG GGGCATGTAC CCTAGGCAGC TGGCTACCGA                        | CGGGCCTGCC<br>CGCAACAGCC<br>AAGTGCAGCT<br>ACTAAGTATA               | : AGTCCTACTT:<br>: TCCTCCAGCA<br>: TCGGGGATGA<br>L CCGCGCGCTC              | TGGCTGTGTG<br>GTTCCTGGAG<br>CCGGCACCTC<br>CAAGTGCCTC   | 840<br>900<br>960<br>1020<br>1080                    |
| 45 | TACTTCCGGG TACGAGTCAG TTCTACCGGG   | AGTGGCTCTA TGGTCACGGG GCCGCATCTG  | CAACTCTCTG<br>TTTCTTCCCC<br>GAACATTCTC<br>CTGCTTCCTT               | TGGTTCCATA TTCTTCCTCA CTCTTCCTGC                                   | AGCACCACCT TTGCCACGGT TGACGGTGCA CAGAGATGAT                                | CTGGATGACC<br>TATACAGCTT<br>GCTGGTGGGC<br>CTTCATGTCC   | 1140<br>1200<br>1260<br>1320                         |
| 50 | ATCAACAAAI<br>CTCATTCCTC<br>TGCCAGGACC<br>GGCTGCTAC  | CTGGCTGGGG<br>TGTCCATCTG  | G CACCTCTGGG<br>GGTGGCAGTT<br>A GACAGAGCTA<br>T CCTCATGCTA         | CGAAAAACCA<br>CTCCTGGAGG<br>GCCTTCCTTG<br>TATCTGGCCA               | A TTGTGGTGAA<br>G GGCTGGCCTA<br>G TCTCTGGGGC<br>A TCATCGCCCG               | CATTGCTACC CTTCATTGGC CACAGCTTAT TATACTGTAT GCGATGTGGG   | 1560   |
| 55 | Seq ID NO  |   | ein seguence   | 2  |  |  | •  |
| 60 | 1  | 11  | 21   | 31   | 41   | 51   |  |
| 60 | LFAFLEHRRI<br>VVDGNROED  | M RRAGQALKL   | P SPRRGSVAL<br>L GGTEQAGPF   | C IAAYQEDPD<br>V WRSNFHEAG   | y lrkclrsaqi<br>E GETEASLQE(   | I ILGLHLLIQS R ISFPDLKVVM MDRVRDVVRA R VLEEDPQVGG  | 120<br>180   |
| 65 | VGGDVQILN<br>DWYHQKFLG<br>YFREWLYNS  | K YDSWISFLS<br>S KCSFGDDRH<br>L WFHKHHLWM   | S VRYWMAFNV:<br>L TNRVLSLGY:<br>T YESVVTGFF                        | E RACQSYFGC<br>R TKYTARSKC<br>P PFLIATVIQ                          | V QCISGPLGM<br>L TETPTKYLR<br>L FYRGRIWNII                                 | Y RNSLLQQFLE<br>W LNQQTRWSKS<br>L LFLLTVQLVG<br>3 RKTIVVNFIG   | 300<br>360<br>420                                    |
| 70 | LIPVSIWVA<br>KKPEQYSLA   | V LLEGLAYTA   | Y CODLESETE  | L AFLVSGAIL  | Y GCYWVALLM  | L YLAIIARRCG   | 540  |
| 75 | Nucleic A<br>Coding se   | : 371 <u>DNA s</u><br>cid Accessi<br>quence: 148  | on #: Eos s<br>-7095   |  | 43   | 51   |  |
| 80 | CAAAAAAA<br>CGGCGAGGG<br>CAGCTCCTC<br>CTTGTTGAF  | C ATTTCCTTC G CCGCAGACC T GTGTTTGCC AG AGATTGGCT AC CATGTAATA                               | C CTCCCCTC C TCTGGAAAT C CCTGGATTC C GTCCTATAC AG CCCAAAACP        | C CTCTCCACI G CGAATCCTA G GCTAATGGA LA GGAGCACTG LA TCTCCTATO      | C TGAGAAGCA<br>AA AGCGTTTCC<br>AT ACTACAGAC<br>SA ATCAAAAA<br>CA ATATTGATG | A AACAAACAAI<br>G AGGAGCCGCI<br>T CGCTTGCAT<br>A ACAGAGAAAI<br>A TTGGGGAAAI<br>A AGATCTTACI<br>C ATCATTGGA | 120<br>180<br>180<br>180<br>180<br>180<br>180<br>180 |

|    | AACACATTCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT  | 480              |
|----|--|------------------|
|    | CTCLCCCCAG GAGTTTCAGA AATGGTGTTT AAAGCAAGCA AGATAACTTT TCACTGGGGA  | 540              |
|    | ANATICANTA TOTONTOTO TOGATORGE CATAGITIAG AAGGACAAAA ATTICCACIT  | 600              |
| _  | CACATCCARA TOTACTOCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA  | 660              |
| 5  | GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTTG  | 720<br>780       |
|    | GATTICAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT<br>TTAGATCCAT TCATACTGTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC   | 840              |
|    | AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT  | 900              |
|    | ACACTTAGCA TOTOTGAAAG COAGTTGGCT GTTTTTTGTG AAGTTCTTAC AATGCAACAA  | 960              |
| 10 | TOTOGETTATO TOATGOTGAT GGACTACTTA CAAAACAATT TTCGAGAGCA ACAGTACAAG   | 1020             |
|    | TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAAGGAAG AGATTCATGA AGCAGTTTGT  | 1080             |
|    | AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTTACA  | 1140<br>1200     |
|    | TGGGAAAGAC CTGGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTTGA CAGATGGCTA TCAAGACTTG  | 1260             |
| 15 | CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTITIGA CAGATGGCTA TCAAGACTAC GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA  | 1320             |
| 13 | TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT  | 1380             |
|    | AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAACTG AAGAAATAAT CAAGGAGGAG  | 1440             |
|    | GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA  | 1500             |
| 00 | AACCAAATCA GGAAAAAGGA ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG  | 1560             |
| 20 | ACGARATACA ATGARGCCAA GACTARCCGA TCCCCARCAR GAGGARGTGA ATTCTCTGGA  | 1620<br>1680     |
|    | AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAGTCAC TAAATTAGCC ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG  | 1740             |
|    | CANCETACTT CAGCCTCTTT ANATGATGGC TCTANAACTG TTCTTAGATC TCCACATATG  | 1800             |
|    | AACTTOTOGG GGACTGCAGA ATCOTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG  | 1860             |
| 25 | ACTITATICA CLACITICAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC  | 1920             |
|    | CONNECTOR CONTINUES CANCELLAGIO AND  | 1980             |
|    | GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC  | 2040<br>2100     |
|    | GAAGATTCAA CTTCATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT<br>GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG   | 2160             |
| 30 | AGCTITCTCC AGACTAATTA CACTGAGATA CGTGTTGATG AATCTGAGAA GACAACCAAG  | 2220             |
| 50 | TOTAL CAGGOCAGE GATGECAGAG GGTCCCTCAG TTACAGATCT GGAAATGCCA  | 2280             |
|    | CATTATTCTA CCTTTCCCTA CTTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC  | 2340             |
|    | TOURGEDAY AGGITTEGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCAACCG  | 2400             |
| 35 | GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC<br>ACCCCTTTGT TGCTTGACAA TCAGATCCTC AACACTACCC CTGCTGCTTC AAGTAGTGAT   | 2520             |
| 22 | TOGGCCTTGC ATGCTACGCC TGTATTTCCC AGTGTCGATG TGTCATTTGA ATCCATCCTG  | 2580             |
|    | TCTTCCTATG ATGGTGCACC TTTGCTTCCA TTTTCCTCTG CTTCCTTCAG TAGTGAATTG  | 2640             |
|    | TTTCCCCATC TCCATACAGT TTCTCAAATC CTTCCACAAG TTACTTCAGC TACCGAGAGI  | 2700             |
| 40 | GATARGETGE CETTGEATGE TTETETGECA GTGGTTGGGG GTGATTTGET ATTAGAGECC  | 2760             |
| 40 | AGCCTTGCTC AGTATTCTGA TGTGCTGTCC ACTACTCATG CTGCTTCAGA GACGCTGGAA  | 2820             |
|    | TTTGGTAGTG AATCTGGTGT TCTTTATAAA ACGCTTATGT TTTCTCAAGT TGAACCACCC<br>AGCAGTGATG CCATGATGCA TGCACGTTCT TCAGGGCCTG AACCTTCTTA TGCCTTGTCT   | 2880             |
|    | AGCAGTGATG CCATGATGCA TGCACGTTCT TCAGGGCCIG AACCTTCTTA IGCCTTGCAC<br>GATAATGAGG GCTCCCAACA CATCTTCACT GTTTCTTACA GTTCTGCAAT ACCTGTGCA  | 3000             |
|    | CATTCTGTGG GTGTAACTTA TCAGGGTTCC TTATTTAGCG GCCCTAGCCA TATACCAAT/  | 3060             |
| 45 | CONSIDER CONTRACTOR TO A TOTAL CONTRACTOR ACCURATION TO CONTRACTOR ACCURATION AND ACCURATION ACCURATION AND ACCURATION ACCURATION ACCURATION ACCURATION AND ACCURATION ACCURATION ACCURATION ACCURATION ACCURATION ACCUR | 3120             |
|    | CCTCATCCCC AATCCTCTGC ACCCTCTTCT GATAGTGAAT TTCTTTTACC TGACACAGA   | . 3180           |
|    | COCCEDENCIA COCCEDIACIT TECTTCACCT GETTCEGIAG CEGAATITAC ATATACAAC   | 1 3240           |
|    | TCTGTGTTTG GTGATGATAA TAAGGCGCTT TCTAAAAGTG AAATAATATA TGGAAATGA   | 3 3300<br>3 3360 |
| 50 | ACTGAACTGC AAATTCCTTC TTTCAATGAG ATGGTTTACC CTTCTGAAAG CACAGTCAT<br>CCCAACATGT ATGATAATGT AAATAAGTTG AATGCGTCTT TACAAGAAAC CTCTGTTTC   | 3420             |
| 50 | ATTICIAGCA CCAAGGGCAT GITTCCAGGG TCCCTTGCTC ATACCACCAC TAAGGTTTT   | 3480             |
|    | GATCATGAGA TTAGTCAAGT TCCAGAAAAT AACTTTTCAG TTCAACCTAC ACATACTGT   | C 3540           |
|    | TCTCAGCAT CTGGTGACAC TTCGCTTAAA CCTGTGCTTA GTGCAAACTC AGAGCCAGC  | A 3600           |
|    | TCCTCTGACC CTGCTTCTAG TGAAATGTTA TCTCCTTCAA CTCAGCTCTT ATTTTATGA   | 3660             |
| 55 | ACCICAGCIT CITITAGTAC TGAAGTATTG CTACAACCIT CCTTTCAGGC TTCTGATGT<br>GACACCITGC TTAAAACTGT TCTTCCAGCT GTGCCCAGTG ATCCAATATT GGTTGAAAC   | T 3720<br>C 3780 |
|    | GACACCTIGC TTAAAACIGT TCTTCLAGCT GIGCCCAGIG AICCARIATI GGTTGAAACCCCCAAAGTTG ATAAAATTAG TTCTACAATG TTGCATCTCA TTGTATCAAA TTCTGCTTC  | A 3840           |
|    | AGTGARACA TGCTGCACTC TACATCTGTA CCAGTTTTTG ATGTGTCGCC TACTTCTCA  | T 3900           |
|    | ATRICACTOR CTTCACTTCA AGGTTTGACC ATTTCCTATG CAAGTGAGAA ATATGAACC   | A 3960           |
| 60 | CTTTCTTAN ANACTONANC TTCCCACCAN GTGGTACCTT CTTTGTACAG TAATGATGA  | G 4020           |
|    | TIGITCCAAA CGGCCAATTI GGAGATTAAC CAGGCCCATC CCCCAAAAGG AAGGCATGI   | A 4080           |
|    | TITGCTACAC CIGITITATC AATTGATGAA CCATTAAATA CACTAATAAA TAAGCTTAT<br>CATTCCGATG AAATTTTAAC CTCCACCAAA AGTTCTGTTA CTGGTAAGGT ATTTGCTGG   | A 4140<br>T 4200 |
|    | ATTCCAACAG TTGCTTCTGA TACATTTGTA TCTACTGATC ATTCTGTTCC TATAGGAAA   | T 4260           |
| 65 | COCONTOTTO CONTROLOC TOTTTCTCCC CACAGAGATG GTTCTGTAAC CTCAACAAA  | G 4320           |
| -  | TTGCTGTTTC CTTCTAAGGC AACTTCTGAG CTGAGTCATA GTGCCAAATC TGATGCCGG   | T 4380           |
|    | TINGTGGTG GTGGTGAAGA TGGTGACACT GATGATGATG GTGATGATGA TGATGATGA  | C 4440           |
|    | AGAGGTAGTG ATGGCTTATC CATTCATAAG TGTATGTCAT GCTCATCCTA TAGAGAATC   | A 4500           |
| 70 | CAGGADARGG TRATGARTGA TTCAGACACC CACGADARCA GTCTTATGGA TCAGARTAR<br>CCARTCTCAT ACTCACTATC TGAGARTTCT GARGARGATA ATAGAGTCAC ARGTGTATC   | C 4620           |
| 70 | TCAGACAGTC AAACTGGTAT GGACAGAAGT CCTGGTAAAT CACCATCAGC AAATGGGCT   | A 4680           |
|    | TOCABBEC ACATGATES ABARGAGGA ARTGACATTC AGACTGGTAG TGCTCTGC  | T 4740           |
|    | CCTCTCAGCC CTGAATCTAA AGCATGGGCA GTTCTGACAA GTGATGAAGA AAGTGGATG   | A 4800           |
|    | CCCCAGCTA CCTCAGATAG CCTTAATGAG AATGAGACTT CCACAGATTT CAGTTITGC  | LA 4850          |
| 75 | CACACTARTS ARRESTSC TGATGGGATC CTGGCAGCAG GTGACTCAGA AATAACTC  | T 4920           |
|    | GGATTCCCAC AGTCCCCAAC ATCATCTGTT ACTAGCGAGA ACTCAGAAGT GTTCCACG<br>TCAGAGGCAG AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGT   | M3 EUVU          |
|    | TCAGAGGCAG AGGCCAGTAA TAGTAGCCAT GAGACTCGTA TAGGTCTAGC TAGAGGGT<br>GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCT   | T 5100           |
|    | CTAGTGGTTC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACT  | TT 5160          |
| 80 | TACTTAGAGE ACAGTACATC CCCTAGAGTT ATATCCACAC CTCCAACACC TATCTTTC  | CA 5220          |
|    | ATTTCAGATG ATGTCGGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATT  | FA 5280          |
|    | CATGCAAGTA GTGGGTTTAC TGAAGAATTT GAGACACTGA AAGAGTTTTA CCAGGAAG  | <b>rg</b> 5340   |
|    | CAGAGCTGTA CTGTTGACTT AGGTATTACA GCAGACAGCT CCAACCACCC AGACAACA<br>CACAAGAATC GATACATAAA TATCGTTGCC TATGATCATA GCAGGGTTAA GCTAGCAC   | NG 5400          |
|    | CACARGARTC GATACATAAA TATCGTTGCC TATGATCATA GCAGGGTTAA GCTAGCAC  |                  |

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                                                                                   7020
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         TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KPSRQVPSSY
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                                                                                     360
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         RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND
                                                                                     540
         GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS
                                                                                     600
         ENISOGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWPPSSTDI
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         TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP
                                                                                     720
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                                                                                     780
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         ILPQVTSATE SDKVPLHASL PVAGGDLLLE PSLAQYSDVL STTHAASETL EFGSESGVLY
KTLMFSQVEP PSSDAMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG
                                                                                     900
                                                                                     960
                                                                                    1020
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          SLFSGPSHIP IPKSSLITPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS
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LNASLQETSV SISTKGMPP GSLAHTTIKV FDHEISQVPE NNFSVQPTHT VSQASGDTSL
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                                                                                    1140
          KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP
                                                                                    1200
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                                                                                    1260
          TISYASEKYE PVLLKSESSH QVVPSLYSND ELFQTANLEI NQAHPPKGRH VPATPVLSID
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          EPLATLINKL IHSDEILTST KSSVTGKVFA GIPTVASDTF VSTDHSVPIG NGHVALTAVS
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          ENETSTDFSP ADTNEKDADG ILAAGDSEIT PGFPQSPTSS VTSENSEVFH VSEAEASNSS
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                                                                                    1620
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TADSSNHEDN KHKNRYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA
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                                                                                    1800
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                                                                                    1860
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AKRHAVGPVV VHCSAGVGRT GTYIVLDSML QQIQHEGTVN IPGPLKHIRS QRNYLVQTEE
  80
                                                                                     1920
                                                                                     2040
          OYVFIHDTLY EAILSKETEV LDSHIHAYVN ALLIPGPAGK TKLEKQFQLL SQSNIQQSDY
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NEEKLIIQDF ILBATQDDYV LEVRHFQCPK WPNPDSPISK TFELISVIKE EAANRDGPMI 2220 VHDEHGGVTA GTFCALTTLM HQLEKENSVD VYQVAKMINL MRPGVFADIE QYQFLYKVIL 2280 SLVSTRQEEN PSTSLDSNGA ALPDGNIAES LESLV

5 seq ID NO: 373 <u>DNA sequence</u> Nucleic Acid Accession #: built from NM\_002851 Coding sequence: 148-4518

| 10 | 1          | 11 :                         | 21               |  | 41            | 51   |      |
|----|------------|------------------------------|------------------|--|---------------|--|------|
| 10 | 1          | 1                            |                  |  | CONCORPERA    | 7707770777   | 60   |
|    | CACACATACG | CACGCACGAT                   | CTCACTTCGA       | TCTATACACT   | GCACGAT IAA   | AMCAMACAMA   | 120  |
|    | CAAAAAAAAC | ATTTCCTTCG                   | CTCCCCCTCC       | CTCTCCACTC   | TGAGAAGCAG    | AGGAGCCGCA<br>CCCCCCCA   | 180  |
|    | CGGCGAGGGG | CCGCAGACCG                   | TCTGGAAATG       | CGAATCCTAA   | AGCGTTTCCT    | CGCIIGCAII   | 240  |
| 15 | CAGCTCCTCT | GTGTTTGCCG                   | CCTGGATTGG       | GCTAATGGAT   | ACTACAGACA    | TTCCCCAAAA   | 300  |
| 15 | CTTGTTGAAG | AGATTGGCTG                   | GTCCTATACA       | GGAGCACTGA   | ATCAMAMAM     | ACATCTTACA   | 360  |
|    | AAATATCCAA | CATGTAATAG                   | CCCAAAACAA       | TCTCCTATCA   | CCCNTNNNNC    | AUAICIIACA   | 420  |
|    | CAAGTAAATG | TGAATCTTAA                   | GAAACTTAAA       | TTTCAGGGTT   | ACCTCACTA A   | TOACTACCAT   | 480  |
|    | AACACATTCA | TTCATAACAC                   | TGGGAAAACA       | GIGGAAATTA   | ATCTCACTAA    | TCACTACCGI   | 540  |
| 20 | GTCAGCGGAG | GAGTTTCAGA                   | AATGGTGTTT       | AAAGCAAGCA   | AGAIAACIII    | 1 CAC 1 GOGGA  | 600  |
| 20 | AAATGCAATA | TGTCATCTGA<br>TCTACTGCTT     | TGGATCAGAG       | CATAGITIAG   | AAGGACAAAA    | ATTICCACIT   | 660  |
|    | GAGATGCAAA | TCTACTGCTT                   | TGATGCGGAC       | CGATTTTCAA   | MACCCA CACA   | ACAAAATTTC   | 720  |
|    | GGAAAAGGGA | AGTTAAGAGC<br>CGATTATTGA     | TTTATCCATT       | TIGITIGAGG   | COMMONON      | CCACCACCACCA   | 780  |
|    | GATTTCAAAG | TCATACTGTT                   | TGGAGTCGAA       | AGIGITAGIC   | GIIIIGGGAA    | TOTAL CATTOR   | 840  |
| 25 | TTAGATCCAT | TGACATCTCC                   | GAACCTTCIG       | COMMITTEE  | CIGACAAGIA    | TTTTTABACAT  | 900  |
| 23 | AATGGCTCAT | TCTCTGAAAG                   | TCCCTGCACA       | CONTRACTO  | ACTOGRITOI    | AATGCAACAA   | 960  |
|    | ACAGTTAGCA | TCTCTGAAAG                   | CCAGTIGGCI       | CARACAST   | TOCOLCACO     | ACAGTACAAG   | 1020 |
|    | TCTGGTTATG | AGGTGTTTTC                   | GGACTACTIA       | CAMMACMAIL   | ACATTCATCA    | ACCACTTTGT   | 1080 |
|    | TTCTCTAGAC | CAGAAAATGT                   | CICATACACI       | CCACACAATT   | ATACCAGCCT    | TOTTGTTACA   | 1140 |
| 30 | AGTTCAGAAC | CTCGAGTCGT                   | TOAGGCIGAC       | ATCATTCACA   | ACTTTCCACCT   | TTTTTACCAG   | 1200 |
| 30 | TGGGAAAGAC | GAGAGGACCA                   | TIMIGHTACC       | WIGHTIGHOU WILLIAM TO THE TANK | CACATGGCTA    | TCAAGACTTG   | 1260 |
|    | CAGTIGGATG | TCAATAATTT                   | COTT CCCS ST     | ATCACTTATC   | TTCTTCAGAT    | AGTAGCCATA   | 1320 |
|    | GGTGCTATTC | GCTTATATGG                   | BETACCOMI        | CACCAACTCA   | TTCTCCACAT    | CCTACTGAT  | 1380 |
|    | TGCACTAATG | TTGATCTTTT                   | AAAATACAGC       | BACCAACTGA   | ANCHARTANT    | CARGGROCAG   | 1440 |
| 35 | AATCCTGAAC | AAGACATTGA                   | CCCTGAATTA       | ATTOURACTO   | CALCULATION I | CARGGRECTACA   | 1500 |
| 23 | GAAGAGGGAA | GGAAAAAGGA                   | AGAAGGCGCI       | MIIGIGAMIC   | CIGGIAGAGA    | TOGOATAGGG   | 1560 |
|    | AACCAAATCA | ATGAAGCCAA                   | ACCCCAGATI       | TCIACCACAA   | CACCOACTO     | ATTETERA   | 1620 |
|    | ACGAAATACA | TTCCCAATAC                   | ACTAACCGA        | TOCKCHACAA   | ANCCAGTCAC    | TABATTAGCC   | 1680 |
|    | AAGGGTGATG | ATATTTCCTT                   | VICTIIVAVI       | A CONCINCACO   | AACTGCCACC    | TCACACTGTG   | 1740 |
| 40 | ACAGAAAAA  | CAGCCTCTTT                   | AAATCATCCC       | ACIGIONCIO   | TTOTTAGATO    | TCCACATATG   | 1800 |
| 40 | GAAGGTACTT | GGACTGCAGA                   | AMAIGAIGGC       | ACAGEMETCES  | TABCAGAATI    | TGAGGAGGAG   | 1860 |
|    | AACTTGTCGC | CCAGTTTCAA                   | AICCIIMANI       | CGVGCLGVV  | ATTCTTCAG     | CTCCAGTCCC   | 1920 |
|    | AGTTTATIGA | CTATCCCATT                   | CATCTCTCAC       | NACATATOCCC  | ALCCITATA     | ATTTTCCTCC   | 1980 |
|    | GCAACTTCTC | AGACAATAAC                   | AUTOTOTO         | MACAIAICCC   | ANGOGIAIA:    | COTTOCAGE  | 2040 |
| 45 | GAAAACCCAC | A CTTCATCAGG                 | MUCACARCA        | TONOTANACO   | NATCIGCIA:    | CCACCCAAAT   | 2100 |
| 43 | GAAGATTCA  | CTTCATCAGG<br>CTAGCTCTAC     | TTCAGAAGA        | CONCIAMAGG   | ATCCTICIA:    | * ACCUAGAGAG   | 2160 |
|    | GIGIGGITI  | AGACTAATTA                   | AGACATAAC        | CONCRECE   | AIGIIGGAI     | CACAACCAAG   | 2220 |
|    | AGCTTTCTC  | CAGGCCCAGT                   | CACTGAGATA       | CGIGIIGAIC   | TOTACAGAGA    | r ccanarcca  | 2280 |
|    | TCCTTTTCT  | A CCTTTGCCTA                 | GAIGICACA        | CACCURATOR   | TIMENGATE:    | TACCCCATCC   | 2340 |
| 50 | CATTATTCT  | A CCTTTGCCTA<br>C AGGATTTGGT | CTICCCAAC        | A SOUTH CALL   | . ACTCCCAGA   | T ANCOCCANCOG  | 2400 |
| 30 | TCCAGACAA  | G CAGAGGCCAG                 | CICCACGGI        | . AMCGIGGIAI   | COLOCAGA      | r AGCTGAGGGG   | 2460 |
|    | GTATACAAT  | G AGAAGAAGGC                 | TAATAGIAG        | CHICAGICIC   | TOTOLOGIC     | ר מאריייייאיר  | 2520 |
|    | TTGGAATCO  | G AGAAGAAGGC<br>G TTCTTGTGGG | AGITATACC        | CITGIGATO  | A VARCEALCE   | A GACTITIATO   | 2580 |
|    | TGTCTAGTG  | G AGGACAGTAC                 | TATTCTCAT        | . INCIGGAGG  | CACCTCCAA     | THE PROPERTY OF THE PARTY OF TH | 2640 |
| 55 | TTTTACTTA  | G AGGACAGTAC<br>G ATGATGTCGC | ATCCCCTAG        | A GIIMIMICCA   | T TTCCNAACC   | A TOTTO A  | 2700 |
| 33 | CCAATTTCA  | G ATGATGTUGG                 | AGCAATICC        | A WINNAGONG  | TICCHANGE     | T TTACCAGGAA   | 2760 |
|    | TTACATGCA  | A GTAGTGGGT                  | TACTGAAGA        | T TORGACAC   | COTOCANO      | A CCCAGACAAC   | 2820 |
|    | GTGCAGAGC  | T GTACIGITGA                 | CTTAGGTAT        | T ACAGCAGAC  | T ATRICCARCE  | T TAAGCTAGCA   | 2880 |
|    | AAGCACAAG  | A ATCGATACAT                 | CARACTOCAC       | r GCCIAIGAIG   | TTAGCAGG      | A TGTTGATGGC   | 2940 |
| 60 | CAGCTTGCT  | G AAAAGGATGC                 | * CAAACIGAC      | C CARLETAINIC  | TCAAATCCA     | C AGCTGAAGAT   | 3000 |
| UU | TACAACAGA  | C CAAAAGCTTA                 | ACTUBLISHED A    | CONSCION   | TONTENTAL     | C AAACCTOGTG   | 3060 |
|    | TTCTGGAGA  | A IGAIAIGGG                  | MCMINAIGI        | o madacasco  | C ATCCCACTC   | A GGAGTACGGG   | 3120 |
|    | CAGAAAGGA  | A GONGHAMMI                  | CACACACACA       | , GEGCCIGCC  | T ATTATACTG   | T GAGGAATTTT   | 3180 |
|    | AMCITICIO  | A ACACARARA                  | י מעמימומכע      | C TCCCAGAAA  | G GAAGACCCA   | G TGGACGTGTG   | 3240 |
| 65 | MULCIAMON  | T ATCACTAGA                  | CONCTRCC         | T GACATGGA   | G TACCAGAGT   | A CICCCIGCCA   | 3300 |
| 05 | CTCCTCACAC | T AICACIACA                  | CCCACCTA         | T GCCAAGCGC  | C ATGCAGTGG   | G GCCTGTTGTC   | 3360 |
|    | GIGCIGACC  | n crecreater                 | TECANGLE         | A GGCACATAT  | A TTGTGCTAG   | A CAGTATGTTG   | 3420 |
|    | CACCACIGO  | A GIGCIGGAG                  | I DOMESTICAL     | C ATATTTGGC  | T TCTTAAAAC   | A CATCCGTTCA   | 3480 |
|    | CARACARAM  | AL VARIATION OF VICTORY      | 4 22 CTC 26 CC 4 | ር የአልሞልሞርሞር  | T TCATTCATC   | A TACACIGGIT   | 3540 |
| 70 | CAAAGAAA   | I MILIGGIAC                  | A ANCIGAGGA      | C CTGGACAGT  | C ATATTCATO   | C CTATGTTAAT   | 3600 |
| 70 | GAGGCCATA  | L TINGIAMO                   | C AUCIGAGGI      | n acabaceta  | G MGAAACAAT   | T CCAGCTCCTG   | 3660 |
|    | CCACICCIC  | A IICCIGGAC                  | N CACAGGGA       | T TOTALOGIA  | C TABACCAAT   | G CAACAGGGAA   | 3720 |
|    | AGCCAGICA  | W WININGWOOD                 | r carceceren     | T GAAAGATCA  | A GGGTTGGC    | T TTCATCCCTG   | 3780 |
|    | AAGAATUGA  | TO COLOTTOTA                 | T CHICCOIG       | T TOTATATO   | A TGGGCTAT    | A CCAGAGCAAT   |      |
| 75 | AUTUGAGAA  | N TTACCORCA                  | y Cutchering     | ייי רבינותות שי  | A AGGATTTC    | G GAGGATGATA   | 3900 |
| 15 | GAATTCAT   | A TIMOCOGNIC                 | u CCCICICCI      | YE ATTOCATO  | G GCCAAAACI   | T GGCAGAAGAT   | 3960 |
|    | TGGGACCA   | M AIGCCCAAC                  | A TERROTTAL      | מ הווכנומאו  | T GEGAGAG     | T TAAGGTCACT   | 4020 |
|    | GAATTTGT   | C ACTGGCCAA                  | W TWWWGWIGH      | A PAUGECES   | A ADCTTATA    | T TCAGGACTTT   | 4080 |
|    | CTTATGGC   | IG AAGAACACA                 | W WIGICIAL       | ANTONOOM   | T GCCVCTTAIN  | CA GTGTCCTAAA  | 4140 |
| 80 | ATCTTAGA   | NO CINCACAGO                 | TOWLING:         | TA CITCHUSTS   | C TTATABOT    | T TATAAAAGAA   | 4200 |
| 30 | TGGCCAAA!  | L CAGATAGCC                  | C CHITAGIA       | הלה להלה של האה הלים הלה<br>מהיו איריויומנה  | G AGCATGGA    | G AGTGACGGCA   | 4260 |
|    | CONTOCTOC  | THE CARGOGRAGE               | C PYCCLUTCH.     | יה כזוכתוטתי   | G AAAAAGAA    | AA TTCCGTGGAT  | 4320 |
|    | GUAACTTT   | CT GIGCICIGA                 | T GATCALTA       | TO ATGRICACT   | G GAGTCTTT    | C TGACATTGAG   | 4380 |
|    | GT T.LYCCA | CA THACANAGE                 | T GUICHUIC       | TO AGEOGRAPHICATION  | A GCACAAGG    | CA GGAAGAGAAT  | 4440 |
|    | CAGTATCA   | G. EILICIMLA                 | - WATCHICE       |  |               | 4.005  |      |
|    |            |                              |                  |  |               | • ^^~  |      |

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          Protein Accession #: AAD16433.1
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Seq ID NO: 393 DNA sequence Nucleic Acid Accession #: NM\_006180.1 Coding sequence: 352..2820

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| 10  | CTCTTCGCTC | CGGACCAGCT               | CAGCCTCTGA                            | TAAGCTGGAC | TCGGCACGCC  | CGCAACAAGC               | 240          |
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|     |            | AGCGCGGGGA               |                                       |            |             |                          | 360          |
|     |            | GGCATGGACC               |                                       |            |             |                          | 420          |
| 1.5 | GGCTTCTGGA | GGGCCCCTTT               | CCCCTCTCCC                            | ACGTCCTGCA | AATGCAGTGC  | CTCTCGGATC               | 480          |
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|     | GATCCTGAGA | ACATCACCGA               | AATTTTCATC                            | GCAAACCAGA | AAAGGTTAGA  | AATCATCAAC               | 600          |
|     |            | TTGAAGCTTA               |                                       |            |             |                          | 660          |
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| 20  |            | TGACGAGTTT               |                                       |            |             |                          | 780          |
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| 25  |            | ATATGTATTG               |                                       |            |             |                          | 1080         |
| 25  |            | AGGGCTCCTT               |                                       |            |             |                          | 1140         |
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|     |            | GGAGTAACAC<br>AGATCCCTGT |                                       |            |             |                          | 1860         |
|     |            |                          |                                       |            |             |                          | 1920         |
| 40  |            | ACACATTTGT<br>GAGCCTTTGG |                                       |            |             |                          | 1980         |
| 0   |            | TCTTGGTGGC               |                                       |            |             |                          | 2040         |
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|     |            | AGTTCCTCAG               |                                       |            |             |                          | 2220<br>2280 |
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| ,,  |            | TGGCGTCCCA               |                                       |            |             |                          | 2400         |
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|     |            | ACAGGAAATT               |                                       |            |             |                          | 2580         |
| 50  |            | TCACCTATGG               |                                       |            |             |                          | 2640         |
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|     |            | CCGAGAAGCT               |                                       |            |             |                          | 3000         |
|     |            | CTTTTTGGCA               |                                       |            |             |                          | 3060         |
|     | TTTCTTTTTT | TAAATTTTCT               | TTTTCTTCTT                            | TTTTTTCGTC | TTCCCTGCTT  | CACGATTCTT               | 3120         |
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| 60  |            |                          |                                       |            |             | CAACTAACAA               | 3240         |
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|     | TCCCATCACC | AGAAATGATA               | GCGTGCAGTA                            | GAGAGCAAAG | ATGGCTT     |                          |              |
| 70  | 0 TD 110   | 204 5                    | ,                                     |            |             |                          |              |
| 70  |            | 394 Prote                |                                       |            |             |                          |              |
|     | Procein Ac | cession #: :             | NP_006171.1                           |            |             |                          |              |
|     | 1          | ••                       | 21                                    | 22         | 43          | <b>61</b>                |              |
|     | 1          | 11                       | 21                                    | 31         | 41          | 51                       |              |
| 75  | MOCMERCE   | I AMADE COST             | I I I I I I I I I I I I I I I I I I I | )          | 002110000   | <u> </u>                 |              |
| , 5 |            |                          |                                       |            |             | GIVAFPRLEP               | 60           |
|     |            |                          |                                       |            |             | FLKNSNLQHI               | 120          |
|     | WEIGHWITH  | TOMOCTOCA                | SETTINGUES                            | CKOLMICACO | LIQUEAKSSPD | TQDLYCLNES<br>DVGNLVSKHM | 180          |
|     |            |                          |                                       |            |             |                          | 240          |
| 80  |            |                          |                                       |            |             | FLESPTSDHH<br>PTHMNNGDYT | 300          |
|     |            |                          |                                       |            |             | TNRSNEIPST               | 360          |
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|     |            |                          |                                       |            |             |                          | 200          |

| 5          |                        |  | NCLVGENLLV<br>VVLWBIFTYG | Kigdfgmsrd<br>Kopwyolsnn | VYSTDYYRVG<br>EVIECITQGR | GHTMLPIRWM                   | 660<br>720<br>780 |
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|            |                        | ACCCCCATTC                             |                          |                          |                          |                              | 180               |
| 15         |                        | GTGCCCGGCG                             |                          |                          |                          |                              | 240               |
|            |                        | CCCCCTGTA                              |                          |                          |                          |                              | 300               |
|            |                        | ACTCTTCGCT                             |                          |                          |                          |                              | 360               |
|            |                        | CACCGAGGAG<br>GCGGCCGGTG               |                          |                          |                          |                              | 420<br>480        |
| 20         |                        | CTGGATAAGG                             |                          |                          |                          |                              | 540               |
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|            |                        | CTGGTGCAGC                             |                          |                          |                          |                              | 660               |
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| 25         |                        | AAAATTTGTG                             |                          |                          |                          |                              | 840               |
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| 30         |                        | ACCTAACCTC                             |                          |                          |                          |                              | 1140              |
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|            |                        | AAGCCACACA                             |                          |                          |                          |                              | 1260<br>1320      |
|            |                        | GATCTCTTGT<br>GCATTTTGCA               |                          |                          |                          |                              | 1320              |
| 35         |                        | TCCATTCACT                             |                          |                          |                          |                              | 1440              |
|            |                        | ATTGAATGAG                             |                          |                          |                          |                              | 1500              |
|            |                        | CGGCTGCCTC                             |                          |                          |                          |                              | 1560<br>1620      |
|            |                        | AATTGACGAT                             |                          |                          |                          |                              | 1680              |
| 40         | ATGGAACTGC             | AGCGAATGAC                             | ATCGGGGACA               | CCACGAACAG               | AAGTAATGAA               | ATCCCTTCCA                   | 1740              |
|            |                        | TGATAAAACC                             |                          |                          |                          |                              | 1800              |
|            |                        | GGGATTTTGC<br>CATGAAAGAT               |                          |                          |                          |                              | 1860<br>1920      |
|            | GTGTTGGCCC             | AGCCTCCGTT                             | ATCAGCAATG               | ATGATGACTO               | TGCCAGCCCA               | CTCCATCACA                   | 1980              |
| 45         |                        | GAGTAACACT                             |                          |                          |                          |                              | 2040              |
|            |                        | CACATTTGTT                             |                          |                          |                          | AACAGTCAGC                   | 2100<br>2160      |
|            |                        | AGCCTTTGGA                             |                          |                          |                          |                              | 2220              |
| 50         | AGGACAAGAT             | CTTGGTGGCA                             | GTGAAGACCC               | TGAAGGATG                | CAGTGACAAT               | GCACGCAAGG                   | 2280              |
| 50         |                        | TGAGGCCGAG                             |                          |                          |                          | GTCAAGTTCT<br>AAGCATGGGG     | 2340<br>2400      |
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| 55         |                        |  |                          |                          |                          | AACTGCCTGG                   | 2580              |
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|            |                        |  |                          |                          |                          | GTCGTGTTGT                   | 2760              |
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| 60         |                        |  |                          |                          |                          | GAGGTGTATG<br>C AAGGGCATCC   | 2880<br>2940      |
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| 65         |                        |  |                          |                          |                          | TTGTTCCTTT                   |                   |
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|            |                        |  |                          |                          |                          | GACAAAGGCC                   |                   |
|            |                        |  |                          |                          |                          | AACTAACAAT<br>TATTTCACTT     |                   |
| 70         | AAACTTTGT              | ACTTCTGCT                              | TACAGATAT                | GAGAGTITC                | T ATGGATTCA              | TTCTATTTAT                   | 3540              |
|            |                        |  |                          |                          |                          | T AAAAAAGAAA                 |                   |
|            |                        |  |                          |                          |                          | G AGAAAGAAGA<br>G CTGGTGTCAG |                   |
|            |                        |  |                          |                          |                          | GCACCTTCCC                   |                   |
| 75         | CTGAGGACCT             | TTCTGAGGAC                             | TAAAAAGAC                | r ACTGGCCTC              | T GTGCCATGG              | A TGATTCTTT                  | 3840              |
|            |                        |  |                          |                          |                          | r GAGACACAAG                 |                   |
|            |                        |  |                          |                          |                          | A TAGCACTGGT<br>G AGGTGGATTC |                   |
| 00         |                        | 3 CTCATTTCG                            |                          |                          |                          |                              |                   |
| 80         | n                      | . 300 5                                |                          | _                        |                          |                              |                   |
|            | Seq ID NO<br>Protein A | : 396 Prote                            | AAL67965.1               |                          |                          |                              |                   |
|            |                        |  |                          |                          |                          |                              |                   |
|            | 1                      | 11                                     | 21                       | 31                       | 41                       | 51                           |                   |

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                                                                                          300
        WCIPFTVKGN PKPALOWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT
        LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST
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        DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKDFSMF GFGKVKSRQG
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                                                                                          1260
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## EIYEVPWENR RSLVKSRCQE S

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Seq ID NO: 404 Protein sequence Protein Accession #: NP\_003967.1

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Seq ID NO: 409 <u>DNA sequence</u> Nucleic Acid Accession #: Eos sequence Coding sequence: 1..1746

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|     |    | TTCCACAACA       | ACCACAACCT               | CCAGAGACTC                 | TACCTGTCCA                  | ACAACCACAT              | CTCCCAGCTG                     | 780          |
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| 25  | 5  | ጥጥ/ ነገር የነው ጥረያጥ | TEGECEAACCT              | GCAGAACATC                 | TCCCTGCAGA                  | ACAATCGCCT              | CAGACAGCTC                     | 1140         |
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| 30  | )  | CCCCXCTCCC       | <b>ጥር እጥር እጥር እጥ</b>     | CAATGTCAAC                 | GTTGCTGTTC                  | CAAGCGTCCA              | TGTCCCTGAG                     | 1440         |
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| 4   | U  | GGATTTCCG        | A TTCATACCC              | TGGGCTTCCT                 | COCAGAGGGG                  | CTCCGGGCCT              | AATCCTCCCC                     | 2100         |
|     |    | ACTTACTO         | A CAGOCTGCTC             | ACTTCGTGGG                 | AATAGTTCTC                  | CGCTGAGATA              | GCCCCTCTCG                     | 2160         |
|     |    | CCTABGTATT       | T አጥሮፕልልሮፕፕር             | ATTICCCTTC                 | TTTTGTTTCT                  | CTTGTTTGTC              | CTATGGCTTG                     | 2220         |
|     | _  | ACCCAGCATO       | G TOCCOTCAA!             | TGAAAGTTCT                 | CCCCTTGATT                  | TTCTGCTCCT              | GAAGGCAGGG                     | 2280         |
| 4   | 5  | TONGTO           | T CCTCAAAGAX             | GACTTCAAAC                 | CATTTAACTG                  | GTTTCTTAAC              | AGCCGTCAAT                     | 2340<br>2400 |
|     |    | CAGCCTGGT        | T TTGGGGATG              | TATGAAAGAG                 | AGAAGGAAAA<br>TOTTOTOTOTOTO | ATCATGCCGC              | CAGTTCCTGG<br>GGAAGAAACA       | 2460         |
|     |    | AGACAGAAG        | A GCCGTCATCA             | CTTTTAGAC                  | AAGGATATTI                  | CCAAACTGC               | AACTTTGCTT                     | 2520         |
|     |    | TODADACTT        | T AGCCCTTTA              | GGAATGAAA                  | CATGTAGAA1                  | TTTGGACTT(              | TAAAAACATT                     | 2580         |
| 5   | 0  | ABBATCACC        | ጥ ጥልጥጥልጥ ጥ               | GGATAGAGA                  | A AGAAATCTGG                | TGCCTGGGGG              | 3 TCCCTGTGTT                   | 2640         |
|     |    | CACCCTAG         | A CTTTCTTTT              | AAATTTTAA                  | A TTGAAGCATO                | : TGAAGTGTA             | C STGCAGAAAA                   | 2700<br>2760 |
|     |    | GTGGGAACA        | T GATAGTGTA              | r GGCTTGGTG                | 3 ATTTTCACA                 | ACTGAACAT               | A CCTGTGTAAT<br>C TTTTCCCAGA   | 2820         |
|     |    | CAGCATCTA        | G ACCCAGACC              | 2 AGAGCATCA                | CTGGGACCTC                  | CCCCCCATG               | A GCCAGGACGG                   | 2880         |
| 5   | 5  | TOTOTOTO         | A CTCACCCTC              | T GCAAAGGCC                | C CGTGGCCAGO                | GGTGGAGGA               | G AATATGTGGG                   | 2940         |
| _   | •  | TETECACAC        | C ATCCCAGACAC            | r gregeetea                | A CAGGAGATT                 | TATTATATC               | T GGAGACCCTG                   | 3000         |
|     |    | ACAGACC          | C AGACCTGGG              | G CACCATGGC                | T GGCCAGGTC                 | <b>A GAAGCATCC</b>      | T GACTGCAGAG                   | 3060<br>3120 |
|     |    | GTCCGTGCA        | G CCACACCCT              | C TTCCCTGCC                | A GCAAGTIGIV                | TGCGGCTCA               | T CGGAGGCCCC<br>T TTCATTCTTC   | 3120         |
| 6   | 60 | ACTTACCC         | A GCCTTCTAT              | G GACGIGAIA<br>G CTCAGAGAT | G AGATOCTTT                 | ATTGAAAAC               | G AAGTGTAACG                   |              |
| •   | ,0 | CAATCTAGT        | G TOTTTCTAA              | T GTGGTAAAA                | T TCTCCATCA                 | A CATCACAGT             | C AGCTGGCAGC                   | 3300         |
|     |    | TGAACTTC         | G AATCTCACT              | T ACAGCAGGC                | G ACACGGGGG                 | r acaccgatg             | G GTCACACTGG                   | 3360         |
|     |    | GTCTGGGGG        | C TCCCTGGAG              | C TCCTCCTGC                | G TGTGGTCTG                 | G TTAGGAGTT             | G AGTIGTITGC                   | 3420         |
| -   | 55 | TCCAGGGT         | TA TTCTCCTCC             | T CGAGTCACA                | G TCACACGAA                 | T ACCTGCCTI             | C TCTGGCTTTC<br>C GTGTGTCTTT   | 3480<br>3540 |
| •   | )) | CTGCTATAC        | A CATATICAC              | A TEGELECTEA               | A GARGIIAGG<br>A ATGGAGAAT  | T TCAGGTCTC             | C ACGTCTGCCC                   | 3600         |
|     |    | AGCAAACA         | AC TTCAGCTGA             | C TCCACGGGG                | A TCTGGAAAT                 | C CACGACCAA             | T CCCGATCGGC                   | 3660         |
|     |    | TOTATE           | さい かいいいいいいい              | Y ACABGACAC                | C TGTGCTTTG                 | G AAATCCACC             | A CCAATCCCGA                   | 3720         |
| _   | 70 | TCGGCTCT         | TA TTAGCTCCC             | C GCTCCACAA                | G ACACCTGTG                 | A TCTGGAAAT             | C TACCACCAAT                   | 3780         |
| - 1 | 70 | CCCGATCG         | GC TCTTATTAC             | C TCCCCGCTC                | C ACAAGACAC                 | C ACARARACATO           | C TCCAGGGCCA<br>C TCCAGAGGGC   | 3840<br>3900 |
|     |    | CAGGAGCA         | CG TGCTGACCA             | G TTTTCCCTI                | TO CAGTICCIG                | C ACAAAAAAG             | G AATCTAGGAG                   | 3960         |
|     |    | ACATCACC         | CC CGTCAGAG              | C AAGAGATG                 | C ATCCCCCCA                 | g ggtctcca?             | NG GCATTTCCAC                  | 4020         |
|     |    | እርጥ አጥተርነር፤      | TO COACCTEG              | C GACATGCAC                | C AAGGCTTGC                 | C AGAGCCAA              | LA GGAAGTGAGC                  | 4080         |
| •   | 75 | CCACACCA         | TG GCACATGAG             | C ATCACCCG                 | T GATGGTGGC                 | C TGCTGTGC              | T GGTGCCAACA                   | 4140         |
|     |    | CCCCCATC         | CC GGCCCGTAG             | C CCTCCAGAC                | LA GGAAGCATG                | G GTTTGCCC/             | AC AGACCTGTCG                  | 4200         |
|     |    | GGTGCTCC         | TG TGAGTGGC              | T CCAGATGT                 | TIGIGCATA                   | A ATCTTABO              | EG GCCAGGGCTG                  | 4200         |
|     |    | COTATTCC         | TO CONGTACO              | CA TYPACATTO               | A GCACCTTCC                 | T CTCCAGCC              | AG AGGCTGACCT                  | 4380         |
|     | 80 | CACCCCCA         | CT GTCCTCAG              | AT GACACCAC                | CC AGGAGCACO                | C TAGGTGAG              | 3G GTGAGGGCCC                  | 4440         |
|     | -  | CCTTATGT         | GA ACCTCTTG              | CC TCTTCCTT                | IC TCCCATCAC                | A GTGGTTGG              | AT GGAGCCATTG                  | 4500         |
|     |    | COUTOUT          | THE CHITCAGOG            | GG CCCTTCAA                | CC TCTCTGCAG                | C ATGTTGTC              | IG GCTGAGGAGC                  | 4560         |
|     |    | TACTAGAA         | AA GCTGAGTG              | GA GTCTCCTT                | TO CAACAGGAT                | T CCCGTACA              | GC TCAATTCTCA<br>GA GTTCAGTTTI | 4680         |
|     |    | GGGCTGGA         | MI GWGCCGGC              | GICCCCA                    | ou unactague                |                         |                                |              |

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CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA
        GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCACTA TTTTTAAAAA GTGCTTACTG
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        TIGICITGGG CITICGTCAT TANACCANAG GANATGGANG CCATTCCCCT GITGCTCTCC
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Protein Accession #: BAB84587.1
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                                                                                                300
                                                                                                360
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|     | TGTTGTGAAG C    | TGATTTCCC A                                | ACCGGGAGTG '                 | FCAGCAGCCC C        | CACTACTACG       | GCTCTGAAGT   | 1140       |
|-----|-----------------|--|------------------------------|---------------------|------------------|--------------|------------|
|     | CACCACCAAA A    | TGCTATGTG (                                | CTGCTGACCC (                 | CCAATGGAAA <i>I</i> | ACAGATTCCT       | GCCAGGGAGA   | 1200       |
|     | CTCAGGGGGA C    | CCCTCGTCT (                                | STTCCCTCCA .                 | AGGCCGCATG A        | ACTTTGACTG       | GAATTGTGAG   | 1260       |
| _   | CTGGGGCCGT G    | GATGTGCCC '                                | rgaaggacaa                   | GCCAGGCGTC 7        | PACACGAGAG       | TCTCACACTT   | 1320       |
| 5   | CALIFO CALLEG B | TOTTCAGTC                                  | ACACCAAGGA .                 | AGAGAATGGC (        | CTGGCCCTCT       | GAGGGTCCCC   | 1380       |
|     | AGGGAGGAAA C    | GGGCACCAC                                  | CCGCTTTCTT                   | GCTGGTTGTC A        | ATTTTTGCAG       | TAGAGTCATC   | 1440       |
|     | TCCATCAGCT G    | TAAGAAGAG                                  | actgggaaga '                 | TAGGCTCTGC A        | ACAGATGGAT       | TTGCCTGTGG   | 1500       |
|     | CACCACCAGG G    | TGAACGACA                                  | ATAGCTTTAC                   | CCTCACGGAT A        | AGGCCTGGGT       | GCTGGCTGCC   | 1560       |
|     | CAGACCCTCT G    | GCCAGGATG                                  | GAGGGGTGGT                   | CCTGACTCAA (        | CATGTTACTG       | ACCAGCAACT   | 1620       |
| 10  | TGTCTTTTTC T    | rggactgaag                                 | CCTGCAGGAG                   | TTAAAAAGGG (        | CAGGGCATCT       | CCTGTGCATG   | 1680       |
|     | GGCTCGAAGG C    | BAGAGCCAGC                                 | TCCCCCGACC                   | GGTGGGCATT '        | TGTGAGGCCC       | atggttgaga   | 1740       |
|     | AATGAATAAT T    | TCCCAATTA                                  | GGAAGTGTAA                   | GCAGCTGAGG '        | TCTCTTGAGG       | GAGCTTAGCC   | 1800       |
|     | AATGTGGGAG (    | CAGCGGTTTG                                 | GGGAGCAGAG                   | <b>ACACTAACGA</b>   | CTTCAGGGCA       | GGGCTCTGAT   | 1860       |
|     | ATTCCATGAA      | <b>IGTATCAGGA</b>                          | AATATATATG                   | TGTGTGTATG '        | TTTGCACACT       | TGTTGTGTGG   | 1920       |
| 15  | GCTGTGAGTG      | DADTOTGAG                                  | TAAGAGCTGG                   | TGTCTGATTG          | TTAAGTCTAA       | ATATTTCCTT   | 1980       |
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|     | ATCCCTTCCT      | TTTAGCCTAG                                 | TTCATCCAAT                   | CCTCACTGGG          | TGGGGTGAGG       | ACCACTCCTT   | 2220       |
| 20  | ACACTGAATA      | TTTATATTTC                                 | ACTATTTTA                    | TTTATATTT           | TGTAATTTTA       | AATAAAAGTG   | 2280       |
|     | ATCAATAAAA '    |  |                              |                     |                  |              |            |
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| 0.5 | Protein Acc     | ession #: N                                | P_002649.1                   |                     |                  |              |            |
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| 30  | YCRNPDNRRR      | PMCXAOAGTK                                 | PLVQECMVHD                   | CADGKKPSSP          | PEELKPQCGQ       | KTERPREKII   | 180        |
|     | GGEFTTIENQ      | PWFAAIYRRH                                 | RGGSVTYVCG                   | GSLISPCWVI          | SATHCPIDIP       | KKEDIIVIDG   | 240        |
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|     | PSMYNDPQFG      | TSCRITGFGK                                 | ENSTDYLYPE                   | <b>GPKWIAAKPI</b>   | SHRECQQPHI       | DUCTET DATE  | 360<br>420 |
| 25  | CAADPQWKTD      | SCOGDSGGPL                                 | VCSLQGRMTL                   | TGIVSWGRGC          | ALKOKPGVYT       | RVSHPLPWIR   | 420        |
| 35  | SHTKEENGLA      | L  |                              |                     |                  |              |            |
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|     | Seq ID NO:      | 415 DNA 8                                  |                              | 1433 1              |                  |              |            |
|     | Nucleic Aci     |  |                              | 1422.1              |                  |              |            |
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|     | 0000111001      | 1<br>2220000000000000000000000000000000000 | CCATCACACC                   | CAGGOGCTTC          | ACACAACCTA       | AGAAAAGCAC   | 60         |
|     | CGCCAAAGGA      | AAAGCCCCTT                                 | GON I GHOUSE                 | CAGGCGCIIC          | CACCACCCC        | CCCAGACTGC   | 120        |
| 45  | CTCTCCGCGC      | GCCCCACCTC                                 | CICCGCCICG                   | CGCICCICCI          | CCCCCCC          | CTCGGCCCGC   | 180        |
| 73  | GCTCCGGCCG      | CACCCCTCTC                                 | CATCCACCCA                   | GCCCGCCCC           | COGGCTCCTG       | GAACGGAGCC   | 240        |
|     | GACCIGCCCC      | CARCCCICIC                                 | CATGGAGGCA                   | ATCTTABTAT          | TTGCCAGTG        | TGCCTGCAAA   | 300        |
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|     | AATGIGACAT      | COMMENCACO                                 | TO CALCULATION OF THE STREET | ATTCATTCAA          | GTGATCCTG        | CTTCCAAATT   | 420        |
| 50  | CIGAMAGAGI      | COLLING                                    | TAGADAGOGT                   | י ארדיטידוריטידי    | TGTCCTCGG        | GAAGAGAAGT   | 480        |
| 50  | TIGGMGGMIG      | TACTTTCCA                                  | CACTGAGAAC                   | CAAGAAAAGA          | AGAAAATATI       | TGTCTTTTTG   | 540        |
|     | TITACCATAT      | CARRETTE                                   | DADGAAAG                     | CATACTAAAG          | AAAAAGTTCT       | AAGGCGCCC    | 600        |
|     | AACACAACAAA     | CHARGGICCI                                 | TOTAL CARROLL OF             | ATGCTAGAAA          | ACTCCTTGG        | TCCTTTTCCA   |            |
|     | WAGWGWAGWI      | ANCACCUTCA                                 | ATCTCACAC                    | CCCAAAACT           | ATACCATATA       | CTATTCCATA   | 720        |
| 55  | ACACCTCCTC      | CACTTGACC                                  | AGAACTCG                     | AATTTATTTT          | ATGTGGAGAG       | AGACACTGGA   | 780        |
| 55  | ADROGICCIO      | CTACTCCTC                                  | TOTAGATOG                    | GAGCAGTATG          | AATCTTTTG        | GATAATTGCC   | 840        |
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|     | CACCATGAAA      | ATGATAACT                                  | CCCAATTTT                    | CACAGAAGAAA         | CTTATACTT        | TACAATTTTT   | 960        |
|     | CANANTTYCA      | CAGTGGGCAG                                 | TACTGTGGG                    | CAAGTGTGTG          | CTACTGACA        | AGATGAGCCT   | 1020       |
| 60  | GACACGATGC      | ACACACGCC                                  | CAAGTACTC                    | CATCATTGGGG         | AGGTGCCAC        | CATCACCCACC  | 1080       |
| ••• | CTATTTTCTA      | TGCATCCAA                                  | TACAGGCGTY                   | ATCACCACAL          | CATCATCTC        | A GCTAGACAGA | 1140       |
|     | GAGTTAATTG      | ACAAGTACC                                  | GTTGAAAAT                    | A AAAGTACAAC        | ACATGGATG        | 3 TCAGTATTTT | 1200       |
|     | GGTCTACAGA      | CAACTTCAA                                  | TTGTATCAT                    | r aacattgat(        | ATGTAAATG        | a ccactigcca | 1260       |
|     | ACATTTACTC      | GTACTTCTT                                  | A TGTGACATC                  | A GTGGAAGAA         | A ATACAGTTG      | A TGTGGAAATC | 1320       |
| 65  | TTACCACTTA      | CTGTTGAGG                                  | TAAGGACTT.                   | A GTGAATACT(        | 3 CTAACTGGA      | G AGCTAATTAT | 1380       |
|     | ACCATTTTAA      | AGGGCAATG                                  | a aaatggcaa                  | TTTAAAATTO          | <b>TAACAGATG</b> | C CAAAACCAAI | 1440       |
|     | CANCCACTTC      | THYCHCTAG                                  | TAAGCCTTT                    | G AATTATGAAG        | 3 AAAAGCAAC      | A GATGATCTTG | 1500       |
|     | CAAATTGGTG      | TAGTTAATG                                  | A AGCTCCATT                  | T TCCAGAGAG         | G CTAGTCCAA      | G ATCAGCCATG | 1560       |
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| 70  | CCAATACAGE      | CTGTTCGCA                                  | T GAAAGAAAA                  | T GCAGAAGTG         | G GAACAACAA      | G CAATGGATAT | 1680       |
|     | TATATATA        | ACCCAGAAA                                  | C AAGAAGTAG                  | C AGTGGCATA         | a ggtataaga      | A ATTAACTGAT | 1740       |
|     | CCAACAGGG       | r GGGTCACCA                                | T TGATGAAAA                  | T ACAGGATCA         | A TCAAAGTTT      | T CAGAAGCCTC | 1800       |
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|     | CAAGGAGGG       | A GAACATGTA                                | C GGGGACACT                  | G GGCATTATA         | C TTCAAGACG      | T GAATGATAA( | 1920       |
| 75  | AGCCCATTC       | A TACCTAAAA                                | A GACAGTGAT                  | C ATCTGCAAA         | C CCACCATGI      | C ATCTGCGGA  | 3 1980     |
|     | ልሞምርምሞርያርዊያ     | TTGATCCTG                                  | A TGAGCCTAT                  | C CATGGCCCA         | C CCTTTGACT      | T TAGTCTGGAG | 3 2040     |
|     | AGTTCTACT       | r CAGAAGTAC                                | A GAGAATGTC                  | G AGACTGAAA         | G CAATTAATO      | a tacagcagc  | A 2100     |
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| 80  | GAAAATGAC       | T GCACACATO                                | G TGTAGATCO                  | A AGGATTGGC         | G GTGGAGGAG      | T ACAACTTGG  | A 2280     |
|     | AAGTGGGCC       | A TCCTTGCAA                                | T ATTGTTGGG                  | C ATAGCATTG         | C TCTTTTGC       | T CCTGTTTAC  | G 2340     |
|     | СТССТСТСТ       | מ הממכידיוניוני                            | G GACGTCTAZ                  | A CAACCAAAA         | G TAATTCCTO      | A TGATTTAGC  | C 2400     |
|     | CAGCAGAAC       | C TAATTGTAT                                | 'C AAACACAGA                 | LA GCTCCTGGA        | G ATGACAAAC      | T GTATTCTGO  | 3 2460     |
|     | AATGGCTTC       | A CAACCCAA                                 | C TGTGGGCGG                  | T TCTGCTCAG         | G GAGTTTGT(      | G CACCGTGGG  | A 2520     |
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| 9         | couring acqu           | 101100. 2                | •••                |                            |                            |                                |              |
|-----------|------------------------|--------------------------|--------------------|----------------------------|----------------------------|--------------------------------|--------------|
|           | 1                      | 11                       | 21                 | 31                         | 41                         | 51                             |              |
|           | 1                      | 1                        | 1                  |                            | 1                          | .1                             |              |
|           | ATGGACACTG             | TGCTGGTGCT               | GCTCCTGGGC         | CTGCAGGCCT                 | TGGCCGGACC                 | CAGTCCGAAG                     | 60           |
| 10        | CCCCACAACG             | P CALCALCALCA            | ACA CTCCCCCC       | ATTGTGTTGA                 | TCACTCTCAC                 | TTTGGTGGCA                     | 120<br>180   |
|           | GCAATTGTCA             | GCCTAATGTA               | CGGTATCAAG         | AAGGCCTGCC                 | AGTTCCGGAG                 | CGAGATGAGT                     | 240          |
|           | CTGGGGTGTG             | GCTGTGGCTC<br>ACTCTTGTCA | TGTGACCCCT         | TACAGCAGCC                 | CACGTGCTAC                 | TACATTCCAA                     | 300          |
|           | AGCCAGCGCT             | AAACTGGGGA               | AATGAAAGCI         | TCCGATCACA                 | TATTTCCCCT                 | CACTCCAGGC                     | 360          |
| 15        | WAL LAMAGEMENT         | CTATCCCTTT               | TGATCACATT         | GTTCTGCATT                 | CAGGACAAAG                 | ACCICCAGAG                     | 420          |
| 13        | CTCCCTAAAT             | CTACAGAAAT               | CCATGAGCAA         | AAACGCCACT                 | GCAACACCAC                 | ACGCCATTCT                     | 480          |
|           | A A CCCCA B CTC        | ACAAGCCTAC               | AGGCAACTCC         | AAAACTATAG                 | ACCACAAAAG                 | CTCTACAGAT                     | 540          |
|           | AATCATCACC             | CTCCTCCCAC               | TTCTGAAGAA         | AACTCCAGCA                 | ACCAAGGGAA                 | AGACCCAATG                     | 600          |
| 20        | ATCCGGAACC             | AGCGCTCTGT               | TGATCCTGCT         | GACTCCACTA                 | CCACACATAA                 | CTCCACACA                      | 660<br>720   |
| 20        | GGAAAAAAAC             | ATATAACGCC<br>CGGTAACAAG | AGCACCCAAG         | AGCAAAATAA                 | CACCTTTTCGA                | AAAGTCCATG                     | 780          |
|           | GGCAAATCAA             | NTANCACAAG               | TACCAGCTCA         | CATAAGACTA                 | CAACTTCCTT                 | CCACAACTCA                     | 840          |
|           | CCCNNTTCNC             | AGACCAAGCA               | AAAAAGCACA         | TCTTTTCCAG                 | AAAAAATCAC                 | AGCAGCCTCA                     | 900          |
|           | *******                | * ACAAGACCAC             | AGGAACCCCA         | GAAGAGTCAG                 | AAAAAACTGA                 | AGATTCCAGA                     | 960          |
| 25        | ACAACAGTTG             | CCTCAGACAA               | GCTCCTGACA         | AAAACTACAA                 | AAAACATACA                 | AGAGACCATA                     | 1020         |
|           | TORCOORDING            | ACCTCACACA               | ATCTCTAGCA         | GAGCCTACAG                 | AACATGGAGG                 | AAGGACAGCC                     | 1080         |
|           | AATGAGAACA             | ACACACCATO               | CCCAGCAGAG         | CCTACAGAAA                 | ATAGAGAAAG                 | GACAGCCAAT                     | 1140<br>1200 |
|           | GAGAACACCA             | CACTATCCCC               | AGCAGAGCCT         | CAGAAAATA                  | BAGAMAGGAC                 | AGCCAATGAG<br>CAATGAGAAT       | 1260         |
| 30        | AACACCGCAC             | CATTCCCAGC               | CCCTACACA          | CATCCAGAA                  | GGACAGCCA                  | TGAGAACACC                     | 1320         |
| 50        | አሮአሮሮስቸርናና             | CACCAGAGCC               | TACAGAACAT         | ' GGAGAAAGGA               | CAGCCAATG                  | GAACACTACA                     | 1380         |
|           | CCATCCCCAC             | 2 (200200772)            | ' AGAACATGG        | GAAAGGACCC                 | CATTTGCCA                  | TGACAAAACC                     | 1440         |
|           | 3 C3 TC3 TCC7          | P CAGCAGAGTO             | TACAGAACAT         | 'GGAGAAAGGA                | CCCCACTGG                  | CAACGAGAAC                     | 1500         |
|           | 3 CC3 C3 CC3 5         | P CCCCXCCXCX             |                    | AAADADATAA                 | GGACAGCCA                  | TGAGAACACC                     | 1560         |
| 35        | ACACCATCC              | CAGCAGGGCC               | TACAGAAAA          | AGAGAAACGA                 | CAGCCAACG                  | GAAGACCACA                     | 1620<br>1680 |
|           | CTATCCCCAC             | TAGAGCCTAC               | AGAAAATAG          | GAAACAACAC                 | TTCCCAATGAGA               | GACCACACCA<br>GAAAACCACA       | 1740         |
|           | TCCCCAGCAG             | 3 AGCCTACAGA             | AAATGGACAA         | A WOONCECK!                | CACTGGCCA                  | TGAGAACACC                     | 1800         |
|           | 3 C3 CC3 PCC           | C CACCAGAGC              | י אמרמממאמאי       | r agagaaaggi               | L CAGCCAATG                | A GAAGACCACA                   | 1860         |
| 40        | CCATCCCA               | C CACAGCCTA              | AGAAAATGG          | A GACAGGACTO               | CTTTGGCCA                  | A TUAGAAGACC                   | 1920         |
| . •       | NC3CCNTCT(             | C TAGCAGAGC              | 'AAAADA''          | r ggacaaagg/               | A CCCCATTIG                | CAATGAGAAG                     | 1980         |
|           | አ ርርስ ርስ ፕሮስ           | T CCTCAGCAG              | CCCTACAGA          | A CACGAAGAA                | A GGACTCCAC                | r ggccaatgag                   | 2040         |
|           | AACACCACA              | C CATCCCCGG              | 2 AGAGCCTAC        | A GAAAATAGA                | 3 AAAGGACAG                | C CAATGAGAAC                   | 2100<br>2160 |
| AE        | ACCACACCA              | T CCCCAGCAG              | GCCTACAGA          | A AATAGAGAA                | A TGACAGCCA                | A CGAGAAGACC<br>A GAAGACCACA   | 2220         |
| 45        | ACACTATTC              | C CAGCAGAGC              | C TACAGAAAA        | T AGAGAAAGG                | CAGCCAATG                  | A TGAGAAAACC                   | 2280         |
|           | TCATCCCCA<br>NCATCATCC | C CAGAGCCIA              | C TACAGAACA        | C GGAGAAAGG                | A CCCCACTGG                | C CAATGAGAAC                   | 2340         |
|           | A CCA CA CTA           | T CCCCAGCAG              | A GCCTACAGA        | A AATAGAGAA                | a ggacagcca                | A TGAGAAGACC                   | 2400         |
|           | 3 (2) ((2) 1000)       | C CACCAGAGC              | C TACAGAAAA        | T AGAGAAAGG                | A CAGCCAATG                | A GAACACCACA                   | 2460         |
| 50        | CONTROCCO              | C CACACOCTA              | C AGAAAATGG        | A GACAGGACT                | C CATTGGCCA                | A TGAGAAGACC                   | 2520         |
|           | <b>みぐみぐぐみなぐて</b>       | TAGCAGAGC                | C TACAGAAAA        | T GGAAAAAGG                | A CCCCATITE                | C CAATGAGAAG                   | 2580<br>2640 |
|           | ACCACATCA              | T CCTCAGCAG              | A GCCTACAGA        | A CACGCAGAA                | A GGACTCCAC                | T GGCCAATGAG                   | 2700         |
|           | AACACCACA              | T CATCCCCAG              | C AGAGCCTAC        | A GAAAATAGA<br>A AATAGAGAA | A GCACAGCCA                | C CAATGAGAAG<br>A TGAGAAGACC   | 2760         |
| 55        | አርአር ርር አጥተና           | TO CAGCAGAGG             | С ТАСАБАААА        | T AGAGAATGG                | A CAGCCAAT                 | A GAACACCACA                   | 2820         |
| 33        | CTATCYCE               | CAGAGCCTA                | C AGAACATGA        | A GAAATGACC                | C CATTGGCC                 | A TGAGAAGACC                   | 2880         |
|           | N CN CTTN TYCY         | TO CRECREAGE             | TACAGAAAA          | T GGAGAAAGG                | A CCCCATTT                 | C CAATGAGAAG                   | 2940         |
|           | N CON CRECE            | ጥ ሮሮፕሮኔፎሮኔር              | A GOOTACAGE        | A CATGGAGAA                | A GGACCCCAC                | T GGCCAATGAG                   | 3000         |
| <b>CO</b> | 200200000              | C CATCCCCAC              | C AGAGCCTAC        | 'A GAACATGGA               | G AAAGGATAG                | C CAATGAGAAG                   | 3060<br>3120 |
| 60        | GCCACACC               | AT CCCCAGCA              | A GCCTACAG         | A CATGGAGAA                | A CGACAGIC                 | A TGAGGACACC<br>CCAATGAGAAC    | 3180         |
|           | ACACCATC               | CT CAGCAGAGO             | C TACAGAAA         | T GGAGAAAGG                | A CCCCACIG                 | A TGAGAAGACC                   | 3240         |
|           | 3 C3 CC3 TC            | CC CAGCAGAGG             | TACAGAAC           | AT GGAGAAAGO               | IA CACCATCA                | SC CAATGAGAAG                  | 3300         |
|           | 3 CC 3 T 3 CC          | አም (ምርር እርር እ            | A COUTACAGE        | AA CACGAAGAA               | LA TGACCCCA                | rc ggccaatgag                  | 3360         |
| 65        | A A CA CCA C           | AC CATCCCCA(             | T ABACCCTA         | CA GAACATGG!               | AG AAAAGACT                | AC ATTGGCCAAT                  | 3420         |
|           | CHCHNCKT               | CB CBCTBTCC              | יר אפאאפפפר        | T ACAGAACA                 | ng gagcaaaa                | AC TACGTCGGCC                  | 3480         |
|           | AATGAGAA               | ga tcacacca              | C CCTAGCAA         | AG CCTACAGAI               | AC ATGGAGAA                | AG GACCACATCA                  | 3540<br>3600 |
|           | בערת מיייים            | רא אכאדרארי              | rc atctgcag        | CA GAGTCTAC                | ig vacution                | OW TWOOGCTWCW                  | 3000         |
| 70        | TCAGCCAA               | TG TGATCACA              | CC AGCCCCAG        | CA GAGCCTATA               | TA AACAIGCA                | AA AAGGACCACA<br>CC AGAAAAGACC | 3720         |
| 70        | TIGGCCCA               | TG AGAAGATG              | AC ACAAGICA        | CA GAAAAGIC                | C CTACGCTA                 | TA CTCAGAGAAG                  | 3780         |
|           | እ <b>ርር</b> አጥልጥ?      | CA CCABAGGG              | AA AAACACAC        | CA GTCCCAGA                | AA AGCCTACA                | ga aaacctgggg                  | 3840         |
|           | A A CA CCA C           | AC TOACCACT              | CA CACCATAA        | AA GCCCCAGT                | AA AGTCCACA                | ga aaacccagaa                  | . 3900       |
|           | AAAACAGC               | AC CACTCACA              | AATATOAD AA        | AA CCTTCAGT                | CA AGGTCACA                | GG AGACAAATCI                  | 3960         |
| 75        | רייר א רייד א ר        | אוים עריידוריים אויי     | <b>ርኔ ጥርፕልልልፕል</b> | AA ACTGAAGT                | TA CTCATCAG                | GL CCCACIGGI                   | 4020         |
|           | ጥርማማማርስር               | ለግልሞዋልግቱ ግግ              | тс тьсььксь        | AG CTGAGTTC                | TA TCACATCA                | GA AGCCACAGGA                  | 4000         |
|           | AACGAGAG               | CC ATCCATAC              | CT CAATAAAG        | AT GGCTCACA                | UM AMGGTATO<br>TA TTOTOGTO | CA CGCTGGACAG                  | 4200         |
|           | ATGGGAGA               | GA ATGATTCA              | TT CCCTGCAT        | TOURTHOT OUR               | CT CCTATATO                | AT GCGGACACGC                  | 4260         |
| 80        | CCC2 C2 C2             | ממסמסמת מחד              | מר מרמפדמרם        | AT GATGCAGA                | GG ATGAGGG1                | GG CCCCAATTC                   | . 4340       |
| 50        | TACCCC                 | CT ACCTGATE              | GA GCAGCAGA        | AT CTTGGCAT                | GG GCCAGATO                | CC TTCCCCACGO                  | 4380         |
|           | TGA                    |                          |                    |                            |                            |                                |              |
|           |                        |                          |                    |                            |                            |                                |              |

Seq ID NO: 428 Protein sequence Protein Accession #: XP\_069480.1

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| -  | ACCOUNTATA TOCATTORIC RESCRICTOT GATTGTARAG CTCAGTGTAR ACARGO   | CACC 3180                  |   |
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|    | CTCAACATT CTCCATCTCC ACTTCTTGT CCAGAAGGAA AATTCTCGCG TTCTGG   | GTTA 3360                  |   |
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|    | TONDOTTONO TROUBLE TO TACTATTTC CGTGGATTTG GGCATCTGGA GTTGT   | TAAAT 3540                 |   |
|    | TGTCCTTCTG AGGTTTTCCA TGAATGCTTC TTTAACCCTT GCCACAATAG TGGAAC   | CTGC 3600<br>AGTGT 3660    |   |
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|    | ACCUSTOCICA TOCCACCTCC TTTGGAGAAT GGCTTCCATT CAGCCGATGA CITCI   | ATGCT 5100                 |   |
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| 40 | TTCTSTACAG ATAATGCGAG CTGGAACGGC GTTTCACCAT CCTGCCTTGA TGTCG  | ATGAG 5220                 |   |
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|    | TGTAAGGCTC CAGGAAATCC GGAAAATGGC CACICCTCAG GTGAGATTTA TACAC  | TAGGT 5400<br>TCACA 5460   |   |
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| 45 | TETTTGGAGT CTGGAGAATG GAATCATCTA ATACCATATT GTAAAGCTGT TTCATAAACCGGCTA TTCCAGAAAA TGGTTGCATT GAGGAGTTAG CATTTACTTT TGGC   | AGCAAA 5580                |   |
|    | AAACCEGCTA TTCCAGAAAA TEGTTECATT GAGGAETTAG CATTACTT TOGE<br>GTGACATATA GGTGTAATAA AGGATATACT CTGGCCGGTG ATAAAGAATC ATCC  | GTCTT 5640                 |   |
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7920

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|----|--|--|--|---|--|--|--|
| 10 | Seq ID NO:<br>Protein Acc  |  |  |   |  |  |  |
| 15 | <br>MAEAKTHWLG<br>YIENLRQQAH<br>AENEPQSAPK<br>RTNEIVEEQY                               | 1  | YQGVSVPLQQ<br>KNPPMDMSDD<br>VFQELGKLTG                           | KENGDESHLP<br>YETQQWPERK<br>PNNQKRERMD                  | ERDSLSEEDW<br>LKHMQFPPMY<br>EEQKLYTDDE                             | MRIILEALRQ<br>EENSRDNPFK<br>DDIYKANNIA                             | 60<br>120<br>180<br>240<br>300                       |
| 20 | DQLSDDVSKV<br>PPEDLIEMLK<br>RAGTEALPDG<br>AAWIPHVENR                                   | IAYLKRLVNA<br>TGEKPNGSVE<br>LSVEDILNLL<br>QMAYENLNDK<br>LNQGSSQETD | AGSGRLQNGQ<br>PERELDLPVD<br>GMESAANQKT<br>DQELGEYLAR             | NGERATRLFE<br>LDDISEADLD<br>SYFPNPYNQE<br>MLVKYPEIIN    | KPLDSQSIYQ<br>HPDLFQNRML<br>KVLPRLPYGA<br>SNQVKRVPGQ               | LIEISRNLQI<br>SKSGYPKTPG<br>GRSRSNQLPK<br>GSSEDDLQEE               | 360<br>420<br>480<br>540<br>600                      |
| 25 | KAEKGREHIA   |  |  | 70111111211   |  |  | -  |
| 30 | Nucleic Aci  | id Accession<br>lence: 19  | #: NM_006  | 398.1   |  |  |  |
| 35 | GAGGAATGGG<br>GAACATGTCC   | 11<br> <br>CTGCAGAGAT<br>ATTTAATGAC<br>GGTCTAAGAC                  | CTTTGATGCC<br>CAAGGTTCCT   | AACCCATATG<br>GTGCAGGACC                                | ACAGCGTGAA<br>AGGTTCTTTT   | AAAAATCAAA<br>GCTGGGCTCC   | 60<br>120<br>180                                     |
| 40 | CACCTTACCC<br>TCAGGTGATG<br>GTGAAAGCAA<br>AATGGAAAGA                                   | AGGCAAAGAG<br>TGATCGAGAC<br>GACTGGAAGA                             | GAAGCCCAGT<br>GCACCTCCTC<br>TAAGACGGGT<br>TGGGAAGATG             | GATGAGGAGC<br>CAGGTGCGAA<br>ATAATCCCTG<br>ATGGCAGATT    | TGCCCTTGTT<br>GGTCCAGCTC<br>AGACCCAGAT<br>ACGGCATCAG               | TCTTGTGGAG<br>AGTGGCACAA<br>TGTGACTTGC<br>AAAGGGCAAC<br>GGGTGTTGGC | 240<br>300<br>360<br>420<br>480<br>540               |
| 45 | AGGGGTCAAA<br>TCCCAAAATT<br>AGTATATTGC   | AAGCTTATTT<br>AATGAGAATG   | CTTTTAATCT<br>AGATGAGTAG<br>GTTTCTTTGA                           | CTTACTCAAC<br>AGTAAGATTT<br>TTCTAACACA                  | GAACACATCT<br>GGGTGGGATG<br>ATTAATTAAG                             | TCTGATGATT<br>GGTAGGATGA<br>TGACATGATT                             | 600<br>660<br>720                                    |
|    |  | 470 Prote cession #: 1   |  |   |  |  |  |
| 50 | 1  | 11   | 21<br>   | 31<br>  | 41   | 51<br>   |  |
| 55 | RSLSSYGIDK   |  | VKPSDEELPL   | KKIKEHVRSK<br>PLVESGDBAK                                | RHLLQVRRSS   | LLGSKILKPR<br>SVAQVKAMIE   | 60<br>120  |
|    | Nucleic Ac   | 471 <u>DNA s</u><br>id Accessio<br>uence: 19                       | n #: XM_094  | 741.1   |  |  |  |
| 60 | 1<br> <br>ATGAAGGCCA<br>TCCCTGCAGO   |  |  |   |  | 51<br> <br>CGACTGGCCT  | 60<br>120  |
| 65 | TTCCTCTGCC<br>CTGGCCAACC<br>TGCGCATCGC<br>CGCGCGGCCG                                   | ACCTGGCCTT TGCGCGGACC TGGCTCTGGG CAGTGTGCCG                        | GGTAGACGCC<br>AGCGCTCTGC<br>TTCGGCCGAA<br>CCCGCTGCGC             | GGCTTCACTA CTGCCGCGCA TGCGTCCTCC TATGCGGGGG             | A CTAGCGTGGT<br>A GCCACTGCAC<br>C TGGCGGTGAT<br>C TCGTCTCCCC       | CATGTACTAC GCCGCCGCTG GGCCCAGCTG GGCTCTGGAC GCGCCTATGT             | 300<br>360<br>420                                    |
| 70 | CTCCTGGCTG<br>CCGCCCGCC<br>GCCGCCCGCC  | AGCGGCCGCI<br>TCAAGCTGGC<br>TGGTCATCCI<br>CTGTCTGTTC               | GTGCGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC                           | CGCCTGCTGC<br>CGACGGAGACA<br>CTTTGCCGTCA<br>CAGCGGAGGCC | A CCACTTCA:<br>A CTACCGAGA!<br>A TCCTGGCCTC<br>C GGAGGAGGG         | C GCAAACCGCG CTGTGAGCTG CCAGATGTTC CTACGGTGCC CGTGGGCACG           | 540<br>600<br>660<br>720                             |
| 75 | CAGCCCGCGC<br>GTCACACCTC   | AGOGCTACA  | CCAGGCACGC GCTCATCTAG  | GCAAGTTCC<br>ACCCTCAGG                                  | 3 TATCGCTCT<br>A ATAAGAAAG   | A CACCTACCTG<br>I CTACACCGTG<br>I GAAGGGGGCA                       | 840  |
| 80 |  | : 472 Protection #:  |  |   |  |  |  |
|    | 1  | -11  | 21<br>   | 31<br>  | 41<br>   | 51<br>}  |  |
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                                                                                             2520
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                                                                                            2580
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                                                                                      1080
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                                                                                       1800
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| 5  | TTTCTGAATC<br>CAGTATATCT<br>TAGAAAAAA<br>TATGACATCA                | TTTCCACATT<br>GATTTGTATA<br>AGCACAGAGA<br>AAGATAGACT                         | ATATTATAAA<br>AGTAAGTTGA<br>AATGTTTAAC<br>TTTGCCTAAG          | AAATATCATA<br>ATATGGAAAT<br>TGAGCTTCTC<br>TGTTTGACTC<br>TGGCTTAGCT<br>TCCAAATCAT            | GTCAGTTTAT<br>TCTACAACAT<br>TTATGATACT<br>GGGTCTTTCA                    | CTCCCCTCCT<br>TTCTAGAAAA<br>TCTTGGAAAC<br>TAGCCAAACT                     | 2100<br>2160<br>2220<br>2280<br>2340  |
|----|--|--|---|---|---|--|---------------------------------------|
| 10 | Seq ID NO:<br>Protein Acc  |  | n sequence<br>P_056322  |   |   |  | •                                     |
| 15 | CEATCEPGCK<br>LSGHMLMPDA<br>GKVICPYNRR<br>GSFKCKCKQG               | LLLSWVAGGF<br>FGECVGPNKC<br>TCVNSRTCAM<br>CVNTFGSYYC<br>YKGNGLRCSA           | RCFPGYTGKT<br>INCQYSCEDT<br>KCHIGFELQY<br>IPENSVKEVL          | 31<br> <br>LLASARQPGV<br>CSQDVNECGM<br>EEGPQCLCPS<br>ISGRYDCIDI<br>RAPGTIKDRI<br>GKKGNEEKMK | KPRPCQHRCV<br>SGLRLAPNGR<br>NECTMDSHTC<br>KKLLAHKNSM                    | NTHGSYKCFC<br>DCLDIDECAS<br>SHHANCFNTQ<br>KKKAKIKNVT                     | 60<br>120<br>180<br>240<br>300<br>360 |
| 20 | SLRGDVFFPK<br>WNPADRDNAI   | VNEAGEFGLI<br>GPYMAVPALA<br>WEKTTSEDEK                                       | LVQRKALTSK<br>GHKKDIGRLK                                      | LEHKOLNISV<br>LLLPDLQPQS<br>GTDATKSIIF  | DCSFNHGICD<br>NFCLLFDYRL  | WKQDREDDFD<br>AGDKVGKLRV   | 420<br>480<br>540                     |
| 25 | Nucleic Act  | 495 <u>DNA se</u><br>id Accession<br>Jence: 259.                             | #: NM_003   | 1506.1  |   |  |                                       |
| 30 | TTAGACGGGG<br>CTCATTTTCA   | ACGGGAAGGG<br>GGAAAGCCTG   | ACAGCGGCCT<br>AAAATGAGTA                                      | 31<br> <br>CCGTCTCAGG<br>TCGACCGCCC<br>AAATAGTGAA   | CCCGAGTAAT<br>ATGAGGAATT  | TGACCCAGGA<br>TGAACATTTT   | 60<br>120<br>180                      |
| 35 | ATCAGGAATT<br>CTCCTAAGAG<br>ATGGCCTACA<br>GCGGTGGAAA               | TGAAGAAAAT<br>GGCACAGTCT<br>ACATGACGTT<br>TGGAGCATTT                         | GGAGATGTTT<br>CTTCACCTGT<br>TTTCCCTAAT<br>TCTTCCTCTC          | AAGAGTGATT<br>ACATTTTTGT<br>GAACCAATTA<br>CTGATGGGTC<br>GCAAATCTGG                          | TGACGTGTAT<br>CTGTTCCCAG<br>ATTATGACCA<br>AATGTTCACC                    | TTTTCTACCC<br>ATGTATGAAA<br>GAGTATTGCC<br>AAACATTGAA                     | 240<br>300<br>360<br>420<br>480       |
| 40 | TGTCGTAAAC<br>ATCCGATGGC<br>GTAACTTTTG                             | TTTGTGAGAA<br>CTGAGGAGCT<br>ATCCACACAC                                       | AGTATATTCT<br>TGAATGTGAC<br>AGAATTTCTT                        | GGTCCTCAGA  | AATTAATTGA<br>ACTGTGATGA<br>AGAAAACAGA                                  | GGTTCCACCT CACTTTTGGG GACTGTTCCT ACAAGTCCAA AGGATATAAG                   | 540<br>600<br>660<br>720<br>780       |
| 45 | TTTCTGGGAA<br>CTAGAGTTTG<br>TTCACATTCC<br>ATATATTACT               | TTGACCAGTG CAAAAAGTTT TTACTTTTTT CTGTCTGTTA                                  | TGCGCCTCCA<br>TATTGGAACA<br>AATTGATGTA<br>CAGCATTGTA          | TGCCCCAACA GTTTCAATAT AGAAGATTCA TCTCTTATGT   | TGTATTTAA TTTGTCTTTG GATACCCAGA ACTTCATTGG                              | AAGTGATGAG TGCAACTCTG GAGACCAATT ATTTTTGCTG CACTGTTGTC                   | 840<br>900<br>960<br>1020<br>1080     |
| 50 | CTAGGCTCTC<br>GCTGGCACTC<br>TGGAGTTGTC<br>CCAGGTTTCC<br>GGAGTTTGCT | : AAAATAAGGC<br>: TGTGGTGGGT<br>: AAGCCATCGA<br>: TGACTGTTAT<br>: TTGTTGGCCT | TTGCACCGTT GATTCTTACC GCAAAAAGC GCTTCTTGCT TTATGACCTC         | TTGTTCATGC ATTACTTGGI GTGTGGTTTC CTGAACAAAG GGTGCTTCTC                                      | TTTTGTATTT TCTTAGCTGC ATGCTGTTGC TTGAAGGAGA GCTACTTTGT                  | TTTCACAATG AGGAAGAAAA ATGGGGAACA CAACATTAGT ACTCTTGCCA                   | 1260<br>1320<br>1380                  |
| 55 | CATGTTCGAC<br>ATTCGAATTC<br>TACGTCTATC<br>CGTCAGTACC               | AAGTCATACA<br>GAGTCTTCAC<br>AGCAAGTGAA<br>ATATCCCATC                         | ACATGATGGG<br>GCGCTTGTAT<br>ACAGGATTACG<br>GTCCTTATCAG        | CGGAACCAAG<br>CTTGTGCCAT<br>CTGGGAGATAA<br>GGCAAAAGCAA                                      | AAAAACTAAA<br>TAGTGACACT<br>CTTGGGTCTC<br>AAAGCTCGACC                   | TTCCTTAAAT A GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT                 | 1500<br>1560<br>1620<br>1680          |
| 60 | GGAAGCAAA<br>CCAATCAGTO<br>TCTAAAGTTI<br>TCCAAATCCI                | A AGACATGCA<br>A AAAGTCGAAA<br>A AACACAAAA<br>A TGGGAACCA                    | AGAATGGC<br>AGTACTACA<br>AGAAGCACTA<br>AGAAGGAGC<br>AGAAGGAGC | r gggiltitti<br>3 gaatcatgi<br>1 aaaccaagi<br>1 acagcaaan                                   | A AACGAAATCO<br>B AGTTTTTCT:<br>C CACACAAGC:<br>C ATGGCACTTO            | CTTCTGGGTT CAAGAGAGAT AAAGCACAAT GAAGGTCATT GAAGGTCATT                   | 1800<br>1860<br>1920<br>1980          |
| 65 | ACATCAATGI<br>TGTGGTGAA<br>GGGAAGGGC<br>AAGAGTGAT                  | A GAGAGGTGA:<br>C CTGCCTCGC:<br>C AGGCAGGCA:<br>A TTACTGACA:                 | A AGCGGACGG<br>C AGCAGCATC<br>C TGTATCTGA<br>C TGGCCTGGC      | A GCTAGCACC<br>C ATCTCCAGA<br>A AGTGCGCGG<br>A CAGAGCAAC                                    | C CCAGGTTAA<br>C TCTCTGGGG<br>A GTGAAGGAA<br>A ATTTGCAGG                | C CTCACCAGAA G AGAACAGGAC A ACAGGTCGAC G GATTAGTCCA T CCCAGTTCT          | 2100<br>2160<br>2220<br>2280          |
| 70 | AGAAAAGAG<br>CAGAAGCAA<br>TACGTTCTT<br>TCAAGAATA                   | C AGGGAGGTG<br>A TTTGTGTTA<br>C TTTTGCACT<br>A TATGACTCA                     | 3 TTGTCATTC<br>C ACTGGAAGT<br>T AAAGTTGCA<br>T TTCACACAA      | A GATACTTGA<br>G ACCTATGCA<br>T TGCCTACTG<br>A GGTTAATGA                                    | A GAACATTTT<br>C TGTTTTGTA<br>T TATACTGGA<br>C AACAATATA                | T TTCAGGAGTO C TCTCGTTACT A GAATCACTGT A AAAATAGAGT C CTGAAAACAC         | 2400<br>2460<br>2520<br>2580          |
| 75 | CCTTTTCTA<br>TTTACCTTT<br>GTATCTTTT<br>ATTCAAGTA                   | T TTATGAAGA<br>T TGATATAAA<br>T ATACATATT<br>T TTTTATCAT                     | T TCTACTCTT<br>A TCAAGATAT<br>T GAAAATAAG<br>G CTATTGTGA      | G GTAAGAGTA<br>T TCTTTGCTG<br>C TTATATGTA<br>T ATTTTAGCA                                    | T TTTAAGATG<br>A AGTATTTAA<br>T TTGAACTTT<br>C TTTGGTAGC                | A GAGGAATCTI T ACTATGCTAT A TCTTATCCTI T TTGAAATCCTI T TTTACACTGI        | 7 2700<br>7 2760<br>7 2820<br>A 2880  |
| 80 | GTCTTATAA<br>TGTGATTTT<br>GGTGCTTAC<br>ATATTTAAA                   | T AGGAATTTA<br>T ATAGTCTCG<br>T CAAAGAGTG<br>A TAAAATGTC                     | A CTTTAAAAA<br>T TTTAGGAAT<br>T CCACTATTO<br>C TAAAGGGTT      | C CCACTTATT T TCACAGATC A TTGTATTAT A GTAGACAAA   | G ATACCTTAC<br>T AAATTATGT<br>G CTGCTCACT<br>A TGTTAGTCT<br>A CCACCCATT | T ATACCAAAAIC ATCTAAAATCA ACTGAAATAIG ATCCTTCTGGTT TTGTATATTIG ATTGTATTA | 3 3000<br>A 3060<br>C 3120<br>A 3180  |

1148

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| 5  | VLVGGNWVLT<br>LMLLQLRDQA<br>QKKCEDAYPG<br>VYTNICRYLD | WIKKIIGSKG                                      | VRLGDHSLQN<br>LADHCTQPGQ<br>SSKGADTCQG               | KDGPEQEIPV<br>KCTVSGWGTV                             | VQSIPHPCYN<br>TSPRENFPDT                             | SSDVEDHNHD  | 60<br>120<br>180<br>240         |
|----|--|---|--|--|--|---|---------------------------------|
| 10 | Nucleic Aci  | 501 <u>DNA</u> se<br>d Accession<br>dence: 294  | #: NM_006  | 103  |  |   |                                 |
|    | 1  | 11  | 21   | 31   | 41   | 51  |                                 |
| 15 | CGCCTCCTC GAAGACTGGC GGACAGCGAA TCTCTGCCCA           | GTGTGCCCCG<br>TGCGCCGACA<br>AATGATAAGG          | TGCTGTTCGG<br>AGCTCCAGGC<br>ACCTCAAGTG<br>AGGGTTCCTG | CTTCACCCTA<br>TGACCAGAAC<br>CTGCAGCGCG<br>CCCCCAGGTG | GTCTCAGGCA<br>TGCACGCAAG<br>GGCTGTGCCA<br>AACATTAACT | CAGGAGCAGA<br>AGTGCGTCTC<br>CCTTCTGCCT<br>TTCCCCAGCT    | 60<br>120<br>180<br>240<br>300  |
| 20 | CCGCAATGGC<br>CAGGCTGAGC<br>TGCCCTCCCC               | TGTGGGAAGG<br>AGTGAGGAGA                        | TGTCCTGTGT<br>GAAAGTTTCT<br>CTCTGTATTC               | CACTCCCAAT<br>GCCTGGCCCT<br>CCTCTTGGGC               | TTCTGAGGTC<br>GCATCTGGTT<br>TGACCACAGC               | TGAAATGCTG<br>CAGCCACCAC<br>CCAGCCCACC<br>TTCTCCCTTT    | 360<br>420<br>480<br>540        |
| 25 |  | 502 Prote<br>cession #: 1                       |  |  |  |   |                                 |
|    | 1  | 11  | 21   | 31   | 41   | 51  |                                 |
| 30 |  |   |  |  |  | SDSECADNLK<br>CRNGCGKVSC                                | 60<br>120                       |
| 35 | Nucleic Ac   | 503 <u>DNA s</u><br>id Accessio<br>uence: 65    | n #: NM_00   | 2407   |  |   |                                 |
| 40 | CGCCATGAAG   | CTGCTGATGG                                      | TCCTCATGCT<br>AGGACATGGT                             | GGCGGCCCTC GAAAAGACC                                 | CTCCTGCACT   | 51<br> <br>  GCAGCCGCCT<br>  GCTATGCAGA<br>  ACATATCTAT | 60<br>120<br>180                |
| 45 | GGGGAAATTC<br>GATGATGCAT<br>AAGGCGTTTC<br>ACCACTTTTC | AAGCAGTGTT ACAGTGTACC GCTCAGAGGG                | TCCTCAACCE<br>ACAGCATTTC<br>CTACAGACTE<br>TGTCTTTTT  | GTCACATAGA<br>GTGTAATATO<br>TGGCCAGAAO<br>TGTGGAAAC  | A ACTCTGAAA?<br>3 AAGAGTAATT<br>C TCATCTGTTC         | CAGAGGCTAT ACTTTGGACT ACTTTACCC ATTGCTAGAA TGTTGAAACC   | 240<br>300<br>360<br>420<br>480 |
| 50 |  | : 504 Proteccession #:                          |  | <u>1</u>   |  |   |                                 |
|    | 1  | 11  | 21   | 31   | 41   | 51  |                                 |
| 55 |  | <br>  |  |  | b eakertőee.<br>                                     | )<br>I DSDAAAEAMG                                       | 60                              |
| 60 | Nucleic A  | : 505 <u>DNA</u><br>cid Accessio<br>quence: 171 | on #: NM_01  | 4791.1   |  |   |                                 |
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|    | TTGGCGGGC  | <br>G GAAGCGGCC                                 | <br>A CAACCOGGC                                      | <br>G ATCGAAAAG                                      | i<br>A TTCTTAGGA                                     | A CGCCGTACCA  | 60                              |
| 65 | GCCGCGTCT  | C TCAGGACAG<br>C AGGTTCTTT                      | C AGGCCCCTG  | T CCTTCTGTC<br>A AATAAACTT                           | NG GGCGCCGCT<br>NG CAAGAGGAC                         | C AGCCGTGCCC<br>T ATGAAAGATT<br>T GGCTTTGCAA            | 120<br>180<br>240               |
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| 70 |  |   |  |  |  | C TTGAAGAACC  |                                 |
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|    | TGTCAGAAG  | A GGAGACCCG                                     | G GTTGTCTTC  | C GTCAGATAG  | T ATCTGCTGT  | T GCTTATGTGC  | 540                             |
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| 75 | ATCTACAGA  | C ATGCTGTGG                                     | G AGTCTGGCT  | T ATGCAGCAC  | C TGAGTTAAT  | A CAAGGCAAAT  | 720                             |
|    | CATATCTTC<br>GTGGATTTC                               | G ATCAGAGGC                                     | A GATGTTTGG<br>T GATGATAAT                           | A GCATGGGCI<br>G TAATGGCT                            | AT ACTGITATA<br>TT ATACAAGAA                         | T GTTCTTATGT<br>G ATTATGAGAG                            | 780<br>840                      |
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| 80 | TGCAGGTGG  | A CCCAAAGAA                                     | A CGGATTTCT  | A TGAAAAAT(  | T ATTGAACCA  | T CACCTGGATCA   | 960<br>1020                     |
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|    |  |   |  |  |  | SA CAAGCCAGTG<br>TG ACCGCAAGTG                          |                                 |
|    |  |   |  |  |  |   |                                 |

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Seq ID NO: 509 <u>DNA</u> sequence Nucleic Acid Accession #: AB051390.1 Coding sequence: 34..2457

| 5   | 1          | 11           | 21           | 31           | 41          | 51                                      |      |
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|     |            |              | GCTGGCCCTG   |              |             |   | 120  |
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|     |            |              |              |              |             | GGAAGAAGAC                              | 360  |
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|     |            |              |              |              |             | GTGGATCACC                              | 1560 |
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| 50  |            |   |            |            |              | IRSTGSKQRS               | 300        |
| 20  |            |   |            |            |              | PEGYAAYYCE               | 360        |
|     | RNMVVRACGO |   | TUNHETNEET | VPRPCCAPIC | i TWAT2APIED | DSSNVILKKY               | 420        |
|     |            | 519 DNA 8                               | emience    |            |              |                          |            |
| 55  |            | id Accessio                             |            | equence    |              |                          |            |
|     |            | uence: 264.                             |            | •          |              |                          |            |
|     |            |   |            |            |              |                          |            |
|     | ļ          | 11                                      | 21         | 31         | 41           | 51                       |            |
| 60  | 1          | 1                                       |            |            |              | 1                        |            |
| 60  |            |   |            |            |              | ATGAGGAAAC               | 60         |
|     |            |   |            |            |              | TCAACTGACC               | 120        |
|     |            |   |            |            |              | TCCAGCACCC               | 180        |
|     |            |   |            |            |              | CCTGAGCCCC               | 240        |
| 65  |            |   |            |            |              | CATGGCTTAG               | 300        |
| UJ  |            |   |            |            |              | AACTACCTGC               | 360<br>420 |
| •   |            |   |            |            |              | CTCCAGGTTC<br>GAGACTCAGA | 480        |
|     |            |   |            |            |              | ACACCCTCAG               | 540        |
|     |            |   |            |            |              | GATGTGGATT               | 600        |
| 70  |            |   |            |            |              | CTGGACTATG               |            |
| , , |            |   |            |            |              | AAGCCCAGTT               | 720        |
|     |            |   |            |            |              | GTGGCCATGT               | 780        |
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|     |            |   |            |            |              | AACTTTCAGG               |            |
|     |            |   |            |            |              | TCCCCAGGGA               |            |
| 00  |            |   |            |            |              | CATGGTTAAA               |            |
| 80  |            |   |            |            |              | A AGTTTTAAAT             |            |
|     | AAAATAGCA  | A CCACCACCA                             |            |            |              |                          |            |
|     |            |   |            |            |              |                          |            |

Seq ID NO: 520 Protein sequence Protein Accession #: Eos sequence

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51
                                  21
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        PGELKNDSPL DYENIKEITD YVNVNPERHK PSFWYFVNPA LSEPAEYDQV AM
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                                                                                          300
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Protein Accession #: Eos sequence
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                                                                                           180
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         GTGCTTTTC TTTTCTCTC TFTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG
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                                                                                           720
                                                                                           780
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                                                                                          1200
                                                                                          1260
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         CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGGAATCTAA CCCAGACACT 1860
GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA
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         Seq ID NO: 524 Protein sequence
         Protein Accession #: Eos sequence
 75
         MLRSSLSTSI VLFLFSSFST INESISSRKR HRPLEQLDSD GTITIEEQIV LVLKAKVQCE
                                                                                            60
          LNITAQLQEG EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW
         DFMHSLNKTW ANYSDCLRFL OPDISIGKOE FFERLYVMYT VGYSISFGSL AVAILIIGYF
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 80
          RRLHCTRNYI HMHLFVSFML RATSIFVKDR VVHAHIGVKE LESLIMODDP ONSIEATSVD
                                                                                            240
          KSQYIGCKIA VVMFIYPLAT NYYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPAA
                                                                                            300
          FVAAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILFLNTVRV LATKIWETNA
          VGHDTRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFFV
SIIYCYCNGE VQAEVKKMWS RWNLSVDWKR TPPCGSRRCG SVLTTVTHST SSQSQVAAST
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SRPMESNPDT EGCOGETEDV L Seq ID NO: 525 DNA sequence 5 Nucleic Acid Accession #: NM\_005048 Coding sequence: 143..1795 51 41 10 GGCCGGTGGC CCGGGCCCGA CCACCCCAGC TGCGCGTCGT TACTGGCCAC AAGTTTGCTC TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120 TCTTCCTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG 180 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCCAGCTG GATTCTGATG GCACCATTAC 240 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 15 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTTGTTG GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCCATGC CCTCCTTATA TTTATGACTT 420 CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600 20 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTTACTTCA GACGATTGCA 660 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTT GTGGCTTTCT TTTCGGACAC 900 25 960 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACTTA GTGCTGGAGA CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1080 1140 30 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG 1260 AGTGCATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA 1320 1380 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT CTCCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCCGC AGATGCGGCT CAGTGCTCAC 1500 35 CACCGTGACG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620 TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGTTC TCTGAATGGA CATTTGTGGC TGACTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1800 40 1860 ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920 TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 1980 2040 GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100 45 GCTGTAGCTT TCTCTCATAT ATATCACCCT AAATATAATG AAGATCTTTT AGTGTGTATC 2160 ATTITECTIT TAGAAACTAG TATTETETTA TITETTACTT TAATGTACTT CTATCACTGC 2220 ATTTATTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGTGG ACATTGATAA AATAATGCAT 2280 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC 2400 50 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC
TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTCCAAA 2460 2520 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCTTG 2580 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTTAAAAA 55 Seq ID NO: 526 Protein sequence Protein Accession #: NP\_005039 60 MAGLGASLHV WGWLMLGSCL LARAQLDSDG TITIEBQIVL VLKAKVQCEL NITAQLQEGE 60 GNCFPEWDGL ICWPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA NYSDCLRFLQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180 MHLPVSFMLR ATSIFVKORV VHAHIGVKEL ESLIMODDPO NSIEATSVDK SQYIGCKIAV VMPIYFLATN YYWILVEGLY LHNLIFVAFF SDTKYLMGFI LIGMGFPAAP VAAWAVARAT 240 65 300 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360 LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFFVS IIYCYCNGEV 420 OAEVKKMWSR WNLSVDWKRT PPCGSRRCGS VLTTVTHSTS SOSOVAASTR MVLISGKAAK 480 IASROPDSHI TLPGYVWSN9 EQDCLPHSFH EETKEDSGRQ GDDILMEKP9 RPMESNPDTE 70 GCOGETEDVL Seq ID NO: 527 <u>DNA sequence</u> Nucleic Acid Accession #: XM\_036683 Coding sequence: 38..3655 75 31 GCTTTGCCCA GTAGTTGGAA AGTGAACTCG ACTCGTGATG GTTCTCCTGT CACTTTGGTT GATAGCAGCC GCTCTGGTAG AGGTTAGGAC TTCAGCTGAT GGACAAGCTG GTAATGAAGA 120 80 AATGGTGCAA ATAGATTTAC CAATAAAGAG ATATAGAGAG TATGAGCTGG TGACTCCAGT 180 CAGCACAAAT CTAGAAGGAC GCTATCTCTC CCATACTCTT TCTGCGAGTC ACAAAAAGAG GTCAGCGAGG GACGTGTCTT CCAACCCTGA GCAGTTGTTC TTTAACATCA CGGCATTTGG AAAAGATTTT CATCTGCGAC TAAAGCCCAA CACTCAACTA GTAGCTCCTG GGGCTGTTGT 300 360 GGAGTGGCAT GAGACATCTC TGGTGCCTGG GAATATAACC GATCCCATTA ACAACCATCA

RMVLISGKAA KIASROPDSH ITLPGYVWSN SEODCLPHSP HEETKEDSGR QGDDILMEKP 540

|     |  | GCTACGTATA   |                   |                  |              |              | 480  |
|-----|--|--------------|-------------------|------------------|--------------|--------------|------|
|     |  | ATCGTGGACA   |                   |                  |              |              | 540  |
|     |  | ATAAAAAGTG   |                   |                  |              |              | 600  |
| -   |  | GAAGAAAAAG   |                   |                  |              |              | 660  |
| 5   |  | GACATGTCCA   |                   |                  |              |              | 720  |
|     | TGATCTAGGT   | ACTGTTTATG   | GCAACATCCA        | CCAGCAGCTG       | AATGAAACAA   | TGAGACGCCG   | 780  |
|     | CAGACACGCG   | GGAGAAAACG   | ATTACAATAT        | CGAGGTACTG       | CTGGGAGTGG   | ATGACTCTGT   | 840  |
|     | GGTCCGTTTC   | CATGGCAAAG   | AGCACGTCCA        | AAACTACCTC       | CTGACCCTAA   | TGAACATTGT   | 900  |
|     |  | TACCATGATG   |                   |                  |              |              | 960  |
| 10  |  | GGATATGCAA   |                   |                  |              |              | 1020 |
|     |  | GTGTGTCGCT   |                   |                  |              |              | 1080 |
|     |  | CATGCAATTT   |                   |                  |              |              | 1140 |
|     |  | GTCACCGGCA   |                   |                  |              |              | 1200 |
|     |  | TCTGCTTTTG   |                   |                  |              |              | 1260 |
| 15  |  | GGCAACAGGT   |                   |                  |              |              | 1320 |
| 13  | CCTACAACAA   | GCATTCCATC   | CTTTTCCACTC       | CTCCCCATCC       | ACTCCTCAAG   | AACTGAAAAG   | 1380 |
|     |  | TCCTATGACT   |                   |                  |              |              | 1440 |
|     |  |              |                   |                  |              |              | 1500 |
|     |  | CCTGGAATCA   |                   |                  |              |              | 1560 |
| 20  |  | ATGTGCACCG   |                   |                  |              |              |      |
| 20  | CCATCCTGAT   | PARTCCCTACT  | TTTGTAAGAC        | TAAAAAGGGA       | CCTCCACTTG   | ATGGGACTGA   | 1620 |
|     | ATGTGCTGCT   | T GGAAAATGGT | GCTATAAGGG        | TCATTGCATG       | TGGAAGAATG   | CTAATCAGCA   | 1680 |
|     | AAAACAAGAT   | GGCAATTGGG   | GGTCATGGAC        | TAAATTTGGC       | TCCTGTTCTC   | GGACATGTGG   | 1740 |
|     |  | CGTTTCAGAA   |                   |                  |              |              | 1800 |
| 25  |  | GGTGTTAATT   |                   |                  |              |              | 1860 |
| 25  |  | TTCAGAGCAC   |                   |                  |              |              | 1920 |
|     |  | CACTGGTTGC   |                   |                  |              |              | 1980 |
|     | CTGTCAGTC  | AAGGAGACTG   | GAGATGTTGC        | TTACATGAAA       | CAACTGGTGC   | ATGATGGAAC   | 2040 |
|     | GCACTGTTC:   | TACAAAGATC   | CATATAGCAT        | ATGTGTGCGA       | GGAGAGTGTG   | TGAAAGTGGG   | 2100 |
|     | CTGTGATAA  | A GAAATTGGTT | CTAATAAGGT        | TGAGGATAAG       | TGTGGTGTCT   | GTGGAGGAGA   | 2160 |
| 30  | TAATTCCCA  | C TGCCGAACCG | TGAAGGGGAC        | ATTTACCAGA       | ACTCCCAGGA   | AGCTTGGGTA   | 2220 |
|     | CCTTAAGAT  | TTTGATATAC   | CCCCTGGGGC        | TAGACATGTG       | TTAATCCAAG   | AAGACGAGGC   | 2280 |
|     | TTCTCCTCA  | r ATTCTTGCTA | TTAAGAACCA        | GGCTACAGGC       | CATTATATTT   | TAAATGGCAA   | 2340 |
|     | AGGGGAGGA  | A GCCAAGTCGC | GGACCTTCAT        | AGATCTTGGT       | GTGGAGTGGG   | ATTATAACAT   | 2400 |
|     | TGAAGATGA  | CATTGAAAGTC  | TTCACACCGA        | TGGACCTTTA       | CATGATCCTG   | TTATTGTTTT   | 2460 |
| 35  |  | T CAAGAAAATG |                   |                  |              |              | 2520 |
|     |  | A CCTACAATCA |                   |                  |              |              | 2580 |
|     |  | G AAGAGCTGGT |                   |                  |              |              | 2640 |
|     |  | A TGCCGTAGGA |                   |                  |              |              | 2700 |
|     |  | G CCGAAACCTA |                   |                  |              |              | 2760 |
| 40  |  | A GAAGAATGGG |                   |                  |              |              | 2820 |
| 40  | TOGGIAGO   | A CGCTGCCTTC | ARCACIGCAC        | TONTOCCIOL       | ANCOCOTO     | TGCACAGCAA   | 2880 |
|     | 1 CGCACIGI   | G GGTGACOGTC | ACCAPATION O      | 2022002200       | AACACACTCC   | COTCOCOTOC   | 2940 |
|     |  | A ACAGGACCCT |                   |                  |              |              | 3000 |
|     |  |              |                   |                  |              |              |      |
| 45  |  | C CTCTGCAGGG |                   |                  |              |              | 3060 |
| 43  |  | A CIGCCTCCTT |                   |                  |              |              | 3120 |
|     | TCAAATGGA  | A GTGTTGGCAC | GATACTGCTC        | CATACCAGGT       | TATAACAAGI   | TATGTTGTGA   | 3180 |
|     |  | C AAGCGCAGTA |                   |                  |              |              | 3240 |
|     |  | T GTCATCTCTA |                   |                  |              |              | 3300 |
| 50  |  | T TATCATTCAG |                   |                  |              |              | 3360 |
| 50  |  | T CCAAATGCAT |                   |                  |              |              | 3420 |
|     |  | G AGGAGTGCTC |                   |                  |              |              | 3480 |
|     |  | A CCCACCAAGA |                   |                  |              |              | 3540 |
|     |  | A GCCAGTGATT |                   |                  |              |              | 3600 |
|     |  | C ATTGACAACA |                   |                  |              |              | 3660 |
| 55  |  | A AGGCTAGAAA |                   |                  |              |              | 3720 |
|     | ATATGCTTG  | T TTAAAGTGGA | AATCTCTATA        | GATCGTCAGC       | TCATTTTATO   | TGTAATTGGA   | 3780 |
|     | AGAACAGAA  | A GTGCTGGCTC | ACTITCTAGE        | TGCTTTCATO       | : CICCITITG  | TCTGCATTGA   | 3840 |
|     | CTCATTTAC  | C AGAATTCATI | GGAAGAAATC        | CACCAAAGATI      | ATTACAAAAA   | AAAAATATGT   | 3900 |
|     | TGCTAAGAT  | T GTGTTGGTCG | CTCTCTGAAG        | CAGAAAAGGG       | ACTGGAACC    | ATTGTGCATA   | 3960 |
| 60  |  | T TTTTGTTTG1 |                   |                  |              |              | 4020 |
|     | CCTTTACAC  | TTABCAGAL T  | ATTTTCCATA        | TGGAACAAAG       | AATTCTTAG    | CTTGTATTCC   | 4080 |
|     | TATTTATCT  | A TATTAGAAAT | ATTGTATGAC        | CAAATTTGC        | GCTGTTGTG    | AAATACTGTA   | 4140 |
|     | TATTGCAAA  | A ATCAGTATTA | TTTTAAGAGA        | A TGTGTTCTCZ     | AATGATTGT.   | TACTATATTA   | 4200 |
|     | CATTTCTG   | A TGTTCTAGGT | CCTCTCCT          | GAGTATTGC        | TTGTTTGAC    | TTCTATAGGT   | 4260 |
| 65  | TAATTTTC   | A AGCAGAGTAT | TACAAAAGA         | AAGTTAGAAT       | TACAGCTAC    | r gacaatataa | 4320 |
|     | AGGGTTTTC  | T TGAATCAACA | ATGTGATAC         | TAAATTATAG       | AAAAAGAAA    | A GAAACACAAA | 4380 |
|     |  |              |                   |                  |              | A TTTAAAGGAT |      |
|     | TGGTGTCT   | TA GTACACTTC | C GGTCACAGG       | ATCAACGAA        | AGTAAATAA    | GAACTCGTGC   | 4500 |
|     | AAGACAAAI  | C TGAAACCCT  | TTTCCAGGA         | CTCAGTAGG        | ACCGTTGAG    | TGTCCTTTGT   | 4560 |
| 70  | Ambitration Annual Annu |              | L deladed Valenda | T CGCATTGTTY     | ACAGATACA    | A ACAGTTATAC | 4620 |
| , ( |  | T CTARTARY   | י ראשאממשאאי      | A ACTITACICAL    | TAACTTATT    | r GTATGTTGGT | 4680 |
|     | rewich   | T GIVITUMIC  | A CHCHACAAA       | י מכיידידים איני | 2 ጥልጥልርምስሶክ  | G CTTTGGGGCT | 4740 |
|     | MUCTUAGA<br>TOTAL ACCO   | NG GERGENSON | A CICIMONNII      | T GUTUITION      | TOTALOUM A   | CCATATGGTT   | 4800 |
|     |  |              |                   |                  |              | A ATAATTTATG |      |
| 75  |  |              |                   |                  |              |              |      |
| ,.  |  |              |                   |                  |              | G TAGATGTAAA |      |
|     |  |              |                   |                  |              | T TTTTTTCTTG |      |
|     | ATAGTATT   | T TATGTACTA  | A ATATTTACA       | C TAATATCAA      | A ACACATATTT | T GGTAAACTAG | 5140 |
|     |  |              |                   |                  |              | A GCAAACTACT |      |
| 80  |  |              |                   |                  |              | T CTTGCATTTT |      |
| O   |  | GA TATTAAGTT | G ATGACTIGT       | T TCCCTTCAA      | G GAAACATTA  | A ATTGTATGGA | 5220 |
|     | CTCAGCTA   | GC TGTTCAATG | A AATTGTGAA       | T TAGAAACAT      | I TITAAAAGT  | T TTTGAAAGAG | 5280 |
|     | ATAAGTGC   | AT CATGAATTA | C ATGTACATG       | A GAGGAGATA      | G TGATATCAG  | C ATAATGATTT | 5340 |
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|----------|--|---|--|---|--|--|---|
| 20       | 110ccin Acc  |   | _  |   |  |  |   |
| 20       | 1  | 11  | 21<br>   | 31  | 41   | 51   |   |
| 25<br>30 | PVNGAHPTLQ<br>YLLFMIGELV<br>VLSAMISVLL<br>HRHSHSHSLP<br>YKIADPICTY   | ADDDSLLDQD<br>GGYIANSLAI<br>VYILMGFLLY<br>SNSPTRGSGC<br>VFSLLVAFTT  | LPLTNSQLSL<br>MTDALHMLTD<br>EAVQRTIHMN<br>ERNHGQDSLA<br>PRIIWDTVVI   | KVDSCDNCSK<br>LSAIILTLLA<br>YEINGDIMLI<br>VRAAFVHALG<br>ILEGVPSHLN  | SRFNKLRVVV<br>QREILKQRKV<br>LWLSSKSPTK<br>TAAVGVAVNV<br>DLVQSVGVLI<br>VDYIKEALMK<br>FGMYRCTIQL                                     | KARLTIAAVL<br>RFTFGFHRLE<br>IMGFLLNQSG<br>AAYIIRFKPE<br>IEDVYSVEDL   | 60<br>120<br>180<br>240<br>300<br>360<br>420  |
|          | Nucleic Act  | 545 <u>DNA se</u><br>id Accession<br>uence: 124   | #: AB03776   |   |  |  |   |
| 35       | 1  | 11  | 21   | 31  | 41   | 51   |   |
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|          |  |   |  |   |  | AGTGAAATAT<br>AGCAAATATT   | 420<br>480  |
| 45       | ATATTCTCAT<br>TTTGTGTATG<br>ATTGGCTCTG<br>GACTTGACCC   | ATGTAAGAGC<br>GGACTACATA<br>AGGATGTGGA<br>AGCAATGTAG  | CATTGGAATA<br>CCAATTTGTC<br>ATATGCACAT<br>AAGAACACTA   | CCAGAGCACA<br>TTAACCACAG<br>CTCTACTTTT<br>ATGGAACAGC  | GAGCAGTCAT AAATTGCCCT TTCATTGTAA CATTGACTAC  | GGAAGCCGCT<br>TTTGGAAAGT<br>ACTAGTCTTG<br>ACTGAACATT   | 540<br>600<br>660<br>720<br>780   |
| 50       | CAAGTTTCAA<br>GCTACTTATG<br>GCAGGAGTTC<br>GTGGTCTTCA   | CTGTCCATCT AAGCTGATAG TACTCTTGTT AAAGAGCAGA   | CCAACTGGGC<br>AAGAACTGCA<br>AAGGGACTCT<br>AGAGGGAGTT   | TTACCACTGG GAATGGGTTG TTGGAAGTGA CCAGTGGAAT   | CTTGGCGTCT ACATTCCTCA TTTTGGTATT   | AGATCCTCAA TAGCCAACAG TCTGGGAAAA AGATGCTAAT ACATGATGTT   | 840<br>900<br>960<br>1020   |
| 55       | GACAATGACA<br>TTCAGAGATA<br>TTTAATGCAA<br>GTATCCATGG   | TGGAAGGTCC<br>GGAAGAGAAA<br>CAGTGATGGC<br>CATTTTTGCA  | AGATATAGAT<br>ATTACCTTTC<br>TTCTGACAGC<br>ATCCTATATT   | GTTCAGGATC<br>GAACTTACAC<br>ATAGTACTCT<br>GATGTGGCAC  | ATGAAGTGGG<br>TGGAACTAAG<br>TCTATGCTGG<br>TTAAACTGA  | AGAAGATGAA AGAAACTGTT AGAAGAAACA TTGGCAAGCA AGGCACATCT TAAGCAAAAT  |   |
| 60       | GTTACTGAAT<br>GGAATGTTAG<br>GTGAATATAA<br>CTCATCTTGT   | TTCCTATCAT GAACCGAAGA CATCGATCCAT ATTCTAGTGT  | AAAGATGTAG<br>TCTCCTAAAA<br>AGAAGCAGAA<br>GTCAGTATTG   | AAGAAAGGCC<br>ATTTATCCAGC<br>AGAATATTTA<br>GGACTATTT  | AGAACCCAGT<br>TCAACAGGAT<br>AGTGGGGAATT<br>AGTCCAACCAT   | TATCTTATGCT TTCATATCCA TATATAAAGAC GAAAACAGCA TGGAATTTAT   | 1440<br>1500<br>1560<br>1620  |
| 65       | TCTGAAGAAC<br>CTTGCCAGAC<br>GACATAGTTC<br>AATCTTCCC  | ATGTTTTGCT ACACAGAAGC AAATAATAACA GTTATTTCAC  | ACTGTCAACO CAAAATAGAC AGATGCACTO ACTTCAGAA   | AAATATGCTO<br>AAGCATCCCAO<br>AACTGGAAATG<br>AACCATTATTG   | 3 CAAGTCTTCC<br>C TAGCTAGCAG<br>I TTCCGGAAA:<br>A TTTTGTTCAG   | AGCCCTGCTG ACATGCACAA CACTGTGGAA GTGATGGCACT ACTTGGATTCA   | 1740<br>1800<br>1860<br>1920  |
| 70       | TTTACTCCAT<br>TATTTTGATC<br>CAAGTATTTC<br>AAGAAATTAC   | GCTGGTTAAA<br>CCTCTGCCTCG<br>GCATTTCCTTG<br>GAAGCAGGAC  | A TCTAAAGAA<br>C CCTTCCTCT<br>C AGACCAGGC<br>T AGAAAATCA   | r actecagter<br>r cttertite<br>r ataatteaa<br>r ateacaatt   | G GGAGAGGAA<br>G TGAATCTGC<br>G AAAACCTTG<br>T TACCTGCTC   | CTTGAGGGCA TTCAGGTGGC TATTGTGGCTG AAGAATGGAAA CTCAACGTGGC  | 2040<br>2100<br>2160<br>2220  |
| 75       | ACTAGGAAA<br>CATGAAGATA<br>AATAGAAGTA  | TTCCCAAGTY<br>A AATCGGCAG   | 3 TATGAAAGA<br>T CAGAAAAGA   | A ACAGATGTG<br>A CCGATTGAA  | C AGGAGAATG<br>A CTCTGAGAA   | A TAAGGAACAA<br>T AAAGCATTGG<br>A AGAGTTAGGA   | 2340<br>2400  |
| 80       |  | : 546 <u>Prot</u><br>ccession #:  |  |   |  |  |   |
|          | 1  | 11<br>  | 21   | 31<br>i   | 41<br>1  | 51<br>   |   |
|          | 1  | ı   | ı  | ŀ   |  | •  |   |
|          |  |   |  |   | 1  | 1163   |   |

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        Protein Accession #: Eos sequence
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Nucleic Acid Accession #: Eos sequence
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| 5  | GAAGAACCCA<br>TITATCTGTA<br>GACTTATTTG<br>GGTGTCACTG<br>AATGTGTTTT<br>ATCACTGTAG<br>AATGGTGTGC<br>CTGTCTGAAG<br>GGTGCTGTGG<br>CATGGGCAGG | CTITTGCATT CAGTAGCTAA TATTCTTTGC AAAATTACTG TCATTTTGAC TTGGTGGAA CCACGCTTGT TCTGTGCAAC AACCAAGGAC TGATGGTTTT AAATGTTCTA AGCAGACAAC | GTGGTCCCGC TACATGTGA TACACCTATG TCTTTCATCG GTCATTGCTG TCCCTCATT ACACCTCCGAT ACACCTCCGAT TGGATTCGTC CTGCTTTCCT | CTTATCCATA TACTTGACAT GACTTGTA GAATGCTTTG GTTTTCCACA ATTGATTGC TTTATCATTC AAGATTATCT AAGATTATCT GATGGCTATTA GACAATTTCT | IGTCCATCGT ITACTGCTT CATTTGGAAG IGACAAGAGA ITGGTGTAAC TCGGGATAGT CATCAGCCTG CTTGTGTCAT CAAATACTCA CTCTCACAAA | GATTTCTGTA CACCCAAGGG ATTTTGTTAT GGTAATTGCC AGTGATGGTC TCTAGAACTC TTATCTGAAA GCTTCCCATT AGACTGCACC TACCCAGAGG | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200 |
|----|--|--|---|--|--|---|--|
| 15 |  | 554 <u>Protei</u><br>ession #: E   |   |  |  |   |  |
|    | 1  | 11   | 21  | 31   | 41   | 51  |  |
| 20 | SYNIIAGDTL<br>TGLTTLILGI   | <br>PPQFSLVLLI<br>SKVFQRIPGV<br>VMARAISLGP   | DPENVFIGRH<br>HIPKTEDAWV  | FIIGLSTVTF<br>FAKPNAIQAV   | TLPLSLYRNI<br>GVMSFAPICH   | AKLGKVSLIS<br>HNSFLVYSSL  | 60<br>120<br>180   |
| 25 | GVTVILTYPM<br>NGVLCATPLI   | LIHMSIVISV<br>ECFVTREVIA<br>FIIPSACYLK<br>DNFSLTNTSE   | NVFFGGNLSS<br>LSEEPRTHSD  | VFHIVVTVMV<br>KIMSCVMLPI   | ITVATLVSLL   | IDCLGIVLEL  | 240<br>300<br>360  |
| 30 |  | 555 DNA se<br>d Accession<br>dence: 11   | #: Eos se   | quence   |  |   |  |
|    | 1  | 11   | 21  | 31   | 41   | 51  |  |
| 35 | CCAGGGTATC<br>TACAATATAA<br>CCTGAAAACG   | AGAGGCAGGA<br>TGCTCCTCTC<br>TAGCTGGAGA<br>TGTTTATTGG<br>CCTTGTACCG   | TGTTCTTCAG<br>TACTTTGAGC<br>TCGCCACTTC  | TTTTTGTATC<br>AAAGTTTTTC<br>ATTATTGGAC   | CTTTTATAGC<br>AAAGAATCCC<br>TTTCCACAGT   | AATGATAAGT<br>AGGAGTTGAT<br>TACCTTTACT  | 60<br>120<br>180<br>240<br>300   |
| 40 | GGTTTAACAA<br>ATACCAAAAA<br>GTTATGTCTT<br>GAACCCACAG   | CTCTGATTCT<br>CAGAAGACGC<br>TTGCATTTAT<br>TAGCTAAGTG<br>TCTTTGCTAC   | TGGAATTGTA<br>TTGGGTATTT<br>TTGCCACCAT<br>GTCCCGCCTT  | ATGGCAAGGG<br>GCAAAGCCCA<br>AACTCCTTCT<br>ATCCATATGT   | CAATTTCACT<br>ATGCCATTCA<br>TAGTTTACAG<br>CCATCGTGAT   | GGGTCCACAC<br>AGCGGTCGGG<br>TTCTCTAGAA<br>TTCTGTATTT  | 360<br>420<br>480<br>540<br>600  |
| 45 | TTATTTGAAA<br>GTCACTGTCA   | ATTACTGCAG<br>TTTTGACATA<br>GTGGGAATCT   | AAATGATGAC<br>CCCTATGGAA  | CTGGTAACAT<br>TGCTTTGTGA   | TTGGAAGATT<br>CAAGAGAGGT   | TIGITATGGT<br>AATTGCCAAT  | 660<br>720<br>780  |
| 50 | GGTGTGCTCT<br>TCTGAAGAAC<br>GCTGTGGTGA<br>GGGCAGGAAA   | CGCTTGTGTC<br>GTGCAACTCC<br>CAAGGACACA<br>TGGTTTTTGG<br>TGTTCTACTG<br>AGACAACACA   | CCTCATTTTT<br>CTCCGATAAG<br>ATTCGTCATG<br>CTTTCCTGAC  | ATCATTCCAT<br>ATTATGTCTT<br>GCTATTACAA<br>AATTTCTCTC   | CAGCCIGITA<br>GIGTCATGCI<br>ATACTCAAGA<br>TCACAAATAC   | TCTGAAACTG<br>TCCCATTGGT<br>CTGCACCCAT<br>CTCAGAGTCT  | 840<br>900<br>960<br>1020<br>1080  |
| 55 | Seq ID NO:<br>Protein Ac   | 556 Prote<br>cession #:  | in sequence<br>Eos sequenc  | e  |  |   |  |
|    | 1  | 11   | 21  | 31   | 41   | 51  |  |
| 60 | PENVFIGRHF<br>IPKTEDAWVF<br>ICIPPATCGY<br>VFFGGNLSSV<br>SEEPRTHSDK   | PHIVVTVMVI<br>IMSCVMLPIG   | LPLSLYRNIA<br>VMSFAFICHH<br>LFENYCRNDD<br>TVATLVSLLI  | KLGKVSLIST<br>NSFLVYSSLE<br>LVTFGRFCYG<br>DCLGIVLELN   | GLTTLILGIV<br>EPTVAKWSRL<br>VTVILTYPME<br>GVLCATPLIF   | MARAISLGPH  | 60<br>120<br>180<br>240<br>300<br>360  |
| 03 | Seq ID NO:   | S57 <u>DNA s</u><br>d Accessio   |   | 188.1  |  |   |  |
| 70 |  | uence: 769.  |   |  |  |   |  |
|    | 1<br>  | 11<br>   | 21<br>  | 31<br>   | 41<br>1  | 51<br>1   |  |
| 75 | CTCCCCCAAC<br>CTCCCCTGTC<br>CTCCCCTGTC   | TCTGTGTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC   | TCTCTCTCCCC TGGTTTTTGC CCCCCGGCCCC  | CTAAATCTCT ATCCCCCTCT GGACCTCTGC   | GGCCCTCCT<br>GCCCCTTGCC<br>ACCCCCCAGG  | AGTGTCAGTC TTCTGAGTTC TCAGTCAAGT TCGCTGTCCC TGGCGTCTCC TGGAGGATCC   | 60<br>120<br>180<br>240<br>300<br>360  |
| 80 | GCAGGAGGTT<br>CCCAAGATCT<br>GATGGGGTCT<br>TGCCTTGACG   | GCGGCGGCCC TCAAGAAGAA CGCTCTATTC TCCCAAAGTC  | GGGCAGCATO<br>GACCTGCACO<br>CCCAGGCTGT<br>CTTGGATTGT  | GTGGTGCCGG<br>ACGTTCATAG<br>TCTCAAACTC<br>GCCCAGCCGT   | AGAAGGAGCA<br>TTGACTCCAC<br>CTGGGCTCAA<br>CCTTGAAGTT   | GCCTGGGCT GAGCTGGATC AGATCCGGGG GCAGTCCTTC TTGCTCAGAA AACTAGGGGA  | 420<br>480<br>540<br>600<br>660<br>720   |

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|    |            |            | AGCCAGCCGC               |              |            |                          | 1080         |
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| 25 |            |            | AAAGATGGTG               |              |            |                          | 1260         |
|    | AAGGCATCAG | AGACCCCAAC | TCTACAAGGC               | CTTTCCTTTA   | CTGTCAGACC | TGGCGAATTG               | 1320         |
|    |            |            | GGGAGCAGGG               |              |            |                          | 1380         |
|    |            |            | GCTGGTCAGC<br>AACTCTGAGG |              |            |                          | 1440<br>1500 |
| 30 |            |            | CATAAAGGCT               |              |            |                          | 1560         |
|    |            |            | GATAGGAGAT               |              |            |                          | 1620         |
|    |            |            | AGCAGTGTAT<br>GGAAGTTAGC |              |            |                          | 1680<br>1740 |
|    |            |            | AATTTTAGTG               |              |            |                          | 1800         |
| 35 | AGTCAGATTC | TGATATTGAA | AGATGGTAAA               | ATGGTGCAGA   | AGGGGACTTA | CACTGAGTTC               | 1860         |
|    |            |            | TGGCTCCCTT               |              |            |                          | 1920         |
|    |            |            | CACACTAAGG<br>CTCCTTGAAA |              |            |                          | 1980<br>2040 |
| 40 |            |            | AGAGGAGAAC               |              |            |                          | 2100         |
| 40 |            |            | TGGTGCTCAC               |              |            |                          | 2160         |
|    |            |            | CTATGTGCTT<br>CACTGTAAAT |              |            |                          | 2220         |
|    |            |            |                          |              |            | TTTTGGCATA               | 2280<br>2340 |
| 45 |            |            |                          |              |            | GCACAACAAA               | 2400         |
| 45 |            |            | AGCTCCGGTA               |              |            |                          | 2460         |
|    |            |            | AGACATTGGA<br>GCTACAAGTG |              |            |                          | 2520<br>2580 |
|    |            |            | CTTGGTTCCC               |              |            |                          | 2640         |
| 50 |            |            | AGATGTGAAG               |              |            |                          | 2700         |
| 30 |            |            | TCTCCAGGGG<br>TGATGCACAC |              |            |                          | 2760<br>2820 |
|    |            |            | GTTCGCCGTC               |              |            |                          | 2880         |
|    | ATCATCGTTG | CCTTTGGGTC | CCTGATTCTG               | GCAAAAACTC   | TGGATGCCGG | GCAGGTTGGT               | 2940         |
| 55 |            |            | CACGCTCATG<br>GATCTCAGTA |              |            |                          | 3000         |
| 33 |            |            | TCAGAAACGC               |              |            |                          | 3060<br>3120 |
|    |            |            | CTTCATGTAC               |              |            |                          | 3180         |
|    |            |            |                          |              |            | CGGAGCTGGA               | 3240         |
| 60 |            |            |                          |              |            | AATTTGGATT<br>GTCAATCATA | 3300<br>3360 |
|    |            |            |                          |              |            | CTTTAATGAG               | 3420         |
|    |            |            |                          |              |            | AACCATTGAA               | 3480         |
|    |            |            |                          |              |            | TAGTGTTGGA<br>ATTGATTATT | 3540<br>3600 |
| 65 | GATGAAGOGA | CGGCAAATGT | GGATCCAAGA               | ACTGATGAGT   | TAATACAAAA | AAAAATCCGG               | 3660         |
|    | GAGAAATTTG | CCCACTGCAC | CGTGCTAACC               | ATTGCACACA   | GATTGAACAC | CATTATTGAC               | 3720         |
|    |            |            |                          |              |            | GCCGTATGTT               | 3780         |
|    |            |            |                          |              |            | CAAGGCAGAA<br>TCCACATATT | 3840<br>3900 |
| 70 |            |            |                          |              |            | CTTAACTATT               | 3960         |
|    | TTCGAGACAG | CACTGTGA   |                          |              |            |                          |              |
|    |            |            |                          |              |            |                          |              |
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| 75 |            |            | XP_036453.1              |              |            |                          |              |
|    | 1          | 11         | 21                       | 31           | 41         | 51                       |              |
|    | î          | î          | 1                        | ĭ            | 1          | Ĭ                        |              |
| 00 |            |            | RVFFWWLNPL               |              |            | DRSQHLGEEL               | 60           |
| 80 |            |            |                          |              |            | IFLGKIINYF               | 120          |
|    |            |            |                          |              |            | CHMIYRKALR<br>MEIGISCLAG | 180<br>240   |
|    |            |            |                          |              |            | WEKSFSNLIT               |              |
|    | nlrkkeiski | LRSSCLRGMN | LASFFSASKI               | IVFVTFTTYV   | LLGSVITASE | VFVAVTLYGA               | 360          |
|    |            |            |                          |              | 1          | 171                      |              |

|     | מכונו זמנות נתנ   | CATUULCUAT   | UCTOD COMET   | TIDETCODE    | OT DEDCKEMI     | UNIODETA PUD  | 420    |
|-----|-------------------|--|---------------|--------------|-----------------|---------------|--------|
|     | VRLTVTLFFP        | SATERVSEAL   | VSIRRIGIPL    | PERSTAGRAK   | <b>ÖDBƏDĞYY</b> | TAGRE THEAD   |        |
|     | KASETPTLQG        | LSFTVRPGEL   | LAVVGPVGAG    | KSSLLSAVLG   | ELAPSHGLVS      | VHGRIAYVSQ    | 480    |
|     | <b>QPWVFSGTLR</b> | SNILFGKKYE   | KERYEKVIKA    | CALKKDLQLL   | EDGDLTVIGD      | RGTTLSGGQK    | 540    |
|     | ARVNLARAVY        |  |               |              |                 |               | 600    |
| 5   |                   |  |               |              |                 |               |        |
| 3   | SQILILKDGK :      |  |               |              |                 |               | 660    |
|     | SQQSSRPSLK        | DGALESODTE   | NVPVTLSEEN    | RSEGKVGFQA   | YKNYFRAGAH      | WIVPIFLILL    | 720    |
|     | NTAAQVAYVL        |  |               |              |                 |               | 780    |
|     |                   |  |               |              |                 |               | 840    |
|     | ARSLLVFYVL        | VNSSOTLHNK   | WERSTFKWAN    | PLLDKNLICK   | ILINKESKUIG     | UPDDPPETI     |        |
|     | LDFIQTLLQV        | VGVVSVAVAV   | IPWIAIPLVP    | LGIIFIFLRR   | YFLETSRDVK      | RLESTTRSPV    | 900    |
| 10  | FSHLSSSLQG        | TANVAGITMI   | ERCORIATION   | ODLHSEAWEL   | FLTTSRWFAV      | RLDAICAMFV    | 960    |
| 10  | t Tith Soot Ti    |  | encompromi    | Spenoramoe   | A CHICADALI CHI | PRUTEVENI P   | 1020   |
|     | IIVAFGSLIL        | AKTLDAGQVG   | LALSYALTLM    | GWLGMCAKGS   | AE V ENMITS V   | FKAIFIIDDP    |        |
|     | KEAPWEYQKR        | PPPAWPHEGV   | I I FDNVNFMY  | SPGGPLVLKH   | LTALIKSQEK      | VGIVGRTGAG    | 1080   |
|     | KSSLISALFR        |  |               |              |                 |               | 1140   |
|     | HTDEELWNAL        | ODUOL VERTE  | DI DOMONTO    | ARCCOMPOUC   | OPOLUCIADA      | TI DIMINITI T | 1200   |
| 15  | HIDEELWAAL        | GEAGPKELIE   | DIFGRADIEL    | AESGSNESVG   | QXQLVCLIAKA     | TURNASIDII    |        |
| 15  | DEATANVDPR        |  |               |              |                 |               | 1260   |
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|     | FETAL             |  |               |              |                 |               |        |
|     | FEIRO             |  |               |              |                 |               |        |
|     |                   |  |               |              |                 |               |        |
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|     | •                 | <b>†</b> *   | 7.            | 7-           | ;-              | 1             |        |
| 0.5 | 1                 |  | }             | 1            | 1               | 1             |        |
| 25  | GGACAGGCGT        | GGCGGCCGGA   | GCCCCAGCAT    | CCCTGCTTGA   | GGTCCAGGAG      | CGGAGCCCGC    | 60     |
|     |                   | GCCTGATCAG   |               |              |                 |               | 120    |
|     |                   |  |               |              |                 |               | 180    |
|     |                   | CAGGAGGTGA   |               |              |                 |               |        |
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|     |                   | TCAGTGCTGC   |               |              |                 |               | 300    |
| 30  |                   |  |               |              |                 |               | 360    |
| 50  |                   | AAAGAAGTTT   |               |              |                 |               |        |
|     |                   | AAGTGTTACT   |               |              |                 |               | 420    |
|     | GGAAAGTGCC        | AAAGTAATCC   | AGCCCATATT    | TTTGGGAAAA   | ATTATTAATT      | ATTTTGAAAA    | 480    |
|     |                   | ATGGATTCTG   |               |              |                 |               | 540    |
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| 0.5 |                   | CTCATTTTGG   |               |              |                 |               | 600    |
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|     |                   | ATGGGGAAGA   |               |              |                 |               | 720    |
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|     |                   | GATCAGGTGA   |               |              |                 |               | 780    |
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| 40  |                   |  |               |              |                 |               | 960    |
| 40  | GAGTAAAACT        | GCAACTTTCA   | CGGATGCCAG    | GATCAGGACC   | ATGAATGAAG      | TIMIMACIGG    |        |
|     | TATAAGGATA        | ATAAAAATGT   | ACGCCTGGGA    | AAAGTCATTT   | TCAAATCTTA      | TTACCAATTT    | 1020   |
|     | CACAAACAAC        | GAGATTTCCA   | AGATTCTGAG    | AAGTTCCTGC   | CTCAGGGGGA      | TGAATTTGGC    | 1080   |
|     |                   | AGTGCAAGCA   |               |              |                 |               | 1140   |
|     |                   |  |               |              |                 |               |        |
|     |                   |  |               |              |                 | GGGCTGTGCG    | 1200   |
| 45  | GCTGACGGTT        | ACCCTCTTCT   | TCCCCTCAGC    | CATTGAGAGG   | GTGTCAGAGG      | CAATCGTCAG    | 1260   |
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| 65  | CTGGTACTTA        | GGAATTTATT   | CAGGTTTAAC    | TGTAGCTACC   | GTTCTTTTTC      | GCATAGCAAG    | 2460   |
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|     |                   |  |               |              |                 | 3 GAAGAATTTT  |        |
|     | AAATCGTTTC        | : TCCAAAGAC  | TTGGACACT     | r ggatgattt  | 3 CTGCCGCTG/    | CGTTTTTAGA    | 2640   |
|     |                   |  |               |              |                 | COGTGATTCC    |        |
| 70  |                   |  |               |              |                 |               |        |
| 70  |                   |  |               |              |                 | C GGCGATATTT  |        |
|     | TTTGGAAACC        | TCAAGAGAT  | G TGAAGCGCC   | r ggaatctac  | A ACTCGGAGT     | C CAGTGTTTTC  | 2820   |
|     | ניות השתישות עיים | The state of the s | A PURCULATION | CACCATION    | GCATACANA       | CAGAAGAGAG    | 2880   |
|     |                   |  |               |              |                 |               |        |
|     |                   |  |               |              |                 | r tettetttt   |        |
|     | GACAACGTC         | CCCCCCCTCC   | G CCGTCCGTC   | r GGATGCCAT  | C TGTGCCATG     | T TTGTCATCAT  | 3000   |
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| , , |                   |  |               |              |                 |               |        |
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| 80  | AGCACTCAT         | T AAATCACAA  | G AAAAGGTTG   | G CATTGTGGG  | A AGAACCGGA     | G CTGGAAAAAG  | 3360   |
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| 5   | ATGGCCTTCG GACCTGTGC GCATAATGG TCAGCATGGC CATATTTGTG AAAGGATTGA AGACAAAACA AAACATGAAA ACTTTTTAAT AGATTGCCAT Seq ID NO: | TCTTTCCATT AACAGAACTT ATCAAATATT AGACCAGTCC CAATGATTTG GCAATACATC GCAATACATC GAACTTTAAG TGACTGAAAA ACAGCAATCT GGAATCTTGCA 598 Protei | GCCACATACC<br>GTGGAGAATT<br>CACAAGATGT<br>AAAGAAGTTT<br>CCAACCTGG<br>AGTGGTGTGG<br>GAGCACCTGT<br>TCTTATGCTT<br>TTGCTTCCAA<br>AA<br>.n sequence | CAGGTATAAT CCCTAGCTGG CAACCAGTCG GGATCTCAGA CCTGGTGGAT ATGCAGACTC ACTTTTCAAG CTGAATAATC | AGTTTCTAAC AGAAGTCACA TTGTGTGCGG ACAACCTTTC AACCAACAAG TTCTTATTTT CCACTGGAGG AAAGACTAAT | ATTTGCCCAG<br>AAGACTATAG<br>CTGATGTTAA<br>TTGTTAGTAA<br>ATGGGAAGA<br>AAAATCTTTA<br>GAGAAATGGA<br>TTGTGATTTT | 720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200 |
|-----|--|--|--|---|---|---|---|
| 15  | 1  |  | _  | 21  | 41  | r1  |   |
|     | 1  | 11   | 21<br>   | 31  | 41<br>  | 51<br>  |   |
| 20  | GIGEELAYQL<br>ATKAVLQEFG<br>KQGKIVTVNS<br>IVENSLAGEV   | VLCALLLLLV<br>SKLGVSLVLS<br>RIDILVNNGG<br>ILGIISVPLS<br>TKTIGNNGDQ<br>KMGKKRIENF   | ARRVHELERV<br>MSQRSLCMDT<br>IGYCASKHAL<br>SHKMTTSRCV   | KRRCLENGNL<br>SLDVYRKLIE<br>RGFFNGLRTE<br>RLMLISMAND                                    | KEKDILVLPL<br>LNYLGTVSLT<br>LATYPGIIVS  | DLTDTGSHEA<br>KCVLPHMIER<br>NICPGPVQSN  | 60<br>120<br>180<br>240<br>300                                  |
| 25  |  | 599 DNA seid Accession<br>mence: 401.  | #: NM_000  | 793.2   |   |   |   |
| 30  | 1  | 11   | 21   | 31  | 41  | 51  |   |
| 30  | GCCTGCAGAG   | AGAGGCACTT   | <br>TGCACCACAG   | ACAGATAGCA  | AGAAGGGAAA  | <br>GACAGAGAGT  | 60  |
|     |  | AGGAGTCAGT<br>AGTGTGTGTA   |  |   |   | GGAGAAAGAG<br>TACCCTTAAA  | 120<br>180  |
| 35  | GCACATTTAA   | алалалала  | CTCTGGCAAT   | TCAAGAAAGA  | AACAGGCTAC  | GTTTAAAGAG  | 240   |
| 33  |  | ATGAAAGGCT<br>AAGTAGAACT   |  |   |   |   | 300<br>360  |
|     |  | ACAAGGGAAC   |  |   |   |   | 420   |
| 40  | CTATGACTCG   | ACACTGCAAA<br>GTCATTCTGC   | TCAAGCACGT   | GGTGCTGCTG  | TTGAGCCGCT  | CCAAGTCCAC  | 480<br>540  |
| 40  |  | TGGCGGCGCA<br>GCCTACAAAC   |  |   |   |   | 600<br>660  |
|     |  | AGTACAGAAG   |  |   |   |   | 720   |
|     |  | ACATGCCACC<br>GCCACTTGAC   |  |   |   |   | 780<br>840  |
| 45  | GGAAGAGTTC   | TCCTCAGTGG   | CTGACTTCCT   | GCTGGTCTAC  | ATTGATGAGG  | CTCATCCATC  | 900   |
|     |  | GCGATACCGG<br>CGATGTGCAG   |  |   |   |   | 960<br>1020   |
|     | GTGCCGAGTT   | GTGGCTGACC   | GCATGGACAA   | TAACGCCAAC  | ATAGCTTACG  | GGGTAGCCTT  | 1080  |
| 50  |  | TGCATTGTGC<br>CTTCAAGAAG   |  |   |   |   | 1140<br>1200  |
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|     |  | AAGGAAATTA<br>GAGTTTATCT   |  |   |   |   | 1320<br>1380  |
| 55  | CACTACTCAA   | ATGGCATTGG   | GCTGAGTAAG   | TAACCATATC  | ACCTCTCTTC  | TTAGTAAAAA  | 1440  |
| 33  | TCTGCATTGA   | AAAAGATCCC<br>GAAGGAACTG   | AAGATGGAGA   | GGAAGAAACG<br>TGCATGCTTT  | CTAATTCAGC  | ATGTGTTCAT<br>GAAAAGACTT  | 1500<br>1560  |
|     | ACCTGAATAA   | TTACTACATT   | AGGGAAGCTA   | CTGTCTACGT  | TAAGATAAAG  | GGTATTGCCT  | 1620  |
|     |  | TGGCATGGAT<br>GCCATGTGGT   |  |   |   |   | 1680<br>1740  |
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                                                                                      1800
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|---------------|--|---|--|---|---|---|--|
| 20            | Seq ID NO:<br>Protein Acc  | 608 <u>Protei</u><br>ession #: N  |  |   |   |   |  |
| 25            | LKTVQAFMIL<br>ANRDGTQYHH<br>Seq ID NO:   | 11   VHIATVIMLF SIIFCVIALL GYSYILGWIC 609 DNA se  | VFVFQLFTME<br>FCFSFIIGVL   | SNTVDASVGL<br>KGNRFFLSGA<br>YLVLRKK   |   |   | 60<br>120  |
| 30            |  | ence: 551   |  | 301.2   |   |   |  |
| 35            | TCCAAAGTTC<br>CCTCAGACTG<br>CAGCCTCTGG   | 11<br> <br>GAGCCGCGAC<br>TTCCAGTCCT<br>AATCAAAGAA<br>AAAATCAGCT<br>GCAAACTGCC   | CCTAGGCATC<br>TGAAGCCTCT<br>CCTCTCTGAG   | TTATTGATCC<br>TCCCGTGATG<br>GAAACAAAGT  | TCCAGTCGAG<br>TTGTCTATGG<br>CAACTGAGAC  | GGTCGAGGGA<br>CCCCCAGCCC<br>TGAGACTGGG  | 60<br>120<br>180<br>240<br>300   |
| 40            | GACCACAAAC<br>GTCAACAGCC<br>TCCCAGACCT<br>AATGGCAATG   | TGCGCCCTGG<br>TTGGTCCTCT<br>GGTACGACGA<br>TGGTGAGCCA  | CATTGGAGAG<br>CTCTATCCTA<br>ACGCCTCTGT<br>GCTATGGATC   | AAGCCCACTG<br>GACATGGAAT<br>TACAACGACA<br>CCGGACACCT  | TGGTCACTGT<br>ACACCATTGA<br>CCTTTGAGTC<br>TTTTTAGGAA  | TGAGATCGCC<br>CATCATCTTC<br>TCTTGTTCTG<br>TTCTAAGAGG  | 360<br>420<br>480<br>540   |
| 45            | GTGTTGTACA<br>CCAATGGATT<br>ATGATCTACA   | AGTGGGAAAA  | GACCATTGAT<br>CCCTCTATCT<br>TTTCAAGCTT   | GCCGGATGCT<br>TTCTCTAGCT<br>GAAATCAATG  | CACTCCACAT<br>TTTCCTATCC<br>AGAAGAACTC  | GCTCAGATTT<br>TGAGAATGAG<br>CTGGAAGCTC  | 600<br>660<br>720<br>780<br>840  |
| 50            | GACTTCATGG CAAAACTATG ACAGAGTCTG TTGGGCACCT TATATCGCCA   | TCCCTTCTTC<br>CTCCAGCCCG<br>TTTCTCGTAA<br>TCTGCTTCGT  | TTTCTTCAAT CGTGACCACG GACCTCTCTA GAATTTCCCG CTTCTGCTTC   | GTGAGCAGGC<br>ATGCTCTCCT<br>GGGATCACCT<br>CGTGTCTCCT<br>TGCGCTCTGT  | GGTTTGGCTA<br>GGGTTTCCTT<br>CTGTTCTGAC<br>ATATCACAGC<br>TGGAGTTTGC  | TGTTGCCTTT TTGGATCAAG CATGACCACG CTTGGATTTC TGTGCTCAAC  | 900<br>960<br>1020<br>1080<br>1140   |
| 55            | AATAGCCGTG<br>GAAGCTTTTG<br>TGCTCAGCCC<br>AAGCTGGCCT   | CCCATGCCCG TGTGCCAGAT AGCAGCCCCCC CGTGTGAGTG  | TACCCGTGCA<br>TGTCACCACT<br>TAGCCCAGGT<br>GTGCAAGCGT   | CGTTCCCGAG GAGGGAAGTG AGCCCTGAGG TTTAAGAAGT   | CCTGTGCCCG ATGGAGAGGA GTCCCCGCAG ACTTCTGCAT   | CCAACATCAG<br>GCGCCCGTCT<br>CCTCTGCTCC<br>GGTCCCCGAT  | 1260<br>1320<br>1380<br>1440   |
| 60            | TACTCGAGAG<br>TGCCTTAACT<br>GGTCCAAGCC<br>AGTTTTTCCT   | TTGTTTTCCC TGTAGGTACC CCTTGCCAAC  | AGTGACTTTC AGCTGGTACC GGAGTTGGGC CCAAACAGA   | TTCTTCTTCA<br>CTGTGGGGCA<br>GAAAGCAGCA<br>GCTTGCAGAG  | ATGTGCTCTA<br>ACCTCTCCAG<br>GCAGCAGCAG<br>GGTTTGTCTT  | CCTGGATAAC<br>CTGGCTTGTT<br>TTCCCCAGGA<br>GAGCGACTAG<br>TGCTGCCCCT  | 1500<br>1560<br>1620<br>1680<br>1740   |
| 65            | TCCCCTACC<br>TGCGCCACCT<br>ACTTAGTGAT<br>AATGCTGACC<br>CTTTCGGCCC  | TGGCCATTC CCCTCTTCT CAGCTCCCTA ACCAGACAA AGTTCTGGCC   | CAAGGAGTCTT CAAGGAGCAT AAACCATGCCTTACTGCATTT TCAGCCTCAT  | CTCAGCAGAC<br>CCGTGATGCT<br>CTAAGTACAGC<br>TTCCAGAAGC<br>AAGTGCACCGF  | CATTTCAAAT CAGTGTTCAF GGGATTAGCT CCACTATTGC ACTAGTTGCTT   | TATTAATAAA AACCACAGCC ATCTTCCAAC CTTTGTAGTG GCCTATACCT  | 1860<br>1920<br>1980<br>2040   |
| 70            | TCAGATTATT<br>CACTGGCATT<br>TTCCTCTCTCT  | TATCTCTCAC<br>TATCCCTTTAC<br>TCTGCTGCTC   | TTCTCTCTCC<br>GAAGAGGGGG<br>TGACATCTC  | CTGCTACCCC<br>GGGCAGCAAC<br>CTCTCCTTGC  | TTTCTCTGCI AGAGCCTAT  | C TCTCCTTTGG A GATAGATAGA T TGGGACAGCA TTTCGTCTGC A TTATAGTAAC  | 2160<br>2220<br>2280   |
| 75            | TACTCCCTGC ACTTTCCCAC GCCAAGAAAC ACCCAGGGCC CACTGTTAT  | C TTTATATGO<br>G TGACTTCCC<br>C TAAGGAAAC<br>A CACTGTCGG<br>A CCCGGGGCA   | C ACCCTCTIC<br>C TAGCCCTGA<br>I CGGCTTTGC<br>A GTTCTATCA<br>C TCTAACCAT  | TTCTCTTTGI CCAGGCACTI ACAGGCATTI CTTGCTTGACC ACAATCAATC   | A CCCCTGTGA<br>A GGCCTTGGT<br>A CTCGCCATT<br>C CCTGGACCC<br>C AATCAAATT   | TCTTTCTGTA CTTCCTGGG ATTGGTGCCCA TAAACCAGTCCCCTTAAATTT GGAGCTTCAT   | 2400<br>2460<br>2520<br>2580<br>2640   |
| 80            | GATAGCCTT<br>GAGTCACAG<br>ACCTTCTAG<br>CTCTGCTGG<br>GGCCTGAGG  | G TGACATCTT A TTTCTGTGG A CCACATGAT C ACACCAGTG T GCTCAGACT   | T AGGGCAGGA G ACTGTGGAT A GGGCTAGAC G CAAGGCCCA G CCCCCAAGA  | T TCTTATCCC  C TCACTGGAA  A GCTCAGTTC  G AATGGCGAC  T CAAATCTCT   | C ATTTTGCAG G CTATCCAAG A CCATGATTC C TCTCTTTAG C CTGGCTGTA   | A TGAAAACCTI A GCCCACTGTC I CTTCTGTCAC C TCAATTTCTG G TAACCCAGTG T GTCTGTAATT   | 2760<br>2820<br>2880<br>2940<br>3000   |

Seq ID NO: 610 Protein sequence 5 Protein Accession #: NP\_004952.1 41 31 MLSKVLPVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60 10 TGSRVGKLPE ASRILNTILS NYDHKLRPGI GEKPTVVTVE IAVNSLGPLS ILDMEYTIDI 120 IFSQTWYDER LCYNDTFESL VLNGNVVSQL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180 GKVLYTIRMT IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIYKWENF KLEINEKNSW KLFQFDFTGV SNKTEIITTP VGDFMVMTIF FNVSRRFGYV AFQNYVPSSV TTMLSNVSFW 300 IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIAICFVF CFCALLEFAV LNFLIYNQTK AHASPKLRHP RINSRAHART RARSRACARQ HQEAFVCQIV TTEGSDGEER 360 15 420 PSCSAQQPPS PGSPEGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL DNYSRVVFPV TFFFFNVLYW LVCLNL Seq ID NO: 611 <u>DNA sequence</u> Nucleic Acid Accession #: NM\_021984.1 20 Coding sequence: 572..1753 25 GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCGCGC CGGTCTCCGC GGAAATGTTG 60 TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120 CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCCTTTGT CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 240 300 TCAGACTGAA TCAAAGAATG AAGCCTCTTC CCGTGATGTT GTCTATGGCC CCCAGCCCCA 360 GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420 CAGAGTTGGC AAACTGCCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA 480 540

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Seq ID NO: 612 Protein sequence Protein Accession #: NP\_068819.1

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Seq ID NO: 615 DNA sequence
Nucleic Acid Accession #: NM\_021990.1
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| •    |    | î            | 1             | 41          | 1           | 41               | 31         |      |
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|      |    |              | TTCCAGTCCT    |             |             |                  |            | 120  |
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| 10   | J  | GTGTAAAGAA   | AGCCAAATCA    | AGGACCCGAA  | TGTGAGCAGG  | ACCTCAGAAG       | CCCCCTTTGT | 240  |
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|      |    |              | CTGTCTGTGG    |             |             |                  |            | 480  |
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|      | •  |              | AAAACCGCAA    |             |             |                  |            | 600  |
|      |    |              | TCCTCTCAGC    |             |             |                  |            | 660  |
|      |    |              |               |             |             |                  |            |      |
|      |    |              | TAGAGGCCAA    |             |             |                  |            | 720  |
| 20   | Λ. |              | TTCATTTCAC    |             |             |                  |            | 780  |
| 21   | U  |              | AATAAAAGAG    |             |             |                  |            | 840  |
|      |    |              | TTAAAGAAAT    |             |             |                  |            | 900  |
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|      |    | GAGGCACTAG   | CTGGGGCCCC    | TACAGAGTGC  | AGGGCAGAGC  | TTCATTTTTC       | GTTTGAATGT | 1020 |
| _    | _  | TCTAGGGTCG   | AGGGACCTCA    | GACTGAATCA  | AAGAATGAAG  | CCTCTTCCCG       | TGATGTTGTC | 1080 |
| 2:   | 5  | TATGGCCCCC   | AGCCCCAGCC    | TCTGGAAAAT  | CAGCTCCTCT  | CTGAGGAAAC       | AAAGTCAACT | 1140 |
|      |    |              | CTGGGAGCAG    |             |             |                  |            | 1200 |
|      |    |              | ATTATGACCA    |             |             |                  |            | 1260 |
|      |    |              | TCTCCGTCAA    |             |             |                  |            | 1320 |
|      |    |              | TCTTCTCCCA    |             |             |                  |            | 1380 |
| - 30 | n  |              | TTCTGAATGG    |             |             |                  |            | 1440 |
| -    | •  |              | AGAGGACCCA    |             |             |                  |            | 1500 |
|      |    |              |               |             |             |                  |            |      |
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|      |    |              |               |             |             |                  | CAGGCGGTTT | 1800 |
|      |    |              | CCTTTCAAAA    |             |             |                  |            | 1860 |
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|      | ^  | CTGACCATGA   | CCACGTTGGG    | CACCTTTTCT  | CGTAAGAATT  | TCCCGCGTGT       | CTCCTATATC | 1980 |
| 4    | U  | ACAGCCTTGG   | ATTTCTATAT    | CGCCATCTGC  | TTCGTCTTCT  | GCTTCTGCGC       | TCTGTTGGAG | 2040 |
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| •    |    |              |               |             |             |                  |            |      |
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|      |    |              |               |             |             |                  | CTTCAATGTG | 2460 |
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|      |    |              |               |             |             |                  | ACCCCTTTCT | 3060 |
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| - 6  | 0  |              |               |             |             |                  | TATTTTTGTG | 3240 |
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| 6    | 5  |              |               |             |             |                  |            |      |
| J    | _  |              |               |             |             |                  |            | 3540 |
|      |    |              |               |             |             |                  | AGTTGTGTCT | 3600 |
|      |    |              |               |             |             |                  | CCCCATTTTG | 3660 |
|      |    |              |               |             |             |                  | GAAGCTATCC | 3720 |
| ~    | 0  |              |               |             |             |                  | TTCACCATGA | 3780 |
| 1    | U  | TTCTCTTCTC   | TCACCTCTGC    | TGGCACACCA  | GTGGCAAGGC  | CCAGAATGGC       | GACCTCTCTT | 3840 |
|      |    | TAGCTCAATT   | TCTGGGCCTG    | AGGTGCTCAG  | ACTGCCCCCA  | AGATCAAATC       | TCTCCTGGCT | 3900 |
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|      |    |              |               |             |             |                  | TTTTGTCACC | 4020 |
| _    |    |              | ATGGGGAAAT    |             |             |                  | · <b>-</b> |      |
| 7    | '5 |              |               |             |             |                  |            |      |
| •    | -  | Seg ID NO.   | 616 Prote     | in semience |             |                  |            |      |
|      |    |              | cession #:    |             |             |                  |            |      |
|      |    | 1            | 11            | 21          | 31          | 41               | 51         |      |
| 8    | 0  | ĩ            | ī             | ī           | 1           | ī*               | ĭ          |      |
| _    | -  | MEALLLULANCE | I OTWANDED TO | MOTERCIATE  |             | <br>  Department |            | -    |
|      |    |              |               |             |             |                  | HEHEITMPNQ | 60   |
|      |    | MAKTAKTCK    | LYTIRMTIDA    | GCSLHMLRPF  | FIDSHSCPLSF | SSFSYPENEM       | IYKWENFKLE | 120  |
|      |    |              |               |             |             |                  | NYVPSSVTTM | 180  |
|      |    | LSWVSFWIKT   | ESAPARTSLO    | ITSVLTMTTI  | GTFSRKNFPR  | VSYITALDFY       | IAICFVFCFC | 240  |
|      |    |              |               |             |             |                  | 100        |      |
|      |    | •            |               |             |             | 1                | 188        |      |

|                            | GSDGEERPSC   | LIYNQTKAHA<br>SAQQPPSPGS<br>SRVVFPVTFF   | PEGPRSLCSK   | LACCEWCKRF   | SRACARQHQE<br>KKYFCMVPDC   | AFVCQIVTTE<br>EGSTWQQGRL   | 300<br>360  |
|----------------------------|--|--|--|--|--|--|---|
| 5                          |  | 617 <u>DNA</u> seid Accession<br>mence: 26   | 1 #: NM_004  | 864.1  |  |  |   |
| 10                         | 1  | 11   | 21   | 31   | 41   | 51   |   |
| 10                         | TCAGATGCTC<br>GGCCGAGGCG   | GCAACCTGCA<br>CTGGTGTTGC<br>AGCCGCGCAA   | TGGTGCTCTC<br>GTTTCCCGGG   | GTGGCTGCCG<br>ACCCTCAGAG   | CATGGGGGCG   | CCCTGTCTCT   | 60<br>120<br>180  |
| 15                         | CTGGGAAGAT<br>AGTGCGGCTG<br>GGGGCTCCCC   | TTGCGGAAAC<br>TCGAACACCG<br>GGATCCGGCG<br>GAGGCCTCCC<br>GACGTGACAC   | ACCTCGTCCC<br>GCCACCTGCA<br>GCCTTCACCG   | GGCCCCTGCA<br>CCTGCGTATC<br>GGCTCTGTTC   | GTCCGGATAC<br>TCTCGGGCCG<br>CGGCTGTCCC   | TCACGCCAGA<br>CCCTTCCCGA<br>CGACGCCGTC   | 240<br>300<br>360<br>420<br>480   |
| 20                         | GCCCGCCCTG   | CACCTGCGAC   | TGTCGCCGCC   | GCCGTCGCAG   | TCGGACCAAC   | TGCTGGCAGA   | 540   |
| 20                         | CCGCAGAGCG<br>TCTGCACACG<br>ACGGGAGGTG   | GCACGGCCCC<br>CGTGCGCGCA<br>GTCCGCGCGT<br>CAAGTGACCA   | ACGGGGACGA<br>CGCTGGAAGA<br>TGTGCATCGG   | CTGTCCGCTC<br>CCTGGGCTGG<br>CGCGTGCCCG   | GGGCCCGGGC<br>GCCGATTGGG<br>AGCCAGTTCC   | GTTGCTGCCG<br>TGCTGTCGCC<br>GGGCGGCAAA   | 600<br>660<br>720<br>780  |
| 25                         | CATGCACGCG<br>CTGCTGCGTG<br>GTCGCTCCAG   | CAGATCAAGA<br>CCCGCCAGCT<br>ACCTATGATG<br>CTGTGCACCT   | CGAGCCTGCA<br>ACAATCCCAT<br>ACTTGTTAGC   | CCGCCTGAAG<br>GGTGCTCATT<br>CAAAGACTGC   | CCCGACACGG<br>CAAAAGACCG<br>CACTGCATAT   | AGCCAGCGCC<br>ACACCGGGGT<br>GAGCAGTCCT   | 840<br>900<br>960<br>1020   |
| 30                         | GGGCTCAAGG<br>TTATTTATTA   | TTCCTGAGAC   | ACCOGATTCC<br>GGGGTGACCT   | TGCCCAAACA<br>TCTTGGGGAC   | GCTGTATTTA<br>TCGGGGGCTG   | TATAAGTCTG<br>GTCTGATGGA   | 1080<br>1140<br>1200  |
| 35                         |  | 618 Protes   |  |  |  |  |   |
|                            | 1 ·  | 11   | 21   | 31   | 41   | 51   |   |
| 40                         | EDLLTRLRAN<br>HRALFRLSPT   | GSQMLLVLLV<br>QSWEDSNTDL<br>ASRSWDVTRP<br>GRRARARNG<br>ANMHAQIKTS  | VPAPAVRILT<br>LRRQLSLARP<br>DDCPLGPGRC   | PEVRLGSGGH<br>QAPALHLRLS<br>CRLHTVRASL   | LHLRISRAAL<br>PPPSQSDQLL<br>EDLGWADWVL   | PEGLPEASRL<br>AESSSARPQL<br>SPREVOVIMC   | 60<br>120<br>180<br>240<br>300  |
|                            |  | -  |  |  |  | CACCACTIONS  | 300   |
|                            | LAKOCHCI   | -  |  |  |  | 0.0201.000   | 300   |
| 45                         | Seq ID NO:<br>Nucleic Ac   | 619 <u>DNA</u> solid Accession<br>lence: 254.  | equence  |  |  |  | 300   |
|                            | Seq ID NO:<br>Nucleic Ac   | 619 <u>DNA se</u><br>ld Accession  | equence  |  | 41   | 51   | 300   |
| 45<br>50                   | LAKOCHCI Seq ID NO: Nucleic Act Coding sequents  | 619 <u>DNA se</u> ld Accession lence: 254.   | equence<br>n #: NM_003<br>.1357  | 979.2<br>31  | <b>41</b><br>  | 51<br>   |   |
|                            | LAKDCHCI Seq ID NO: Nucleic Ac: Coding sequence  ATAACAGCAT TCCTTGTCCC ACAACTGCTC  | 619 DNA seld Accession dence: 254.   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGATAG   | 31   TAGGCGTGTC TCCCTCCCTC   | 41<br> <br>CTCTCCCTCG<br>CGGCGAGGGC<br>TCTCCCCCAG  | 51<br> <br>  ACCCTCCCCC<br>CGCCTTTATA<br>CACTGAGGAG  | 60<br>120<br>180  |
| 50                         | Seq ID NO: Nucleic Ac: Coding sequence  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CCTCGCCTGCT   | 619 DNA sid Accession dence: 254.  | equence 1 #: NM_003 .1357 21   GGAACTGGAA CCTCGCTCGT GCGGGGATAG GCGCGGGAAG   | 31   TAGGCGTGTC TCCCTCCCTC CTGTCCAAGG  | 41<br> <br>CTCTCCCTCG<br>CGGCGAGGGC<br>TCTCCCCCA<br>TTCACGGCA  | 51<br> <br>ACCCTCCCC<br>CGCCTTTATA<br>CACTGAGGA<br>ACGCCTTGAGC   | 60<br>120<br>180<br>240   |
|                            | Seq ID NO: Nucleic Ac: Coding sequ  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CCTCGCCTGCT ACTAGGGTCC  | 619 DNA seld Accession sence: 254  | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGATAG GCCGGGAAG CCACAGTCCC  | 31  <br>TAGGGGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACCAG<br>TGATGGTTGC  | 41<br> <br>CTCTCCCTCG<br>CGGCGAGGGC<br>TCTCACGCCA<br>TCTCACGCCCA<br>CGCAATGGCC   | 51<br> <br>ACCCTCCCC<br>CGCCTTTATA<br>CACTGAGGAG<br>ACGCCTTGGC<br>TGAAATCCAA   | 60<br>120<br>180<br>240<br>300  |
| 50                         | Seq ID NO: Nucleic Ac: Coding sequ  ATAACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT   | 619 DNA sid Accession tence: 254.  11    GAAGTGCCGT TCTGCTCACC AGAGTGCGAG GCCTCTTGC AGATGGCTA CTTTGTGATA CTTTGTGATA GTGACCTCGG   | equence 1 #: NM_003 .1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGATAG GCCGGGAAG CCACAGTCCC AGGCTGAAGC  | 31<br>  TAGGGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACCAAG<br>TGATGGTTGC<br>TTGGGGCATC  | 41<br> <br>CTCTCCCTGG<br>CGGCGAGGGC<br>TTCACCCCAG<br>TTCACGGCCA<br>GGCATGGCC<br>GTCCTAGAAA   | 51<br> <br>ACCCTCCCC<br>CGCCTTTATA<br>CACTGAGGAG<br>ACGCCTTGGC<br>TGAAATCCAA<br>CGGTGGCCAC   | 60<br>120<br>180<br>240<br>300<br>360<br>420  |
| 50<br>55                   | LAKDCHCI Seq ID NO: Nucleic Ac: Coding sequ  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CCTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT GCAGGACTCC  | 619 DNA seld Accession lence: 254  11    GAAGTGCCGT TCTGCTCACC AGAGTGCGAG GCCCTCTTGC AGAATGGCTA CTTTGTGATA CTTTGTGACT ACAGGCGAA  | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGAAG CCACAGTCCC AGGCTGAAGC TGGCCTCAT AAATGCTGCC   | 31<br>  TAGGGGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>TGATGGTTGC<br>TTGGGGCATC<br>GCTCACTGTT   | 41<br> <br>CTCTCCCTCG<br>CGGGAGGGC<br>TCTCCCCAG<br>TTCACGCCA<br>CGCAATGGCC<br>GTCCTAGAAA<br>CCGATCCTCG<br>CTCTTCCTCC   | 51<br> <br>ACCCTCCCC<br>CGCCTTTATA<br>CACTGAGGAG<br>ACGCCTTGGC<br>TGAAATCCAA<br>CGGTGGCAC<br>TCTGCAAGGT<br>TCGGAGGTT<br>TCGGTGTGTT   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480   |
| 50                         | Seq ID NO: Nucleic Ac: Coding sequ  ATANCAGCAT TCCTTGTCCC ACAACTGCTC CTGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT GCAGGATCTCTTACAGTA AGCCTGCTTCTTTACAGTACTTCTTTC   | 619 DNA si ld Accession lence: 254.  11   GAAGTGCCGT TCTGCTCACC AGAGTGCGAG GCCTCTTGC AGAATGGCTGA AGAATGGCTGA AGAATGGCTGA AGAATGGCTA AGAGTGAAA GCCTCACCT CTCTTTGGGA GCCTCACCT   | equence n #: NM_003 .1357  21   GGAACTGGAA CCTCGCTCGT GGCGGGATAG GCCGGGAAG CCACAGGTCCC CAGCTGAAGC TGGCCTCAT AAATGCTGCC TCGCCTTCAT TCCTCTTTC  | 31<br>  TAGGCGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACCAAG<br>TGATGGTTGC<br>GCTCACTCTC<br>TACTCAGTTT<br>CATCGGACTT   | 41<br> <br>CTCTCCCTGG<br>GGGGAGGGC<br>TCTCCCCAG<br>TTCACGGCCA<br>GCCAATGCC<br>GTCTTAGAAA<br>CCGATCCTCG<br>CTCTTCCTCC<br>GACGGGAGCA   | 51<br>  ACCCTCCCCC<br>CGCCTTTATA<br>CACTGAGGAG<br>ACGCCTTGGC<br>TGAAATCCAA<br>CGTGGCCAC<br>TCTGCAAGGT<br>TCGGTGTGTT<br>CAGGGCCCAC<br>TGGCTCATGC  | 60<br>120<br>180<br>240<br>300<br>360<br>420  |
| 50<br>55                   | Seq ID NO: Nucleic Ac: Coding sequ  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTACGGGTC GTACTACAGA AGCCGGGGTT GCAGGACTCCT ACGCTTCTTC CGGGCATCTTT ACGCTTCTTC TGTCAGTCTG  | 619 DNA seld Accession lence: 254  11    GAAGTGCCGT TCTGCTCACC AGAGTGCGAG GCCCTCTTGC AGAATGGCTA CTTTGTGATA GTGACCTCGG AACAGGCGAA GGCCTCACCT CTCTTTTGGGA ACCAAGCTCGG  | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGAAG CCACAGTCCC AGGCTGAAGC TGGCCTTCAT AAATGCTGCC TCGCCTTCAT TCCTCTTTTCT TCCGGGGGAG  | 31<br>  TAGGGGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACAAG<br>TGATGGTTGC<br>TTGGGGCATC<br>GCTCACTGTT<br>CATCGGACTG<br>CATCTGCTTC  | 41<br> <br>CTCTCCCTGG<br>CGGGAGGGC<br>TCTCCCGG<br>GCGATGGCC<br>GTCCTAGAAA<br>CCGATCCTGG<br>CTCTTCCTCC<br>GACGGAGCA<br>TCCTGCCTGC   | 51<br> <br>ACCCTCCCC<br>CGCCTTTATA<br>CACTGAGGA<br>ACGCCTTGGC<br>TGAATCCAA<br>CGGTGGCAC<br>TCTGCAAGGT<br>TCGGAGGTGT<br>CAGGGCCAC<br>TGGCTCATGC   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600   |
| 50<br>55                   | Seq ID NO: Nucleic Ac: Coding sequence  ATAACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGTTT GCAGGACTCC GGGCATCTTT ACGCTTCTTC TCTCAGTCTG TCTGCCTGC CATGAATAGG  | 619 DNA selld Accession lence: 254.  11   GAAGTGCCGT TCTGCTCACC AGAGTGCGAG GCCTCTTGC AGAGTGCTA ACTAGGCGAA ACCAAGCTCA ACCAA  | equence n #: NM_003 .1357  21   GGAACTGGAA CCTCGCTCGT GGCGGGAAG CCACAGTCCC AGGCTGAAGC TGGCCTCAT AAATGCTGCT TCCCCTTCAT TCCTCTTTC TCCGGGGGAG TAGTCCAGGA AATCCTTTTC   | 31<br>  TAGGCGTGTC<br>CTGTCCAAGG<br>CAGCACAAGG<br>TGATGGTTGC<br>TTGGGGCATC<br>GCTCACTCTC<br>TACTCAGTTT<br>CATCGGACTG<br>CATCTGCTTC<br>GAAGCCCTT<br>TGTTATCGCT<br>TGGCTTTC  | 41   CTCTCCCTGG GGGGGGGGC TCTCCCCAG TCCACGGCA GCGCATGGCC GTCTTAGAAA CCGATCCTGG GACGGGAGCA TCCTGCTGC TCCTGCTTGG ATTGAATATATA  | 51<br>  ACCCTCCCCC<br>CGCCTTTATA<br>CACTGAGGAG<br>ACGCCTTGGC<br>TGGATGGCCAC<br>TCTGCAAGGT<br>TCGGGTGTGTT<br>CAGGGCCCAC<br>TGGCTCATGC<br>TGGTTCATGC<br>TGATTCCTGGC<br>TGGTTCCTGAG<br>GCAATGAAGA   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>720  |
| 50<br>55<br>60             | Seq ID NO: Nucleic Ac: Coding sequ  ATRACAGCAT TCCTTGTCCC ACTACTGCTC ACTACGGTTC ACTACGGGTTC GCACGACTCCT GCACGACTCTT CGCGCTTCTTC TCTCAGTCTTC  | 619 DNA se Id Accession Lence: 254.  11    GAAGTGCCGT TCTGCTCACC AGAGTGCCGA AGAGTGCCAC AGAGTGCCAC AGAGCTCAC TCTTTTGGATA AACAGCCAAC GCCTTCACC CTCTTTTGGA ACCAGCTCA CTCTTTTGGA ACCAACCTCA CTCACCTC ACCAACCTCAC ACCAACCTCAC ACCAACCTCAC ACCAACCTCAC ACCAACCTCAC ACCAACCTCAC ACTCACCTC   | equence 1 #: NM_003 1357 21   GGRACTGGAA CCTCGCTCGT GGCGGGAAG CCACGGGAAG CCACGGTGAAGC TGGCCTTCAT AAATGCTGCC TCGCCTTCAT TCCTCTTTTC TCCCGGGGAG TAGTCCAGGA ATGTCTTTC  | 31<br>  TAGGGGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACAAG<br>TGATGGTTGC<br>TTGGGCATC<br>GCTCACTCTC<br>TACTCAGTTT<br>CATCGGACTG<br>CATCTGCTTT<br>TGTATCGCT<br>TGAGCTTTCC<br>CTTGATGCGCT   | 41   CTCTCCCTGG CGGCAAGGCC TCTCCCCAG TTCACGGCCA CGCAATGGCC GTCCTTCCTCC GACGGGAGCA TCCTGCTTGG ATTGAATATA GCTCCTCGTTGG CTGACCTTCC CTGACCTTCC CTGACCTTCC CTGACCTTCC CTGACCTTCC CTGACCTTCC CTGACCTTCC CTGACCTTCC CTGACCTTCC  | 51    ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TCTGCAAGGT TCGGGTGTGTT CAGGCCCAC TGGCTCATC TGATTCTGGG TTGTCCTGAC GCAATGAAGA TCATGTCCTT   | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840  |
| 50<br>55                   | Seq ID NO: Nucleic Ac: Coding sequitarian  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT ACGCTTCTTC GGGGCATCTTT ACGCTTCTTC TCTGAGTCTG CATGAATAGG CTTTGTCCTC CTTCACCTTC CTTCACCTTC   | 619 DNA seld Accession sence: 254.  11   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGATAG CAACAGTCCC AGGCTGAAGC TCGCCTTCAT TCCTCTTCT TCGCGGGAA ATGCTCCTCTTTC TCCGGGGAA ATGTCCAGGA ATGTCTTTTC ACGTCCTCTT  | 31<br>  TAGGCGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACCAAG<br>GTGATGGTTG<br>GTCACTCTC<br>CATCTCAGTTT<br>CATCGGACTG<br>CATCTGCTTT<br>GAAGCCCCTT<br>TGTATGCCT<br>TGAGCTTCC<br>CTTGATGGCG<br>CATCTGCTTCC  | 41   CTCTCCCTGG CGGGGAGGGC TCTCCCCAG TTCACGGCCA GCGCAATGGCC GTCCTAGAAA CCGATCCTCG GACGGGAGCA TCCTGCTGG TCCCTGTTGG ATTGAATATA GCTCCTCGTC CTGACCTTCC CGGGCCCTGCA   | 51<br>  ACCCTCCCCC<br>CGCCTTTATA<br>CACTGAGGAG<br>ACGCCTTGGC<br>TGAAATCCAA<br>CGGTGGCCAC<br>TCTGCAAGGT<br>TCAGGGCCCAC<br>TGGCTCATGC<br>TGATTCTCGG<br>TTGTCCTGAC<br>GCAATGAGA<br>TCATGTCCTCAC   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>720<br>780<br>840<br>900  |
| 50<br>55<br>60             | Seq ID NO: Nucleic Aci Coding sequ  ATAACAGCAT TCCTTGTCCC ACTACTGCTC ACTACTGCTC ACTACTGCTC ACTACTGCTC ACTACTGCTC ACTACTGCTC TCACTGCT TCTCGCTTCT TCTCAGTCTT TCTCAGTCTT TCTCAGTCTT CATGAATAGG CATGAATAGG CATGAATAGG CATGAATAGG CATGAATAGG CATGAATAGG CTTCACCTTC TCTCACCTTC TGACCGCAGG  | 619 DNA se Id Accession Lence: 254.  11    GAAGTGCCGT TCTGCTCACC AGAGTGCCGA AGAGTGCCGA AGAGTGCCACT CTTTTGGTATA ACCACCTCACCT  | equence 1 #: NM_003 1357 21   GGRACTGGAA CCTCGCTCGT GGCGGGATAG CCACCGGTCAAG CAACAGTCCC AGGCTGAAGC TGGCCTTCAT TCCTCTTTC TCCGGGGAGA ATGTCTTTTC TCCGGGGGAG ATGTCCTTTTC TCACGGGCTG TCACTTTTC TCACGGCTGTTTC TCACGGCTGTTTC TCACGGCTG   | 31<br>  TAGGCGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACAAG<br>TGATGGTTGC<br>TTCCAGTTT<br>CATCGGACTG<br>CATCTGCTTC<br>CATCGGCTTT<br>CATGGCTTTC<br>TGAGCCTTTC<br>TGAGCTTTCC<br>CTTGATGGCG<br>GAAGAGACAT<br>CTGGATCACC   | 41   CTCTCCCTGG CGGCAAGGCC TCTCCCCAG TTCACGGCCA CGCAATGGCC GTCCTAGAAA CCGATCCTGG CTCTCCTCC GACGGAGAGA TCCTGGCTGG ATTGAATATA GCTCCTGGT CTGACCTTCC GGGGCCCACA CTGCTCATGG   | 51    ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCACGT TCGGAGGTT CAGGCCCAC TGGCTCATC TGATTCTCGC TGATTCTCGC TGATTCTCGC TCACTCAC TCACTCCAC TCCTGACTTTCCTGACT TCCTGACTTTCCTGACT TCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTCCTGACTTTTCCTGACTTTTCCTGACTTTCCTGACTTTTCCTGACTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTTCCTGACTTTCCTGACTTTTCTGACTTCACTACT  | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840  |
| 50<br>55<br>60<br>65       | Seq ID NO: Nucleic Ac: Coding sequilibrian  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGGCT ACTACGGTCC GGACATCTTT ACGCTTCTT ACGCTTCT TCTCGCCTGG TCTCGCCTGG TCTCGCCTG TCTCGCCTG TCTCGCCTG CATGAATAGG CTTTGTCCTC CTTCACCTTC GATGCTCCTT TGACCGCAGG CCTGTTGGCCTG CTGACCGCAGG CCTGTTGGCT   | 619 DNA seld Accession lence: 254  11    GAAGTGCCGT TCTGCTCACC AGAGTGCGAG GCCCTCTTGC AGAATGGCTA CTTTGTGATA ACCAGGCGAA ACCAGGCGAA ACCAAGCTCA GCCTTCACCT TCTGTCACCT TCTGTCACCT TCTGTCACCT TCTGTCACCT TCTGTCACCT TCTGTTCCCA   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGAAG CAACAGTCCC AGGCTGAAGC TGGCCTTCAT TCCTCTTTC TCCGGGGAA ATGTCTTTTC ACGGCTGAAGC TCACGGCTGAAGC TCACGGCTGAAGC TCCGCTTCAT TCCTCTTTTTC TCCGGGGAG TAGTCCTCTT TCACGGCTG TCACGGCTG TCACGGCTG CCCATCCTCAG CCCATCCTCAG  | 31<br>  TAGGGGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACCAG<br>TGATGGTTGC<br>TACTCAGTT<br>CATCGGACTG<br>CATCTGCTTC<br>CATGGCTTC<br>CATGGGCCCTT<br>TGTTATCGCT<br>TGATGGCG<br>CTTGATGGCG<br>CTTGATGGCG<br>CTGGATCACC<br>CTCGCCTTG  | 41   CTCTCCCTCG CGGCGAGGGC TCTCCCCCAG TTCACCGCCA CCGCAATGGCC GTCCTAGAAA CCGAATCCTCG GACGGAGCA TCCTGCTGCT TCCTGTCTGC ATTGAATATA GCTCCTCGTC CTGACCTTCC CGGGCCCACA CTGCTCATGC GCTCCATGC GCTCCATGC GCTCCATGC   | 51<br> <br>ACCCTCCCC<br>CGCCTITATA<br>CACTGAGGAG<br>ACGCCTTGGC<br>TGAATCCAA<br>CGGTGGCAC<br>TCTGCAAGGT<br>TCGGTGTTTC<br>CAGGCCCAC<br>TGATTCTGGG<br>TTGTCCTGAC<br>GCAATGAAGA<br>TCATGTCCTC<br>TCTACCTCAC<br>TCTGCGTCTT<br>CTGGCTTTCTCGCT<br>TCTGCGTGTTT<br>CTGGGGTGTT<br>GCTGGGTGTT   | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020   |
| 50<br>55<br>60             | Seq ID NO: Nucleic Ac: Coding sequ  ATAACAGCAT TCCTTGTCCC ACTACTGCTC ACTACGGCTC ACTACGGCTC ACTACGGCTC TCACTGCTC TCTCCCTGCT CAGGACTCCT TGTCAGTCTC TGTCAGTCTC CTTGCCTGC CATGAATAGG CTTTGTCCTC TTTCACCTTC CATGCCTCCT TGACCGCAGG CCTGTTGGCT TTATCCTGTT TGACCGCAGG CCTGTTTGGCT TTATCCTGTT TGACCGCAGG CCTGTTTGGCT TTATCCTGTT TGACCGCAGG CCTGTTTGGCT TTATCCTGTT TGACCGCAGG  | 619 DNA se Id Accession lence: 254.  11    GAAGTGCCGT TCTGCTCACC AGAGTGCCAC AGAGTGCCAC AGAGTGCCAC AGAGTGCCAC AGAGTGCCAC AGAGTGCAC ACCAGGCGAA ACCAGGCGAA ACCAAGCTCA CTCTTTGGGA ACCAAGCTCA CTGCTCACCT TCTGTTAGCA TCTGTTCACT TCTGTTCACT TCTGTTCACT TCTGTTCACT TCTGTTCACCT TCTGTTCCA TAGGATGCAC TAGGATGCAC TAGGATGCAC TAGGATGCAC TAGGATGCAC TAGGATGCAC TAGGATGCAC TAGGATGCAC TAGGATGCAC TAGGATGCAAC TAGGATGCTCAAC TAGGATGCTCAAC TAGCTCAAC  | equence 1 #: NM_003 1357 21   GGRACTGGAA CCTCGCTCGT GGCGGGATAG GCGCGGAAG CAACAGTCCC AGGCTGAAGC TGCCTTCAT TCCTCTTTC TCCGGGGGA ATGTCCTTTTC TCACGGCTGA TCCTCTTTTC TCACGGCTG CCATCCTTTT TCACGGCTG CCATCCTCAC CCATCCTCAC CCATCCTCAC CCATCCTCAC CCATCCTCAC CCATCCTCAC CCATCCTCAC CCATCCTCAC CCATCCTCAAACC CCAGAATTTTG TCTGTAAACC   | 31<br>  TAGGCGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>TGATGGTTGC<br>TGATGGTTGC<br>TTCCAGTTT<br>CATCAGTTT<br>CATCAGTTTC<br>CATCAGCTTCC<br>GAAGCCCCTT<br>TGATATCGCT<br>TGATATCGCT<br>CTTGATGCC<br>CTTGATGCCC<br>CTTGATCACC<br>CTCCGCCTTG<br>GCTCCCCTC<br>GCTCCCCTTG<br>GCTGCTCACA<br>TCAACTCGTT<br>TCAAGGTTTT  | 41   CTCTCCCTGG CGGCGAGGGC TCTCCCCAG TTCACGGCCA CGCAATGGCC GTCTTCCTCC GACGGGAGCA TCCTGCCTGC TCCTGCTTGG ATTGATATA GCTCCTGGTC CTGACCTTCC GGGGCCCACA CTGCTCATGG ATTGAAAAAAAAAA  | 51    ACCCTCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGTGGCCAC TCTGCAACGT TGGGTGTGTT CAGGCCCAC TGATTCTGGC TGATTCTGGC TGATTCTGGC TCTACCTCAC TCACTCAC TCCTGACTT ACCCCACTGA ATGGTGTGGA ATGGTGTGGA ATGGTGTGGA ATGGTGTGGA  | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>660<br>720<br>840<br>900<br>840<br>900<br>1020   |
| 50<br>55<br>60<br>65       | Seq ID NO: Nucleic Ac: Coding sequitary  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT ACGCTTCTTC CGGGCATCTTT ACGCTTCTTC CATGAGTATAGG CTTTGTCCTC CTTCACCTTC GATGCTCCTT GATGCTCCTT TGACCGCAGG CCTGTTGGCT TTATCCTGT TGACAGAGCC CTTATGCCCC CTTAGCCCCC  | 619 DNA seld Accession lence: 254  11    GAAGTGCCGT TCTGCTCACC AGAGTGCGAG GCCCTCTTGC AGAATGGCTA CTTTGTGATA ACCAGGCGAA GGCCTCACCT CTCTTTGGGA ACCAACGTCA ACCAACGTCA CTGCTCACCT TGTGGTTCCT TCTGTCACT TGTGGTTCCT TCCATTGCCA TGGGATGACA TATGTTAGTC GAGGATGCTA TATGTTCACAC TTATCTCAAG TATTCTCAAG   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGAAG CAACAGTCCC AGGCTGAAGC TGCCTTCAT TCCTCTTTC TCCGCTTCAT TCCTCTTTTC TCCGGGGAA ATGTCTTTTC TCACGGCTG TCACGGCTGAAGC CCAACTCTCAT TCACGGCTGT TCACGGCTGAAACC AGGAAATCAC   | 31<br>  TAGGGGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACAGG<br>CAGCACAGG<br>TATTGGTTGC<br>CATCTGCTTT<br>CATCTGGTTT<br>CATCTGGTTT<br>CATCTGGTTTC<br>CTTGATGGC<br>GAAGGCCTT<br>TGTATGGC<br>CTTGATGGC<br>CTCGGCTTG<br>CTGGATCACC<br>TCAGGTTTCC<br>CTCGCCTTG<br>GCTGCTCACA<br>TCAACTCGTG<br>TCAAGGTTTT   | 41   CTCTCCCTGG CGGGAGGGC TCTCCCCGG TTCACGCCA GCGAATGGCC GTCTTAGAAA CCGAATCCTGG GACGGGAGCA TCCTGCTGC GACGGGACCA CTCCTCGTTGG ATTGAATATA GCTCCTCGTC CTGACCTTCC GGGGCCCACA CTGCTCATGC GCTCCAATG GCTCCAATG GCTGCCAATG GCTGCCAATG CCTGCAGAGACAGA AAGAAGAGACGA   | 51  ACCCTCCCC CGCCTTTATA CACTGAGGA ACGCCTTGGC TGAAATCCAA CGGTGGCAC TCTGCAAGGT TCGGTGGTT CAGGCCCAC TGGCTCATCC TGATTCTGG TTGTCCTGAC TCATCTCAC TCATCTCAC TCATCTCAC TCATCTCAC TCCTGACTT ACCCCAAC ACCCCATGGA ATGGTGTGA ATGGTGTGA  | 60<br>120<br>180<br>240<br>360<br>420<br>6600<br>6600<br>720<br>780<br>840<br>960<br>1020<br>1080   |
| 50<br>55<br>60<br>65       | Seq ID NO: Nucleic Ac: Coding sequitable  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGTTT ACGCTTCTTC GGGCATCTTT TCTGCCTGCT CATGAGTCTC CTTCACCTTCTC GATGCTCTCT CTTCACCTTC GATGCTCCTC TGACCGCAGG CTTTGTCCTC TGACCGCAGG CTTTGTCCTC CTTCACCTTC GATGCTCCTC TGACCGCAGG CCTGTTGGCT TTATCCTGTT GAACAGAGCC CTATGCCCCC CATCCCACGG   | 619 DNA seld Accession sence: 254.  11   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGATAG GCACGGAAG CAACAGTCCC AGGCTGAAGC TCGCCTCAT TCCTCTTCT TCGCGTGAG ATGCTGCC TCGCCTCAT TCCTCTTTTC TCACGGGAG ATGTCTTTTC ACGTCCTCTT TCACGGCTG TCACGGCTGCCCAT TCTCTCAG  | 31<br>  TAGGCGTGTC<br>CTCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACCAAG<br>GTCACTGTT<br>CATCAGTTT<br>CATCAGACTG<br>CATCTGCTTT<br>GAAGCCCCTT<br>TGTATCGCT<br>TGAGCTTCC<br>CTTGATGCG<br>GAAGAGACAT<br>CTGGATCAC<br>CTCGCCTTG<br>GCTGCTCACA<br>TCAACTCGTG<br>TCAACTCGTG<br>TCAAGGTTTT<br>GCAGAACCAG   | 41   CTCTCCCTGG CGGGGAGGGC TCTCCCCAG TTCACGGCCA GCGCAATGGCC GTCTTAGAAA CCGATCCTCG GACGGGAGCA TCCTGCTGTTGG CTCCTCTTGTG CTCCTCTTGTG CTGGCCACA CTGCTCATGC GGGGCCCACA CTGCTCAATG AAGAACGAA AAGAAGACG GAAGACAC TCCCCCCAAA TGAAGACAC TCCCCCCAAA TGAAGACACA TATGAAGACAC CTCCCCCCAAA   | 51   ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TCTGCAAGGT TCGGTTGTC TGGTTTCTGG TCTATCCTCAC GCAATGAAGA TCATGTCCTC TCTACCTCAC TCTACCTCAC TCTCCCATCG ACGGGTGTT ACCCCATCGA ATGGTGTGAA ATGGTGTGGA GGGACACGCT AGGAATTCTCC AGGAATTCTCAAC AGGAATTCTCAAC AGGAATTCTCAAC AGGAATTCTCAAC AGGAATTCTCAAC AGGAATTCTCAAC AGGAATTCTCAAC AGGAATTCTCAAC AGGAATTCTCAACACACACACACACACACACACACACACA   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1140<br>1200<br>1320   |
| 50<br>55<br>60<br>65<br>70 | Seq ID NO: Nucleic Aci Coding sequ  1   ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCSCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT ACGCTTCTTC TCTCAGCTTC TCTCAGCTTC CATGAGTAGG CTTGACTCTC CATGAGTAGG CTTGACCTC GATGATTGGCT TTATCCTTC TGACCGCAGG CCTGTTGGCT TTATCCTGT TGACCGCAGG CCTGTTGGCT TTATCCTGT TCAACAGGCC CATCCACAGG CAGCTAACTC CTCAACGGT CAGCTCACCG CAGCTAACTC TCAACAGGAT TCAAAGGGAT  | 619 DNA se Id Accession lence: 254.  11    GAAGTGCCGT TCTGCTCACC AGAGTGCCGA AGAGTGCCGA AGAGTGCCAC AGAGTGCCAC AGAGTGCCAC ACCACCTC CTCTTTGGAA ACCAACCTCA CTCTCACC ACCAACCTCA TCTCATCCCA TCTGTTAGTA ACGAGTCAC TCTCATCCCA TCTGTTAGTA TATCCCAAC TATCCCAAC TATCCCAAC TATCCCAAC TATCCCAAC TATCCCAAC TATCCCAAC TATCCCAAC TCTCAAC TCTCAAC TCTCAAC TCTCAAC TCTCAAC TCTCAAC TCTCAAC TCTCCAAC TCTCCAAC TCTCAAC TCTCCAAC TCTCCTCAAC TCTCTCAAC TCTCTCTC | equence 1 #: NM_003 1357 21   GGRACTGGAA CCTCGCTCGT GGCGGGAAG CAACAGTCCC AGGCTGAAGC TGCCTTCAT TCCTCTTTC TCCGGGGGAG ATGTCCTTTTC TCACGGGTGAGC CCATCCTCTT TCACGGGTGAGC CCATCCTCAT ACGTCTTTT TCACGGCTGAGAAATCAC AGGAAATCAC AGGAAATCAC AGTTTCAGCT GGCCGAGCCA ATCTTCAGCT AGGAAATCAC AGTTTCAGCT AGTGGACAA   | 31<br>  TAGGCGTGTC<br>TCCCTCCCTC<br>CTGTCCAAGG<br>CAGCACAAG<br>TGATGGTTGC<br>GCTCACTCTC<br>TACTCAGTTT<br>CATCGGACTC<br>CATCGGTTTC<br>CATCGGTTTC<br>CATGGCTTCC<br>CTTGATGCCT<br>GAAGCCCCTT<br>GCTGATCACC<br>CTCGCTCACA<br>TCAACTCGTG<br>TCAACTCGTG<br>TCAACTCGTG<br>TCAACGTTTTC<br>GCTGCTCACA<br>TCAACTCGTG<br>TCAACGTTTT<br>GCAGAACCAG<br>TTACAACAGGTTTTCCACACCACCACCACCACCACCACCACCACCACCAC   | 41   CTCTCCCTGG CGGCAAGGCC TCTCCCCAG TTCACGGCCA CGCAATGGCC GTCCTTCGTCG GACGGGAGCA TCCTGCTTGG ATTGAATATA GCTCCTCGTC GGGGCCCACA CTGACCTTCC GGGGCCCACA CTGCTCATGG AAGAAGACGA AAGAAGACGA AAGAAGACGA TATGAAGTAA CCTCCCCCAAA TATGAAGTAA CCTCCCCAAA CCTCCCCAAA CCTCCCCAAA CCTCCCCAAA CCTCCCCAAA CCTCCCCAAA CCTCCCCAAA CCTCCCCCAAA CCTCCCCCCAAA CCTCCCCCCCC   | 51    ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TCTGCAAGGT TGGGTGTTT CAGGCCCAC TGATTCTGGA TGATTCTGGA TCATCTCCTGAC TCATCTCCTGAC TCATCTCCTGAC TCATCTCCTGAC TCATCTCCTGAC TCCTGACTT GCTGGGTTT ACCCCATGGA ATGGTGGGA ATGGTGGGA ATGGTGGGA ATGGTGGGA TGGCGGAGC TAGCGGGGGT TAGCGGGGGG TAGCGGGGGA CCCCT CACAACGGGA   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>600<br>660<br>780<br>900<br>900<br>1020<br>1080<br>1140<br>1200<br>1260<br>1380  |
| 50<br>55<br>60<br>65       | LAKDCHCI Seq ID NO: Nucleic Ac: Coding sequitary ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTACGGTTCC GGACATCTTT ACGCTTCTTC GGAGGACTCCTTC TGTCAGCTTGTCTC TGTCAGCTTGTCTC CATGAATAGG CTTTGTCCTC CTTCACCTTC GAACAGAGC CTTTTGTCCTC TAACCGCAGG CCTTTTGCCCTC CTAACGCAGG CCTATGCCCC CATCCCACGG CAGCTAACTC TCAAAGGGAT ACAGTTTTGCC TCAAAGGGAT ACAGTTTTGCC TCAAAGGGAT   | 619 DNA seld Accession lence: 254.  11   GARGEGCGT TCTGCTCACC AGAGTGCGAG GCCTCTTGC AGACTCGC ACCACGTCACCT TCTGTGAA ACCAAGCTCA CTGCTCACCT TCTGTGAC ACCAACGTCA CTGCTCACCT TCTGTGTACACT TGTGGTCACCT TCTGTGTACACT TGTGGTCCT TCCATTGCCA GCGATGACA TATGTTAGTC GAGGATGACA TATGTTAGTC TACTCCAAGCTTACCAAGCTTATCCAAGCTTACCAAGCTTTTCCTCAAGCTCCCAGCTTTCCTGAAGACATCCCCAGCTTTCCTGAAGACATCCCTCCAAGCTCCAAGCTCCAAGCTCCCAGGCTAATCCCAAGCTCCAAGCTCCCAGGCTAATCCCCAAGCTCCCAGGCTAATCCCCAAGCTCCCAAGCTCCCAAGCTCCCCAGGCTAATCCCCCAAGCTCCCCAAGCTCCCCAAGCTCCCCACGCTTCCCCAAGCCCCACCCCCCCC   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGAAG CAACAGTCCC AGGCTGAAGC TGGCCTCAT TCCTCTTTC TCCTCTTTTC ACGTCCTCT TCACGGGGA ATGTCTTTTC ACGTCTCTT TCACGGCTG TCAGGTGGC ACGTCTTTT TCACGGCTG TCTGGTGAACC ACGTCTTT TCACGGCTG TCTGGTAAACC AGGAAATCAC AGGAAATCAC AGTTTTCAGCT GCCCAAGCCC AGTTGGGACAA TCTTGAGTCT CCTCAACCAC  | 31   TAGGCGTGTC TCCCTCCCTC CTGTCCAAGG CAGCACCAAG TGATGGTTGC TACTCAGTT CATCGGACTG CATCTGCTTC GAAGCCCCTT GAAGCCCCTT TGTATCGCT TGTATGGC CTTGATGGC CTCGCCTTG GAAGCACAC TCAAGTTTC CATCGATTTC CATCGCTTC CAAGGTTTCC TTGATGGC TTGATGGC TTGATGGC TCAAGGTTTCC TCAGCTGC TCAAGGTTTCC TCAGCATCAC TCAAGGTTTACAAGGT TTACAAAGAC TTACAAAGAC ATGCAGCAGG TCTGAGAACAA AATTCTTCCA   | 41   CTCTCCCTCG CGGCGAGGGC TCTCCCCCAG TTCACGCCA GTCTAGAAA CCGATCCTCG GACGGGAGCA TCCTGCTGC GACGGGACCA TCCTGCTGC GACGGACCA ATGAATATA GCTCCTCCTC GGGCCCCACA CTGCTCATGC GCTCCCATGC GAGGAGACA AAGAAGAGCT GAAGGACCA AAGAAGAGCT CTACCCCCAAA ATGAAGTAA GCGCAGATC CTCTCCCCAAA GCTCCCCCAAA CCTCCCCAAA CCTCCCCAAA GCTCCCCAAA GCTCCCCAAA CCTCCCCAAA GCGCAGATC CTGTACAAGGA CCTCCCCAAA GCGGCAGATC CTGTACAAGGA CTGCTGCGGGCT CTGTTACAAGGA  | 51   ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TGGGTGTT CAGGGCCCAC TGGTTCTGGG TTGTCCTGAC TCTACCTCAC TCCTGACTT GCTGGGTGTT ACCCCATGG ATGGTGTT ACCCCATGGA ATGGTGTGGG TCATGCTCAC TCCTAGCTT ACCCCATGGA ATGGTGTGGA ATGGTGTGGA TCATGGGATTCT AGGAATCCTC AGGAATCCTC AGGAATCCT AGGAATCTCT AGGAATCTCT AGGAATCTCT AGGAATCTCT AGGAATCTCT AGGAATCGGA TAGCGGGAGC CACTACCGGA CACTACCGGA CACTACCGGA CACTACCGGA CATTACGGGA CACTACCGGA CACTACCGCA CACTACCGGA CACTACCGGA CACTACCGCA CACTACCGCA CACTACCGCA CACTACCGCA CACTACCGCA CACTACCGCA CACTACCGCA CACTACCGCA CACTACCGCA CACTACCCA CACTACCGCA CACTACCCA CACTACCA CACTACCCA CACTACCCA CACTACCCA CACTACCCA CACTACCA CACTACCA CACTACCCA CACTACCA  | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1140<br>1200<br>1320   |
| 50<br>55<br>60<br>65<br>70 | Seq ID NO: Nucleic Ac: Coding sequitable  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGGT ACTAGGGTCC GTACTACAGA AGCCGGGGTT ACGCTTCTTC TGTAGTCTC TGTAGTCTC TGTAGTCTC CATCAGTCTG CATGACTCT TCAGCTCTC GATGCTCTC GATGCTCCTC TGACCGCAGG CCTTTGTCTCT CATCCTCC TGACCAGG CCTTAGCCTC TAACCGCAGG CCTACCCCTC CATCCACGC CATCCACGC CATCAAGAGCC CATCAAGGGAT ACAGTTTGCC AGTAAGAGCT TCAAAGGGAT ACAGTTTGCC AGTAAGAGCT ACAGTTTGCC AGTAAGAGCT ACAGTTTGCC AGTAAGAGCT   | 619 DNA selld Accession sence: 254.  11  | equence    #: NM_003   1357  21   GGAACTGGAA CCTCGCTCGT GGCGGGATAG GCSCGGGATAG CAACAGTCCC AGGCTCAT TCATTCAT TCACGGCGGA ATGTCTCAT TCCTCTTTC TCACGGGGGA ATGTCTCAGGC CCAACTCTTG TCACGGCTG TCATCTCAGC CCGAGTTTTG TCTCAGGGAA ATGTTTTAAACC AGGAAATCAC ATTTTCAGGT AGGAAATCAC ATTTTCAGGT AGGCCGAGCCC AGTGGGACAA TCTTGAGTCT CCCCAACCAC AGGCCCTAACCA AGGCCCTTAACCC AGGCCCTTAACCC AGGCCCTTAACCC AGGCCCTTAACCC AGGCCCTTAACCC AGGCCCTTAACCC AGGCCCTTAACCC AGGCCCTTAACCCT AGGCCCTTAACCCT AGGCCCTTAACCCT AGGCCCTTAACCCT AGGCCCTTAACCCT AGGCCCTTAACCCT AGGCCCTGTAACCCT AGGCCTGTAACCCT AGGCCTTCT AGGC | 31<br>  TAGGCGTGTC<br>CTCCCCCCCC<br>CTGTCCAAGG<br>CAGCACCAAG<br>GAGACCAAG<br>TATGGGGCATC<br>GCTCACTCTC<br>CATCTGGACTG<br>CATCTGCTTC<br>GAAGGCCCCTT<br>TGTATCGCT<br>TGAGGCACAT<br>CTGATCACC<br>CTCGCCTTG<br>GCAGAACAC<br>TCAACTCGTG<br>TCAAGGTTTT<br>GCAGAACCAG<br>TTACAAAGAC<br>ATCCAGCCGG<br>TTACAAAGAC<br>ATCCAGCCGG<br>TCTCAGAAAA<br>AATTCTTCCA   | 41   CTCTCCCTGG CGGGGGGGGC TCTCCCCCAG TTCACGGCCA GCGCAATGGCC GTCCTAGAAA CCGATCCTCG CTCTCTCTCC CACCTGTTGG TCCCTGTTGG CTCCTCTTCTCC CTGACCTTCC GGGGCCCACA ATGAATATA AAGCAACGAA AAGAAGACT GAAGACACAA TATGAAGACA CCTCCCCAAA TATGAAGTAA TATGAAGTAC CTGTCCCCAAA TATGAAGTAC CTGTCCAGAGT CTGTCCAGAGT CTGTACAAGA TGCTGCGGGCT TTTTTTGTCT  | 51   ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGTGGCCAC TCTGCAAGGT TCGGGTGTGT TGGGTTATCT TGGTTATCTGG TCATCTCAC CCATCGAATTCCTC TCCTCACTCAC TCCTCGACTT ACCCCATCGA ATGGATTTT ACCCCATCGAC TCATGTCTC AGAAACACG TAGGGGGAGC CACTACGGGA GATGTGGGCA CATCTCCGACT AGGAATTCTC AGAAACACG AGGAATCTC AGGAATCTCT CAGAAGAGGG TAGCGGGAGC CACTACGGGA CATCTTTGG CATCTTTTGG   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>660<br>780<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560   |
| 50<br>55<br>60<br>65<br>70 | Seq ID NO: Nucleic Ac: Coding sequitary  ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTACTGCTC GGAGACTCCT GGAGGACTCC GGGCATCTTT ACGCTTCT TCTCGCCTG TCTCGCCTG TCTCGCCTG TCTCGCCTG TCTCGCCTG CATGATAGG CTTTGTCCTC TGACCGCAGG CCTGTTGGCCT TTATCCTGTT GAACAGAGCC CTATGCCCC CATCCCACGG CAGCTAACTC TCAAAGGGT ACAGTTTTGCC ATACTTCTT ACACTTCTT TCAACTTCTC TCAACTGC CATGCTAAGTT ACAGTTAGCCC CATCCCACGG AGTAACTC ATACTTCTTT GTTTTTTTGAA   | 619 DNA seld Accession lence: 254  11   GARGEGEGET TCTGCTCACC AGAGTGCGAG GCCTCTTGC AGACTGGAA ACCAAGTCA CTTTTGGATA ACCAAGTCA TGGGATGACA TGGGATGACA TATGTTAGTC GAGGATGACA GCCACGCTT TCTCATAG GCCACGCT TCTCATAGACA GCCACGCTT TCTCATAGACA TATGTTAGTC GAGGATGACA TATGTTAGACA TATGTCTCAAG GCCACGCTT TCTCATAG GTGGGCGAAA TCCCTCCAG ACAGTCTTAGACA AGAGTGGAGAA ACAGGATCTTAGAAG AGAGTGCGAAA ACAGGATCTTAGAAG AGAGTGCGAAA ACAGGATCTTAGAAGAACAGATAGTGGAGAAAACAGGATCTTAGAAGAACAGGATCTTAGAAGAACAGGATCTTAGAAGAACAGGATCTTAGAAGAACAGGATCTTAGAAGAACAGGATCTTAGAAGAACAGGAGAAAATAGTGGGAGAAAACAGGATCTTAGAAACAGGATCACACACA   | equence    #: NM_003   1357  21   GGAACTGGAA   GGCGGGAAG   GCGGGAAG   GACAGTCCC   AGGCTGAAGC   TGCCTTCAT   TCCTCTTTC   TCCTCTTTTC   ACGTCCTCTTTTC   ACGTCCTCTTTTC   ACGTCCTCTTTTC   ACGTCCTCTTTTC   ACGTCCTCTTTTC   ACGTCCTCTTTTCACGGAAATCAC   ACGTCTCAGGAAATCAC   AGGTGGAACCAC   AGTTGGACCAC   AGTTGGACCAC   AGTTGGACCAC   AGTTGGACCAC   AGTTGGACCAC   AGTTGAGCTCT   CCTCAACCAC   AGGCGCTGTA   ACGTCTCAGCAC   AGGCGCTGTA   ACCTCAGCAC   AGGCGCTGTA   ACCTCAGCCAC   ACCTCAGCCAC   ACCTCAGCCAC   AGGCGCTGTA   ACCTCAGCCAC   ACCTCAGCAC   ACCTCAGCCAC   ACCTCAGCCAC   ACCTCAGCCAC   ACCTCAGCAC   A | 31   TAGGGGTGTC TCCCTCCTC CTGTCCAAGG CAGCACCAG CAGCACCAG TAGGGCATC GCTCACTCTC TACTCAGTT CATCGGACTG CATCTGCTTC CAAGGCTTTC CATCGGCTTC CAAGGCTTTC CTGATGGC CTGATGCC CTTGATGGC TCAGATCACC CTCGCCTTG TCAAGGTTTC TCAAGTTTTC TCAAGTTTTT TCAAGTTTTT TCAAGTTTTT TCTCAAGTTTTT CTCAAGTTTTT CTCAAGTTTTT CTCAAGTTTTT CCAGCTTGA  | 41    CTCTCCCTGG CGGGAGGGC CTCTCCCCGG CGGCAGGGC CTCTCCCCGG GTCCTAGAAA CCGAATCCTGG GACGGGAGCA TCCTGGTGG ATTGAATATA GCTCCTCGTC CTGACCTTCG GGGGCCCACA CTGCTCATGG GCTCCAATG GCTCCCCAAA AAGAAGACA AAGAAGACA CTCCCCCAAA ATTGAATATA CCTCCCCAAA CCTTCCCCAAC CTCCCCTACCT CCTCCCTACCT CCTCCCTC  | 51   ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TGGGTGGTT CAGGGCCCAC TGGCTATTC TGGTTGTT CAGGGCCCAC TGGTCATCC TGATTCTGG TTGTCCTGA TCATGTCTC TCTACCTCAC TTCCTGACTT GCTGGGTGTT ACCCCATGGA ATGGTGTGGA TAGCAGGGAGC CACTACCGGG CATCTTTGG CTTTTTTTTTT   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>720<br>780<br>960<br>1020<br>1080<br>1140<br>1260<br>1320<br>1320<br>1340<br>1500<br>1500                                       |
| 50<br>55<br>60<br>65<br>70 | Seq ID NO: Nucleic Ac: Coding sequitable  ATRANCAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGGT ACTAGGGTCC GTACTACAGA AGCCGGGGTT ACGGTCTTT ACGCTTCTTC TGCAGTCTGT CATGAGTCTGT CATGAGTCTGT CATGAGTCTGT CATGAGTCTGT CATGACTCTTC GATGACTCTT GAACGCAGG CTTTGTCCTC GATGCTCCT TGACCGCAGG CCTGTTGGCT TTATCCTGTT GAACAGAGCC CATCCCACGG CAGCTAACTC TCAAAGGGCC CATCCCACGG CAGCTAACTC TCAAAGGGCC AGTAACTC ATACTTCTT GTTTTTTTGA CCCAGTGCAG CACGTGCAG CACGTGCAG CACGTGCAG CACGTGCAG CACGTGCAG CACGTGCAG CCCAGTGCAG CCCAGTGC | 619 DNA seld Accession sence: 254.  11   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGGATAG CAACAGTCCC AGGCTGAAG TCGCCTCAT TCCTCTTTT TCACGGGGAA ATGTCTCAGGA ATGTCTCTTTT TCACGGGTG TCAGCTCCTCAT TCTCTATTC ACGTCTCTTT TCACGGGTG CCAACTCTCAG TCTTAAACC AGGAAATCAC AGTTTTAAACC AGGAAATCAC AGTTTAAACC AGGAAATCAC AGTTTAAACC AGGAAATCAC AGTTTAAACC AGGACTCTCAACCAC AGTCGCACAC CCTCAACCAC CCTCAACCAC CCTCTCACCAC CCTCTCTCAACCAC CCTCTCTCT  | 31   TAGGCGTGTC CTGTCCAAGG CAGCACAAG GAGACCAAG GATCTACTCT TACTGGTTC CATCTGGTTC CATCTGGTTT CATCGGACTG CATCTGCTTC GAAGCCCCTT GGAGACCAC TGAGATCAC CTCAGCTTC GCAGACCAC TCAGCTTC GCAGACCAC TCAGCTGT TCAAGGTTTT GCAGACCAC TCAAGGTTTT GCAGAACAC ATCAAGGCCGG TTACAAAGAC ATGCAGCCGG TTACAAGAC ATGCAGCTTCC GTATTTTTT CTCAAGTTTA CCAGGCTTGA   | 41   CTCTCCCTGG CGGGGAGGGC TCTCCCCCAG TTCACGGCCA GCGCAATGGCC GTCCTAGAAA CCGATCCTCG GACGGGAGCA TCCTGTTGG GACGGGACA TCCTGTTGG GGGCCCAATG CGGCCCAATG AAGAACGAA AAGAAGACG GAAGAGACG GTCCCCCAAA GCGCCAATG TATGAAGACA CCTCCCCAAA GCGCAGATC TATGAAGAC TTTTTTGTCT GACCCTTACT GTGCAGTGCT CTCCCACAC TCCTCCCACAC TCCTCCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCCACAC TCCTCCCCACAC TCCTCCCACAC CCTCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCCCACAC CCTCCCCACC CCCCCCACAC CCTCCCCCACC CCCCCCCC   | 51   ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TCTGCAAGGT TCGGTGTTTCGGTTTCGGTTCTCAC GCAATGAGA TCATGTCCTCAC TCTACCTCAC TCCTACCTCAC TCCTACCTCAC TCCTACCTCAC TCCTACCTT ACCCATCGA ATGGATCTCG AGGAATTCTC AGGAATTCTC AGGAATTCTC AGGAATTCTC CAGCATGAGG CATCTACGGA CATCTTTGGT CATCTTTTGTTT CCGATCACAC CTTTTTTTTT CCGATCACAC CTTTTTTTTT CCGATCACAC CTTTTTTTTT CCGATCACAC CTTTTTTTTT CCGATCACAC CTTCTTTTG CTTTTTTTTT CCGATCACAC CTCCTTTTG CTTTTTTTTT CCGATCACAC CTCCTTTTG CTTTTTTTTT CCGATCACAC CTCCTTTTG CTCTTTTTTT CCGATCACAC CTCCTTTTG CTCTTTTTTT CCGATCACAC CTCCTTTTTTT CCCAACAC CTCCTTTTTTT CCCAACAC CTCCTTTTTTTT   | 60<br>120<br>180<br>240<br>360<br>420<br>540<br>600<br>6600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560<br>1560<br>1680<br>1740                |
| 50<br>55<br>60<br>65<br>70 | Seq ID NO: Nucleic Aci Coding sequ  1   ATRACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT GCAGGACTCTT TGTCAGTCTG CTTGCCCTGC CTTGACCTGC CTTGACCTCC CTTGACCTCC CTTCACCTTC CATGCCTCC CTTCACCTTC GATGCTCCTC TTATCCTCT TGACCGCAGG CCTGTTGGCT TTATCCTTT TGACCGCAGG CAGTACAGC CATCCACAGG CAGTACAGC CAGTACAGC TCAAAGGGAT ACAGTTTTGC TCAAGGGAT ACAGTTTTT GTTTTTTTTTAA CCCAGTGCAG CTGGGATGAG CCTGGGATGAG CCTGGGATGAG CCTGGGATGAG CCTGGGATGAG  | 619 DNA se id Accession lence: 254.  11    GAAGTGCCGT TCTGCTCACC AGAGTGCCGA GCCCTCTTGC AGAGTGCGAA ACCAGGCGAA GCCCTCACCT CTCTTTGGGA ACCAGCTCACCT CTCTTTGGGA ACCAACGTCA CTGCTCACCT TCCATTGCCA TAGGTCACCT TCCATTGCCA TAGGTCACCT TCCATTGCCA TAGGTCACCT TCCATGCCA CAGGATGCTT TCCATGCCA CAGGTCACCT TAGCTCACCT TAGCTCACC TAGTCACC TAGCTCACCT TAGCTCACC TAGTCACAC TATCCCAC CCCCCCGAC TATCCCAC CCCCCCCACGCTT TCCCTCCACC CAGGTTCTTAG TAAGTGGGAG ACAGGATCTT CCTCGACCA ACAGGATCTT CCTCCACCA ACAGGATCTT CCTCCACCA ACAGGATCTT CCTCCACCAC ACGGCTCAC ACGCGTGAGC ACCCGCTGACCAC ACCCGCTGACCAC ACCCGCTGACCAC ACCCGCTCAC ACCCGCTCACC ACCCGCTCACC ACCCGCTCACC ACCCGCTCACC ACCCGCTCACC ACCCGCTCACC ACCCGCTCACC ACCCGCTCACC ACCCGCTCACC ACCCCCC ACCCCCCC ACCCCCC ACCCCCC ACCCCCC   | equence 1 #: NM_003 1357 21   GGRACTGGAA CCTCGCTCGT GGCGGGATAG GCCGGGAAG CAACAGTCCC AGGCTGAAGC TGCCTTCAT TCCTCTTTTC TCCGGGGGAG ATGTCCTTTTC TCACGGCTG CCATCCTTTTC TCACGGCTG CCATCCTTTTC TCTTAAACC CCATCCTCAG AGGAATCAC ATTTTCAGCT AGGCCGAGCCC AGGCCAC ATCTTAGCT AGGCCACAC ATCTTAGCTC CCTCAACCAC AGGCCCTAACCAC AGGCCCTAACCAC AGCCCTCAACCAC AGGCCTCTAACCAC AGGCCTCTAACCAC AGGCCTCTCAACCAC AGCCTCTCAACCAC AGCCTCTCAACCAC AGCCTCTCAACCAC AGCCTCTCAACCAC AGCCTCTCAACCAC AGCCTCTCAACCAC AGCCTCTCAACCAC AGCCTCTTCAACCAC AGCCTCTCTCAACCAC AGCCTCTCTCAC ACACAGCTCCC  | 31  TAGGCGTGTC TCCCTCCCTC CTGTCCAAGG TGATGGTTGC TGCACAGG TGATGGTTGC TACTCAGTTT CATCGGACTG CATCGCTTC GAAGCCCCTT GGTATGCTTC GAAGCCCCTT GGATACCCTT GTATCGCT GCTGATCACA TCAACTCGTG GCTGCTCACA TCAACTCGTG TCAACTCTGC TCACAGTTTA CCAGGCTTGA GCAATCCTCC AGCCTGGGCC   | 41    CTCTCCCTGG CGGCGAGGGC TCTCCCCAG TTCACGGCCA CGCAATGGCC GTCCTAGAAA CCGATCCTGG TCCTGCTGG ATTGATATA GCTCCTGGTGG GTGCTAGCAGAC CTGACCTTCC GGGGCCCACA CTGCTCATGG GAAGAGACAG GAAGAGACAG GAAGAGACAG TCTCATGC GAGGCGTATG GAGGCAGATC TTTTTTGTCT GTGCAGTGGT GACCTTACT GTGCAGTGGT CATTCCCATC CTTCATCCATC CTTCATCATCATC CTCTCCATC CTCTCCTCATC CTCTCCATC CTCTCCTACT CTCTCCTTC CTCTCCTTCCT   | 51    ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TCTGCAACGT TGGGTGTGTT CAGGCCCAC TGATTCTGGC TGATTCTGGC TCTACCTCAC TCACTCAC TCACTCAC TCACTCAC TCACTCAC   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>600<br>660<br>720<br>780<br>840<br>900<br>1020<br>1140<br>1200<br>1140<br>1320<br>1380<br>1440<br>1560<br>1620<br>1680<br>1680<br>1680 |
| 50<br>55<br>60<br>65<br>70 | LAKDCHCI  Seq ID NO: Nucleic Ac: Coding sequital sequitation se | 619 DNA seld Accession sence: 254.  11   | equence 1 #: NM_003 1357 21   GGAACTGGAA CCTCGCTCGT GGCGGAAGG CAACAGTCCC AGGCTGAAGC TGGCCTCAT TCCTCTTTTC TCCGGGGGA ATGTCCTGTTTC ACGTCCTCTTTC ACGTCCTCTTTC ACGTCCTCTTTC TCACGGCTG TCACGGCTGAACC CCATCCTCAG TCTCAGGCAA ATGTCTTTTC ACGTCTCTTTC ACGTCTCTTTC ACGTCTCTCAG TCTCAGGCAAC ACGTCCTCTAACC AGGAAATCAC ATTTTCAGCTC AGGCAGCC AGGCGCCC AGGCGCCC AGGCGCCC AGGCGCCC AGGCGCCC CCTCTCACAC CCCTCTCAC CCCATCCCAC CCATCTCAGCCA CCCATCCCC CATCTCAGCCA CCTCTCCC CATCTCAGCC CATCTCAGCC CATCTCAGCC CATCTCAGCC CATCTCAGCC CATCTCAGC CA | 31   TAGGCGTGTC CTGTCCAGG CAGCACCAGG CAGCACCAGG TATGGGGCATC GCTCACTCTC GCTCACTCTC GCTCACTCTC GCTCACTCTC GAAGCCCCTT TGTATGGCT TGAGCTTCC CTTGATGGCG GAAGAGCAC CTCCGCCTTG GCAGACCAC TCAAGTTTT CCAGCTTGC TCAAGGTTTT CCAGCTTGC TCAAGGTTTT CCAGCTGGC TTACAAGGC TTACAAGGC ATGCAGCCGG TTACAAGGCC ATCCAGCTTGA GCATTCTCC GCTTTGAGCAC ATGCAGCCTGAGCCC ACGCTTGAC ACCACGCTTGC ACCACGCTGCC ACCCTGGCC CACGCTTGCC CACGCTTGGCC CACGCTGGCC CCCTGGCCC CCCTGCCC CCCCTGCC CCCTGCCC CCCTGCCC CCCTGCCC CCCTGCCC CCCTGCCC CCCTGCCC CCCCTGCC CCCCTGCC CCCTGCC CCCTGCC CCCCTGCC CCCCTGCC CCCCTGCC CCCCTGCC CCCCTGCC CCCCTCCC CCCCTGCC CCCCTGCC CCCCTGCC CCCCTGCC CCCCTGCC CCCCTGCC CCCCC CCCCTGCC CCCCCC CCCCCC CCCCCCC CCCCCCC CCCCCC | 41   CTCTCCCTGG CGGGAGGGC TCTCCCCAG TTCACGGCCA GCGCAATGGCC GCAATGGCC GTCCTAGAAA CCGATCCTCG GACGGGAGCA TCCTGCTGC GACGGGACA TCCTGTTGG GGGCCCACA CTGCTCATGG GCTGCCAATG AAGAAGACAG AAGAAGACAG CCTCCCCAAAA TCTACAGGCCT TTTTTTGTCT GACCCTTACT GACCATACT CTTAATCTTG CACACAGGCAC CACACAGCACC CACACAGGCAC CACACAGCACC CACACAGGCAC CACACAGCACC CACACACA  | 51   ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TCTGCAAGGT TCGGGTGTTT TGGGTGTTCTGG TGATTCTGG TCATGCCTAC GCAATGAGA TCATGCCTC TCTACCTAC TCCTGACTT ACCCCATCGA ATGGTGTGA CACCTACGGA ATGTTGCTC CATCTTTTGTT GCGATCACAG CTTTTTTTT TGGGGCCTC CTGTTATTTT TAGGGGCCTC CTGCTTTTTTT TAGTTT TAGTTT TAGGGGCCTC CTGCTTTTTTT TAGTTT TAGTTT TAGTTT TAGTTT TAGTTT TAGTTT TAGTTT TAGTTT TAGTTT TAGTT TAGTTT TAGTT TAGT TAGTT TAGT TAGT TAGTT TAGTT TAGTT TAGTT TAGTT TAGTT TAGTT TAGTT TAGTT TAGT T | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>600<br>660<br>780<br>900<br>960<br>1020<br>1140<br>1200<br>1140<br>1500<br>1560<br>1620<br>1680<br>1680<br>1860<br>1860                |
| 50<br>55<br>60<br>65<br>70 | Seq ID NO: Nucleic Aci. Coding seq.  1   ATAACAGCAT TCCTTGTCCC ACAACTGCTC CTCGCCTGCT ACTAGGGTCC GTACTACAGA AGCCGGGGTT GCAGGACTCCT TGTCAGTCTG CATGAGTCTG CATGAGTCTG CATGAGTCTG CATGAGTCTG CATGACTGCTC CATCACCTTC GATGCTCCTC TTATCCTGT TGACCGCAGG CCTGTTGGCT TTATCCTGT TGACGGAGGC CTATGCCCCC CATCCACCGG CAGGTAACTC TCAAAGGGAT ACAGTTTTGC TCAAAGGGAT ACAGTTTTGC TCAAAGGGAT ACAGTTTTTT GTTTTTTTTAA CCCAGTGCAG CCTGGGATGAC CCTGGGATGAC CCATGGACTA CCCCTCTAAC GAGCAAAAAT   | 619 DNA se id Accession lence: 254.  11    GAAGTGCCGT TCTGCTCACC AGAGTGCCGA AGAGTGCCGA AGAGTGCGAA ACCAGGCGAA ACCAGGCGAA ACCAGGCGAA ACCAAGCTCA CTCTTTGGGA ACCAAGCTCA CTCTCTCACCT TCCATTGCCA TCCATTGCCA TCCATTGCCA TAGGTCACCT TCCATTGCCA TAGGTCACCT TCCATTGCCA TAGGTTCAT TACTCTCAAG TATTCCACAC GCCCACGCTT TGTCCTGAAG GTGGGCGAAA TCCCTCCCAG CAGTTCTTAG TAAGTGGGAG ACAGGATCTT CCTCGACCA CAGGTCTTAC TAAGTGGGAG ACAGGATCTT CCTCGACCA AGGCGTGAGC AAGGTCTGGT TCACAGTGGGAG ACACGTTGGGAGAAAGGCC AGCAGGTTGGGAGAAAGGCT   | equence 1 #: NM_003 1357 21   GGRACTGGAA CCTCGCTCGT GGCGGGATAG GCCGGGATAG CAACAGTCCC AGGCTGAAGC TGCCTTCAT TCACTCTTTC TCACGGGAG ATGTCTTTTC TCACGGCTGA CCATCCTCTT TCACGGCTGA CCATCCTCAT TCTGTAAACC AGGAAATCAC AGGAAATCAC AGGCCAGCC AGGCCAGCCC CATCTAGCAC CCGTCAGCCC CCTCAACCAC CCGTCAGCCC CCTCAACCAC CCGTCAGCCC CCTTCAGCCAC CCGTCAGCCC CCTTCAGCCAC CCGTCACCAC CCTCTCACCAC CCGTCCCC CATCTGAGCT CTTTTTGAGGCT TTTTTGAGGCT TTTTTGAGGCT TTTTTGAGCT TCTCAGCCAC CCTCTCAGCCT CCTCAGCCC CATCTAGCCT CCTCAGCCC CATCTAGCCT CTCTCAGCCT CCTCTCAGCCT CCTCTCACCAC CCTCTCCTCAC CCTCTCCTCAC CCTCTCCTCAC CCTCTCCTCAC CCTCTCCTCAC CCTCTCTCACC CCTCTCTCCT CCTCTCCTCC CCTCTCTCT   | 31    TAGGCGTGTC TCCTCCCTC CTGTCCAAGG TGATGGTTG TAGGCATGG TGATGGTTG GCACCAGG TGATGGTTT CATCAGTTT CATCAGTTT CATCAGTTT CATCAGCTTC GAAGCCCCTT TGATATCGCT TGAGCTTCC CTTGATGCC GAAGCCCTT GCAGCCTTG GCTGCTCAC TCAACTCGTG TCAAGGTTT GCAGAACAG TTACAAAGAC ATCAGCCGG TCTAGGAAAA AATCCTTCC ATCAGCTTTC CAGGCTTGC CACGCTTGCC CACGCTTGCC CACGCTTGCC CACGCCTGCC CACGCCTGCCC CACTGCCC CACGCCTGCCC CACGCCCCC CACGCCCCC CACGCCCCC CACGCCCCC CACGCCCCC CACGCCCCC CACGCCCCC CCCCCCCC  | 41   CTCTCCCTGG CGGCGAGGGC TCTCCCCGGG TCTCCCCGGG TCTCAGAAA CCGAATGGCC GTCTTCCTCC GACGGGAAGCA TCCTGGCTGG CTGCTGTGG ATTGATATA GCTCCTGGTC GGGGCCCACA CTGCTCAGAGA AGGAAGAGCA CTGCCAATG AAGCAGAAG CCTCCCCAAA TATGAAGTAA GCGCAGATC CTGTCGGGGC TTTTTTGTCT GTCCAGTGGT CATTCCATC CTTCAATCTCCATC CTTCAACAGA TCTTAATCTTG CACACAGCTC CACACACCTC CACACCTC CACACACCTC CACACACCTC CACACACCTC CACACACCTC CACACACCTC CACACCTC CACACACCTC CACACACCTC CACACACCTC CACACACCTC CACACACCTC CACACCTC CACACACC CACACCTC CACACACC CACACCTC CACACACC CACACC CACACACC CACACACC CACACAC CACACACC CACACC CACACACC CACACACC CACACAC CA | 51    ACCCTCCCCC CGCCTTTATA CACTGAGGAG ACGCCTTGGC TGAAATCCAA CGGTGGCCAC TCTGCAACGT TGGGTGTGTT CAGGCCCAC TGATTCTGGC TGATTCTGGC TCTACCTCAC TCACTCAC TCACTCAC TCACTCAC TCACTCAC   | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1020<br>1140<br>1260<br>1380<br>1440<br>1560<br>1680<br>1740<br>1860<br>1980                        |

| 5  | ATTCACAGGT<br>TAATCTCCCC<br>CTCCTTGTCA<br>CTCATCTTGC<br>GTGGGCATGG | GGAGAATTTG<br>ACCCCAACCT  | TTCTTGCACT<br>CCAGGAATTC<br>TAGATCATTC<br>CTGTAAATAG<br>GAGGAGTGTT | GTCCCCAAAC<br>TTTCAGACCT<br>TCACTTCAAA<br>ATTTACCGCA<br>CATTGTATAA | TTGCTGTCAA<br>CACTAGCACA<br>TTCCTGGGGC<br>TTTACGGCTG<br>TAAGTTATTC | TTCCGAGATC AGCCCGGTTG TGATACTTCT CATTCTGTAA ACCTGAGTAT             | 2100<br>2160<br>2220<br>2280<br>2340<br>2400 |
|----|--|---|--|--|--|--|--|
| 10 | Seq ID NO:<br>Protein Acc  | 620 <u>Protei</u><br>ession #: N                                  |  |  |  |  |  |
| 15 | RRKMLPTOFL<br>KLVRGRKPLS<br>LTYVLFLMAL<br>DDTILSSALA               | <br>NGLKSKYYRL<br>FLLGVLGIFG<br>LLVILGLAVG                        | LTFAFIIGLD<br>FSLVQDVIAI<br>GSFTGWKRHG<br>VSPEFWLLTK               | GSTGPTRFFL<br>EYIVLTMNRT<br>AHIYLTMLLS<br>QRNPMDYPVE               | FGILFSICFS<br>NVNVFSELSA<br>IAIWVAWITL<br>DAFCKPQLVK               | CLLAHAVSLT<br>PRRNEDFVLL<br>LMLPDFDRRW<br>KSYGVENRAY               | 60<br>120<br>180<br>240<br>300               |
| 20 |  | 621 <u>DNA se</u><br>id Accession<br>mence: 488                   | #: NM_0024   | 23.2   |  |  |  |
| 25 | 1  | 11  | 21   | 31   | 41   | 51   |  |
| 30 | TGCTGTGTGC<br>GAGGCATGAG   | CCATAGGTCC<br>TGTGTGCCTG<br>TGAGCTACAG                            | CTGCCTGGCA<br>TGGGAACAGG   | GCCTGGCCCT<br>CTCAGGACTA   | GCCGCTGCCT<br>TCTCAAGAGA   | CAGGAGGCGG<br>TTTTATCTCT   | 60<br>120<br>180                             |
|    | TCTTTGGCCT<br>CCAGATGTGG<br>CTTCCAAAGT                             | AACAAAAAT<br>ACCTATAACT<br>AGTGCCAGAT<br>GGTCACCTAC<br>AGTGTCAAAG | GGAATGTTAA<br>GTTGCAGAAT<br>AGGATCGTAT                             | ACTCCCGCGT<br>ACTCACTATT<br>CATATACTCG                             | CATAGAAATA<br>TCCAAATAGC<br>AGACTTACCG                             | ATGCAGAAGC<br>CCAAAATGGA<br>CATATTACAG                             | 240<br>300<br>360<br>420<br>480              |
| 35 | GGAAAGTTGT<br>ACTCCTACCC<br>GTCTCGGAGG<br>GGATTAACTT               | ATGGGGAACT<br>ATTTGATGGG<br>AGATGCTCAC<br>CCTGTATGCT              | GCTGACATCA<br>CCAGGAAACA<br>TTCGATGAGG<br>GCAACTCATG               | TGATTGGCTT<br>CGCTGGCTCA<br>ATGAACGCTG<br>AACTTGGCCA               | TGCGCGAGGA<br>TGCCTTTGCG<br>GACGGATGGT<br>TTCTTTGGGT               | GCTCATGGGG<br>CCTGGGACAG<br>AGCAGTCTAG<br>ATGGGACATT               | 540<br>600<br>660<br>720                     |
| 40 | AACTTTCCCA<br>GAAAGAAATA<br>TGTTGCACAA                             | GGATGATATT<br>GAAACTTCAG<br>TCAGAATTGA                            | AAAGGCATTC<br>GCAGAACATC<br>TAAGCACTGT                             | AGAAACTATA<br>CATTCATTCA<br>TCCTCCACTC                             | TGGAAAGAGA<br>TTCATTGGAT<br>CATTTAGCAA                             | CAAAATTTTA<br>AGTAATTCAA<br>TGTATATCAT<br>TTATGTCACC<br>AAACTCCTTT | 780<br>840<br>900<br>960<br>1020             |
| 45 | ATGGTGTGAC   |   | TCCATCTATG   | AGCTTTGTCA   | GTGCGCGTAG   | ATGTCAATAA   | 1080   |
|    |  | 622 <u>Prote</u><br>cession #: 1                                  |  |  |  |  |  |
| 50 | 1  | 11  | 21   | 31   | 41   | 51   |  |
| 55 | EMQKFFGLPI<br>PHITVDRLVS<br>APGTGLGGDA                             | TGMLNSRVIE<br>KALNMWGKEI  | IMQKPRCGVP<br>PLHFRKVVWG<br>GSSLGINFLY                             | DVAEYSLFPN<br>TADIMIGFAR   | SPKWTSKVVT<br>GAHGDSYPFD   | NANSLEAKLK<br>YRIVSYTRDL<br>GPGNTLAHAP<br>VMYPTYGNGD               | 60<br>120<br>180<br>240                      |
| 60 | Nucleic Ac   | 623 <u>DNA s</u><br>id Accessio<br>uence: 204.                    | n #: NM_031  | 457.1  | ,  |  |  |
|    | 1  | 11<br>  | 21<br>   | 31<br>   | 41<br>   | 51   |  |
| 65 | CAGGAAATAG<br>ATTCTCTCAG<br>ACGTGGCTGC<br>CTGTGTTGGT               | AGGACTTCGG<br>GAAAAAAAAC<br>TGGCAGAGCA<br>GGTGGCACCC              | ATCCTTCTAA<br>AAGGTCCCCA<br>AGCATGAATT<br>CACAATGGTT               | CCCTACCACC<br>CAGCAAAGAA<br>CGATGACTTC<br>ATCCTGTGAC               | CAACTGGCCC<br>AAGGAATAGG<br>AGCAGTTCCG<br>CCCAGGAATT               | GGCCTGCATC<br>CAGTACATTC<br>ATCAAGAGAT<br>GTGGCCAATT<br>ATGTCTCACG | 120<br>180<br>240<br>300                     |
| 70 | TGGTGTCGAA<br>GGGCCATCCA<br>TTCTCGTAGG<br>TGTGGTTTAT               | TGTGAATGGG<br>GATCATCATT<br>GGAATACCTG<br>CATTTCAGGA              | CAGCCTGTGC<br>GGCCTGGCTC<br>TCTATTTCAT                             | AGAAAGCTCT ACATCGGCCT TCTACGGAGG TGGCAGCAGA                        | GAAAGAAGGC<br>CGGCTCCATC<br>CTTTCCCTTC<br>AAATCAGCCA               | CCACCTAGIT AAAACCTTGG ATGGCGACGG TGGGGAGGCT TATTCTTATT             | 420<br>480<br>540<br>600                     |
| 75 | TCATACTCTT CTTACGCCTC TCCTGGAGTT AATCAAGCA                         | CATCACAGAT<br>GGGTGTGAAC<br>TGGCATCGCA<br>TGTGAGTGTC              | CTAAGTATTO<br>CCTGGAATGO<br>TGCGCATCTT                             | CCCACCCATA CGATTTCTGG CCCACTTTGG                                   | TGCCTACCCC CGTGCTGCTC CTGCCAGTTC AGCAAACCC                         | GCAGTTGGAG GACTATTATC GTCTTCTGCC GTCTGCTGTC GTGATCACCC             | 720<br>780<br>840<br>900                     |
| 80 | ACAGATTCTC<br>CCATAACCCA<br>TCTCACCTTC<br>ACAGAGATTT               | GAAGCATCTT<br>A GGTCGTTCCT<br>C ATTCTTCAAT<br>T TAAACAGATC        | TCACTGGGAC<br>GTTCTGACAC<br>TCAGTCTAGG<br>TTAACCAAG                | CAAAAGAAGT<br>CTGAGGAAAC<br>AAACCATGCT<br>AGGACTCCCT               | CCTCCTCCCI<br>GTCTCTCCCI<br>GTTTCTCTAT<br>AGGGCACATC               | AAGTAAGGCT TTCTGGGCTT CTGTTTGTAC CAAGAAGAAG CATCAGCACA CTGCTGCATG  | 1020<br>1080<br>1140<br>1200                 |

|    |  | GGTTAGAGGA<br>ATAAATAGAT   |  |   |  | TTCAATTGTG   | 1320                                   |
|----|--|--|--|---|--|--|--|
| 5  | Seq ID NO:<br>Protein Acc  | 624 <u>Protei</u><br>ession #: N   |  |   |  |  |  |
| 10 | <br>MNSMTSAVPV<br>PVQKALKEGK<br>LSVAAENQPY<br>GMAISGVLLV           | 11<br> <br> <br>ANSVLVVAPH<br>TLGAIQIIIG<br>SYCLLSGSLG<br>FCLLEFGIAC             | <br>NGYPVTPGIM<br>LAHIGLGSIM<br>LNIVSAICSA                         | SHVPLYPNSQ<br>ATVLVGEYLS<br>VGVILFITDL                            | <br>PQVHLVPGNP<br>ISFYGGPPFW<br>SIPHPYAYPD                         | GGLWFIISGS<br>YYPYAWGVNP   | 60<br>120<br>180<br>240                |
| 15 |  | 625 DNA se<br>d Accession<br>ence: 187   | #: NM_005  | 221.3   |  |  |  |
| 20 | <br>ATGACAGGAG   | 11<br> <br>  TGTTTGACAG<br>  CCGCAGCTAT  |  |   |  |  | 60<br>120                              |
| 25 | TCAGCTACCG<br>CCTACCTCGG<br>AACGGCTCCG<br>TACCACCAGT<br>GAAGTGACCG | ATTCTGACTA<br>CTTCCTATGG<br>CCGGGAGCTA<br>ACGGCGGCGC<br>AGCCCGAGGT               | CTACAGCCCT<br>CAAAGCTCTC<br>CCCAGCCAAA<br>CTACAACCGC<br>GAGAATGGTG | ACGGGGGAG<br>AACCCCTACC<br>GCTTATGCCG<br>GTCCCAAGCG<br>AATGGCAAAC | CCCCGCACGG<br>AGTATCAGTA<br>ACTATAGCTA<br>CCACCAACCA<br>CAAAGAAAGT | CTACTGCTCT<br>TCACGGCGTG<br>CGCTAGCTCC<br>GCCAGAGAAA<br>TCGTAAACCC | 180<br>240<br>300<br>360<br>420        |
| 30 | TACCTCGCCT<br>GTGAAAATCT<br>ATGCCCCCGG<br>CCAGCGGTGT               | ATTCCAGCTT<br>TGCCGGAACG<br>GGTTTCAGAA<br>AGCACAGTCC<br>GGGAGCCCCA<br>CCAACCAGTC | CGCCGAGCTG<br>CAAAAGATCC<br>CAGCTCCAGC<br>GGGCTCGTCC               | GCCGCCTCGC<br>AAGATCAAGA<br>GACCCAATGG<br>CGCTCGCTCA              | TGGGATTGAC<br>AGATCATGAA<br>CGTGTAACTC<br>GCCACCACCC               | ACAAACACAG<br>AAACGGGGAG<br>GCCGCAGTCT<br>TCATGCCCAC               | 480<br>540<br>600<br>660<br>720<br>780 |
| 35 | ACAAGTGCAG   | CCAGCTCAAT<br>CCTCCGGGAC   | CAATTCCCAC   |   |  |  | 840                                    |
|    |  | 626 Protei   |  |   |  |  |  |
| 40 | 1<br> <br> MTGVFDRRVP  | 11<br> <br>SIRSGDFQAP  | 21<br> <br> <br>  FQTSAAMHHP                                       | 31<br> <br>SQESPTLPES   | 41<br> <br>SATDSDYYSP  | 51<br> <br>TGGAPHGYCS  | 60                                     |
| 45 | EVTEPEVRMV<br>VKIWFQNKRS   | NPYQYQYHGV<br>NGKPKKVRKP<br>KIKKIMKNGE<br>SYLENSASWY                             | RTIYSSFQLA<br>MPPEHSPSSS   | ALQRRFQKTQ<br>DPMACNSPQS  | YLALPERAEL PAVWEPQGSS  |  | 120<br>180<br>240                      |
| 50 |  | 627 <u>DNA se</u><br>id Accession<br>mence: 118                                  | 3 #: NM_0144   | 120   |  |  |  |
| 55 | AGCCTCGCTT<br>GTGGCGGCCG<br>GACTTCAACA                             | 11<br>  CGACGTGCTG<br>TGGTGACGCA<br>TCCTGCTGGG<br>ACATCAGGAG<br>CGGACTGCAA       | CAGTGCTGGG<br>GCTGAGCTGG<br>CTCTGCTGAC                             | ACCCTCCAGG<br>CTCTGCTCTC<br>CTGCATGGGG                            | AGCCCCGGGA<br>CCCTGGGAGC<br>CCCGGAAGGG                             | TTGAAGGATG<br>TCTGGTCCTG<br>CTCACAGTGC                             | 60<br>120<br>180<br>240                |
| 60 | TTCTGTGCTA<br>GGGACACTCT<br>AGGCAGCTTG<br>GAAAACCAAC               | CATGTCGTGG<br>GTGTGAACGA<br>ATGAGCAAGA<br>CCAAAAGGAA                             | GTTGCGGAGG<br>TGTTTGTACT<br>TGGCACACAT<br>GCCAAGTATT               | AGGTGCCAGC<br>ACGATGGAAG<br>GCAGAAGGAA<br>AAGAAATCAC              | GAGATGCCAT<br>ATGCAACCCC<br>CAACTGGGCA<br>AAGGCAGGAA               | GTGCTGCCCT<br>AATATTAGAA<br>CCCAGTCCAG<br>GGGACAAGAG               | 300<br>360<br>420<br>480<br>540        |
| 65 | TGGACGAAAA<br>AAAGACACTG<br>TGTCGAAGCC                             | CTCAAGCTCC<br>AATTGACCAG   | AGTCCTTTTG<br>AGAAATCTTC<br>CAATCGGCAG                             | GAGGGACAGG<br>CAGCGTTGCG<br>CATGCTCGAT                            | TCTGCTCCAG<br>ACTGTGGCCC<br>TAAGAGTATG                             | TCGTCATTTT AAGAGGGCAT TGGACTACTG CCAAAAAATA AAAAAAAAAA             | 600<br>660<br>720<br>780<br>840        |
| 70 |  | 628 <u>Prote</u><br>cession #: 1   |  |   |  |  |  |
| 75 | PFCATCRGLR<br>QENQPKRKPS   | RRCQRDAMCC   | PGTLCVNDVC<br>EGESCLRTFD   | TTMEDATPIL<br>CGPGLCCARH  | ERQLDEQDGT<br>FWTKICKPVL   | 51<br> <br>KFCLQPRDEK<br>HAEGTTGHPV<br>LEGQVCSRRG                  | 60<br>120<br>180                       |
| 80 | Nucleic Ac.  | 629 <u>DNA s</u><br>id Accession<br>uence: 241.                                  | n #: NM_00   | 2448.1  |  |  |  |
|    | 1  | 11   | 21   | 31  | 41   | 51   |  |

```
GCGCGAGTGC TCCCGGGAAC TCTGCCTGCG CGGCGGCAGC GACCGGAGGC CAGGCCCAGC
       ACGCCGGAGC TGGCCTGCTG GGGAGGGGGG GGAGGCGCGC GCGGGAGGGT CCGCCCGGCC
                                                                                 120
       AGGCCCCGGG CCCTCGCAGA GGCCGGCCGC GCTCCCAGCC CGCCCGGAGC CCATGCCCGG
                                                                                 180
       CGGCTGGCCA GTGCTGCGGC AGAAGGGGGG GCCCGGCTCT GCATGGCCCC GGCTGCTGAC
 5
                                                                                 240
       ATGACTTCTT TGCCACTCGG TGTCAAAGTG GAGGACTCCG CCTTCGGCAA GCCGGCGGG
       GGAGGCGCGG GCCAGGCCCC CAGCGCCGCC GCGGCCACGG CAGCCGCCAT GGGCGCGGAC
                                                                                 360
       GAGGAGGGGG CCAAGCCCAA AGTGTCCCCT TCGCTCCTGC CCTTCAGCGT GGAGGCGCTC
                                                                                 420
       ATGGCCGACC ACAGGAAGCC GGGGGCCAAG GAGAGCGCCC TGGCGCCCTC CGAGGGGCTG
                                                                                 480
10
       CAGGCGGCGG GTGGCTCGGC GCAGCCACTG GGCGTCCCCG CGGGGTCGCT GGGAGCCCCG
       GACGCGCCCT CTTCGCCGCG GCCGCTCGGC CATTTCTCGG TGGGGGGACT CCTCAAGCTG
                                                                                 600
       CCAGAAGATG CGCTCGTCAA AGCCGAGAGC CCCGAGAAGC CCCGAGAGGAC CCCGTGGATG
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       CAGAGCCCCC GCTTCTCCCC GCCGCCGGCC AGGCGGCTGA GCCCCCCAGC CTGCACCCTC
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       CTGGAGCGCA AGTTCCGCCA GAAGCAGTAC CTGTCCATCG CCGAGCGCGC GGAGTTCTCC
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       AGCTCGCTCA GCCTCACTGA GACGCAGGTG AAGATATGGT TCCAGAACCG CCGCGCCAAG
                                                                                 900
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                                                                                 960
       CCACCGGCTG CCTTCGGCCT CTCCTTCCCT CTCGGCGGCC CCGCAGCTGT.AGCGGCCGCG
       GCGGGTGCCT CGCTCTACGG TGCCTCTGGC CCCTTCCAGC GCGCCGCGCT GCCTGTGGCG
                                                                                1080
20
       CCCGTGGGAC TCTACACGGC CCATGTGGGC TACAGCATGT ACCACCTGAC ATAGAGGGTC CCAGGTCCCC ACCTGTGGGC CAGCCGATTC CTCCAGCCCT GGTGCTGTAC CCCCGACGTG
                                                                                1140
                                                                                1200
       CTCCCCTGCT CGGCACCGCC AGCCGCCTTC CCTTTAACCC TCACACTGCT CCAGTTTCAC
                                                                                1260
       CTCTTTGCTC CCTGAGTTCA CTCTCCGAAG TCTGATCCCT GCCAAAAAGT GGCTGGAAGA
                                                                                1320
       GTCCCTTAGT ACTCTTCTAG CATTTAGATC TACACTCTCG AGTTAAAGAT GGGGAAACTG
AGGGCAGAGA GGTTAACAGA TTTATCTAGG GTCCCCAGCA GAATTGACAG TTGAACAGAG
                                                                                1380
25
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       1560
                                                                                1620
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Protein Accession #: NP_002439.1
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                                                       41
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        MTSLPLGVKV EDSAFGKPAG GGAGQAPSAA AATAAAMGAD EEGAKPKVSP SLLPFSVEAL
                                                                                   60
        MADHRKPGAK ESALAPSEGV QAAGGSAQPL GVPPGSLGAP DAPSSPRPLG HFSVGGLLKL
                                                                                 120
        PEDALVKAES PEKPERTPWM QSPRFSPPPA RRLSPPACTL RKHKTNRKPR TPFTTAQLLA
                                                                                  180
40
        LERKFROKOY LSIAERAEFS SSLSLTETOV KIWFONRRAK AKRLOEAELE KLKMAAKPML
        PPAAFGLSFP LGGPAAVAAA AGASLYGASG PFQRAALPVA PVGLYTAHVG YSMYHLT
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        Nucleic Acid Accession #: NM_002557.1
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        Coding sequence: 13..2049
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                                21
                                            31
                                                                    51
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        CACGATGGTG CTGCCCATAA ACTCGTGTGT TATTTCACCA ACTGGGCACA CAGTCGGCCA
                                                                                  120
        GGCCCTGCCT CGATCTTGCC CCATGACCTG GACCCCTTTC TCTGCACCCA CCTGATATTT
                                                                                  180
        GCCTTTGCCT CAATGAACAA CAATCAGATT GTTGCTAAGG ATCTCCAGGA TGAGAAAATT
                                                                                  240
        CTCTACCCAG AGTTCAACAA ACTAAAGGAG AGGAACAGAG AGCTGAAAAC ACTACTGTCC
                                                                                  300
        ATCGGCGGGT GGAACTTTGG CACCTCAAGA TTCACCACTA TGTTGTCCAC ATTTGCCAAC CGTGAAAAGT TTATTGCTTC AGTTATATCC CTTCTGAGGA CACATGACTT TGATGGTCTT
                                                                                  360
 55
        GACCTITICT TCTTATATCC TGGACTAAGA GGCAGCCCCA TGCATGACCG GTGGACTTTT
                                                                                  480
        CTCTTCTTAA TTGAAGAGCT CCTGTTTGCC TTCCGGAAGG AGGCACTGCT CACCATGCGC
                                                                                  540
        CCGAGGCTGC TGCTGTCTGC TGCTGTTTCT GGGGTCCCAC ACATCGTCCA AACATCCTAT
                                                                                  600
        GATGTGCGCT TTCTAGGAAG ACTCCTGGAT TTCATCAATG TCTTGTCTTA TGACTTACAT
 60
        GGAAGTTGGG AAAGGTTCAC AGGACATAAT AGCCCCCTCT TCTCTCTGCC TGAAGACCCC
                                                                                  720
        ARATCTTCGG CATATCCTAT GRATTATTGG AGRARGCTTG GGGCACCCTC AGAGAAGCTC ATCATGGGGA TCCCCACCTA TGGACGTACC TTTCGCCTCC TCAAAGCCTC TAAGAATGGG
                                                                                  780
        TTGCAGGCCA GAGCGATCGG ACCAGCATCT CCAGGGAAGT ACACCAAGCA AGAAGGCTTC
                                                                                  900
        TTGGCTTATT TTGAGATTTG TTCCTTTGTC TGGGGAGCGA AGAAGCACTG GATTGATTAC
                                                                                  960
        CAGTATGTCC COTATGCCAA CAAGGGAAA GAGTGGGTTG GCTATGACAA TGCCATCAGC
TTCAGTTACA AGGCATGGTT TATAAGGCGA GAGCATTTTG GGGGGGCCAT GGTGTGGACA
 65
                                                                                 1020
                                                                                 1080
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                                                                                 1140
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                                                                                 1200
        CTGTCATCTG CTGTGAATTC TTCAAGCACT GACCCTGAAA GGCTGGCTGT GACCACGGCA
                                                                                 1260
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        TGGACCACTG ATAGTAAGAT TTTGCCCCCA GGAGGAGAGG CTGGGGTCAC TGAGATCCAC
                                                                                  1320
         GGAAAGTGTG AAAATATGAC TATAACCCCT AGAGGTACAA CTGTGACCCC TACAAAGGAA
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         ACTGTATCCC TTGGAAAGCA CACTGTAGCT CTAGGAGAGA AGACTGAGAT CACTGGGGCA
                                                                                 1440
         ATGACCATGA CTTCTGTGGG TCATCAGTCC ATGACCCCTG GAGAGAAGGC CCTGACCCCT
                                                                                  1500
         GTGGGTCATC AATCTGTGAC CACTGGACAG AAGACCCTGA CCTCTGTGGG TTATCAGTCT
                                                                                 1560
 75
         GTGACCCCTG GGGAAAAGAC CCTGACCCCT GTGGGTCATC AGTCTGTGAC CCCTGTGAGT
                                                                                 1620
         CATCAGTCTG TGAGCCCTGG AGGAACGACT ATGACCCCTG TCCATTTTCA GACTGAGACC
                                                                                 1680
         CTTAGACAGA ATACAGTGGC CCCTAGAAGG AAGGCTGTGG CCCGTGAAAA GGTGACTGTC
         CCCTCCAGAA ACATATCAGT CACCCCTGAA GGGCAGACTA TGCCTTTAAG AGGGGAGAAT
                                                                                  1800
         TTGACTTCTG AGGTGGGCAC TCACCCCAGG ATGGGTAACT TGGGTCTTCA GATGGAAGCT
GAAAACAGGA TGATGCTGTC CTCCAGCCCC GTCATCCAGC TCCCGGAACA AACTCCTCTA
                                                                                  1860
 80
                                                                                  1920
         GCTTTTGACA ACCGCTTTGT TCCCATCTAT GGAAACCATT CCTCTGTCAA CTCAGTAACC
                                                                                  1980
         CCTCAAACAA GTCCTCTTC TCTAAAAAAA GAAATCCCAG AAAACTCTGC TGTGGATGAA
                                                                                  2040
         GAAGCCTAAG CCCCTCTGGT GTCAGAAACC AGGGAAAACC CTTGTCTTTT CTTCTAAGTG
                                                                                 2100
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## CTCTTTTCCA TTAAATAAAC TGTAAACACA AGAACCCA

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Seq ID NO: 632 Protein sequence
        Protein Accession #: NP_002548.1
        MWKLLLWVGL VLVLKHHDGA AHKLVCYFTN WAHSRPGPAS ILPHDLDPFL CTHLIFAFAS
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IASVISLLRT HDFDGLDLFF LYPGLRGSPM HDRWTFLFLI EELLFAFRKE ALLTMRPRLL
10
                                                                                            180
        LSAAVSGVPH IVQTSYDVRF LGRLLDFINV LSYDLHGSWE RFTGHNSPLF SLPEDPKSSA
                                                                                            240
        YAMNYWRKLG APSEKLIMGI PTYGRTFRLL KASKNGLQAR AIGPASPGKY TKQEGFLAYF
                                                                                            300
        EICSFVMGAK KHWIDYQYVP YANKGKEWVG YDNAISFSYK AWFIRREHG GAMVWTLDMD
DVRGTFCGTG PPPLVYVLND ILVRAEFSST SLPQFWLSSA VNSSSTDPER LAVTTAWTTD
SKILPPGGEA GVTEIHGKCE NMTITPRGTT VTPTKETVSL GKHTVALGEK TEITGAMTMT
                                                                                            360
                                                                                             420
15
                                                                                            480
        SVGHQSMTPG EKALTPVGHQ SVTTGQKTLT SVGYQSVTPG EKTLTPVGHQ SVTPVSHQSV
                                                                                            540
        SPGGTTMTPV HFQTETLRQN TVAPRRKAVA REKVTVPSRN ISVTPEGQTM PLRGENLTSE
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        VGTHPRMGNL GLQMEAENRM MLSSSPVIQL PEQTPLAFDN RFVPIYGNHS SVNSVTPQTS
        PLSLKKEIPE NSAVDEEA
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        AAACTCAGAA TTTTCGCGGG CTCGGTGAGC GGTTTTATCC CTCCGGCCGG CAGGCTGGGC
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                                                                                            180
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         GGCCGTACAG AACAGCAAGA ACGCCAAGGA CAAGAACCTG AAGCGCCACT CCATCATCTC
                                                                                            240
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                                                                                            300
        GCAGCCTAAC AGCAGCTACC AGAACAACAT CACGCACCTC AACAATGAGA ACCTGAAGAA
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ACCCCCGGCC AGCCAGCTCT CGGGTTCCCA GACCGGGGG TCCTCCTCAG TCAAGAAAGC
                                                                                             420
                                                                                             480
35
         CCCTCACCCT GCCGTCACCT CCGCAGGGAC GCCCAAACGG GTCATCGTCC AGGCGTCCAC
                                                                                             540
        CAGTGAGCTG CTTCGCTGCC TGGGTGAGTT TCTCTGCCGC CGGTGCTACC GCCTGAAGCA
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                                                                                             660
         GGGCTGGCAG GACCAGGGCT TCATCACGCC GGCCAACGTG GTCTTCCTCT ACATGCTCTG
                                                                                             720
         CAGGGATGTT ATCTCCTCCG AGGTGGGCTC GGATCACGAG CTCCAGGCCG TCCTGCTGAC
                                                                                             780
40
        ATGCCTGTAC CTCTCCTACT CCTACATGG CAACGAGATC TCCTACCCGC TCAAGCCCTT CCTGGTGGAG AGCTGCAAGG AGGCCTTTTG GGACCGTTGC CTCTCTGTCA TCAACCTCAT
                                                                                             900
         GAGCTCAAAG ATGCTGCAGA TAAATGCCGA CCCACACTAC TTCACACAGG TCTTCTCCGA
                                                                                            960
         CCTGAAGAAC GAGAGCGGCC AGGAGGACAA GAAGCGGCTC CTCCTAGGCC TGGATCGGTG
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Protein Accession #: NP_003876.1
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         MGTVLSLSPS YRKATLFEDG AATVGHYTAV QNSKNAKDKN LKRESIISVL PWKRIVAVSA
                                                                                              60
         KKKNSKKVQP NSSYQNNITH LANENLKKSL SCANLSTFAQ PPPAQPPAPP ASQLSGSQTG
                                                                                             120
         GSSSVKKAPH PAVTSAGTPK RVIVQASTSE LLRCLGEFLC RRCYRLKHLS PTDPVLWLRS
                                                                                             180
55
         VDRSLLLQGW QDQGFITPAN VVFLYMLCRD VISSEVGSDH BLQAVLLTCL YLSYSYMGNE
         ISYPLKPFLV ESCKBAFWDR CLSVINLMSS KMLQINADPH YFTQVFSDLK NESGQEDKKR
                                                                                             300
         LLLGLDR
```

## TABLE 79A:

| 5  | Pkey:<br>ExAccn:<br>UnigeneID:<br>Unigene Till                     |  | nber   | fier number<br>er, Genbank accession number  | ·  |
|----|--|--|--|--|--|
|    | Seq ID No.:  | Sequence id  | entification nur   | nber linking information in Table 79A to sequences in  | Table 80   |
| 10 | Pkey   | ExAcon   | UnigenelD  | Unigene Title  | Seq ID No.   |
| 15 | 424212<br>424503<br>418007<br>418007<br>418738<br>443646<br>409956 | NM_005814<br>NM_002205<br>M13509<br>M13509<br>AW388633<br>AI085198<br>AW103364 | Hs.143131<br>Hs.149609<br>Hs.83169<br>Hs.83169<br>Hs.6682<br>Hs.164226<br>Hs.727 | glycoprotein A33 (transmembrane) Integrin, alpha 5 (fibronectin receptor, matrix metalloproteinase 1 (interstitial matrix metalloproteinase 1 (interstitial solute carrier family 7, (cationic amino Thrombospondin 1 Inhibin, beta A (activin A, activin AB a | Seq ID No. C1 & C217<br>Seq ID No. C2 & C218<br>Seq ID No. C3 & C219<br>Seq ID No. C4 & C220<br>Seq ID No. C5 & C221<br>Seq ID No. C5 & C221<br>Seq ID No. C5 & C222 |
| 20 | 422867<br>444381   | L32137<br>BE387335   | Hs.1584<br>Hs.283713   | cartilage oligomeric matrix protein (pse<br>hypothetical protein BC014245  | Seq ID No. C7 & C223<br>Seq ID No. C8 & C224<br>Seq ID No. C9 & C225   |
|    | 421582   | AI910275   | Hs.350470  | trefoll factor 1 (breast cancer, estroge   | Seq ID No. C10 & C226  |
|    | 411789   | AF245505   | Hs.72157   | Adlican  | Seq ID No. C11 & C227  |
|    | 452281   | T93500   | Hs.28792   | Homo sapiens cDNA FLJ11041 fis, clone PL   | Seq ID No. C12   |
| 25 | 428698<br>421552<br>425247<br>432201<br>447377                     | AA852773<br>AF026692<br>NM_005940<br>AI538613<br>X77343                        | Hs.334838<br>Hs.105700<br>Hs.155324<br>Hs.298241<br>Hs.334334                    | KIAA1866 protein secreted frizzled-related protein 4 martied mizzled-related protein 4 martie metalloproteinase 11 (stromelysin Transmembrane protease, serine 3 transcription factor AP-2 alpha   | Seq ID No. C13 & C228<br>Seq ID No. C14 & C229<br>Seq ID No. C15 & C230<br>Seq ID No. C16 & C231<br>Seq ID No. C17 & C232  |
| 30 | 446921   | AB012113   | Hs.16530   | small inducible cytokine subfamily A (Cy   | Seq ID No. C18 & C233  |
|    | 418888   | AU076801   | Hs.89436   | cadherin 17, LI cadherin (liver-intestin   | Seq ID No. C19 & C234  |
|    | 432179   | X75208   | Hs.2913  | EphB3  | Seq ID No. C20 & C235  |
|    | 422578   | AF239666   | Hs.1545  | caudal type homeo box transcription fact   | Seq ID No. C21 & C236  |
| 35 | 409889   | AW630041   | Hs.56937   | suppression of tumorigenicity 14 (colon  | Seq ID No. C22 & C237  |
|    | 447033   | Al357412   | Hs.157601  | Predicted gene: Eos cloned; secreted w/V   | Seq ID No. C23 & C238  |
|    | 447033   | Al357412   | Hs.157601  | Predicted gene: Eos cloned; secreted w/V   | Seq ID No. C24 & C239  |
|    | 411975   | Al916058   | Hs.144583  | 3'UTR of: dead ringer (Drosophila)-like  | Seq ID No. C25 & C240  |
|    | 434206   | AW136973   | Hs.362915  | ESTs, Wealdy similar to S69890 mitogen i   | Seq ID No. C26 & C241  |
| 40 | 423936<br>447400<br>449032<br>415214<br>443247                     | U77629<br>AK000322<br>AA045573<br>AI445236<br>BE614387                         | Hs.135639<br>Hs.18457<br>Hs.22900<br>Hs.125124<br>Hs.333893                      | achaeta-scufe complex (Drosophila) homol<br>hypothetical protein FLJ20315<br>nuclear factor (erythroid-derived 2)-lik<br>EphB2<br>c-Myc target JPO1  | Seq ID No. C27 & C247<br>Seq ID No. C28 & C243<br>Seq ID No. C29 & C244<br>Seq ID No. C30 & C244<br>Seq ID No. C30 & C245<br>Seq ID No. C31 & C246                   |
| 45 | 422048   | NM_012445  | Hs.288126  | spondin 2, extracellular matrix protein  | Seq ID No. C32 & C247  |
|    | 410418   | D31382   | Hs.63325   | transmembrane probasse, serine 4   | Seq ID No. C33 & C248  |
|    | 446342   | BE298665   | Hs.14846   | solute carrier family 7 (cationic amino  | Seq ID No. C34 & C249  |
|    | 411274   | NM_002776  | Hs.69423   | kallikrein 10  | Seq ID No. C35 & C250  |
|    | 104978   | Al199268   | Hs.19322   | Homo sapiens, Similar to RIKEN cDNA 2010   | Seq ID No. C36 & C251  |
| 50 | 422260<br>409041<br>420344<br>422163<br>437935                     | AA315993<br>AB033025<br>BE463721<br>AF027208<br>AW939591                       | Hs.105484<br>Hs.50081<br>Hs.97101<br>Hs.112360<br>Hs.5940                        | regenerating gene type IV Hypothetical protein, XP_051860 (KIAA119 putalive G protein-coupled receptor prominin (mouse)-like 1 mucin 13, epithelial transmembrane  | Seq ID No. C37 & C252<br>Seq ID No. C38 & C253<br>Seq ID No. C39 & C254<br>Seq ID No. C40 & C255<br>Seq ID No. C41 & C256  |
| 55 | 422330   | D30783   | Hs.115263  | epiregulin   | Seq ID No. C42 & C257  |
|    | 408908   | BE296227   | Hs.250822  | serine/threonine kinase 15   | Seq ID No. C43 & C258  |
|    | 407811   | AW190902   | Hs.40098   | cystelne knot superfamily 1, BMP antagon   | Seq ID No. C44 & C259  |
|    | 437852   | BE001836   | Hs.256897  | putative GPCR  | Seq ID No. C45 & C260  |
|    | 408243   | Y00787   | Hs.624   | interleukin 8  | Seq ID No. C46 & C261  |
|    | 426088   | AF038007   | Hs.166196  | ATPase, Class I, type 8B, member 1   | Seq ID No. C47 & C262  |
| 60 | 439738   | BE246502   | Hs.9598  | sema domain, immunoglobulin domain (lg),   | Seq ID No. C49 & C262  |
|    | 419741   | NM_007019  | Hs.93002   | ubiquifin carrier protein E2-C   | Seq ID No. C49 & C264  |
|    | 450983   | AA305384   | Hs.25740   | ERO1 (S. cerevisiae)-like  | Seq ID No. C50 & C265  |
|    | 417771   | AA804698   | Hs.82547   | refinoic acid receptor responder (tazaro   | Seq ID No. C51 & C266  |
|    | 421379   | Y15221   | Hs.103982  | smati inducible cytokine subfamily B (Cy   | Seq ID No. C52 & C267  |
| 65 | 442006   | AW975183   | Hs.372210  | ESTs, Weakly similar to \$72482 hypotheti  | Seq ID No. C53 & C268  |
|    | 413048   | M93221   | Hs.75182   | mannose receptor, C type 1   | Seq ID No. C54 & C269  |
|    | 443324   | R44013   | Hs.164225  | ESTs   | Seq ID No. C55 & C270  |
|    | 424917   | Al636208   | Hs.96901   | hypothetical protein FLJ23049  | Seq ID No. C56 & C271  |
|    | 424917   | Al636208   | Hs.96901   | hypothetical protein FLJ23049  | Seq ID No. C57 & C272  |
| 70 | 444527   | NM_005408  | Hs.11383   | small inducible cytokine subfamily A (Cy   | Seq ID No. C58 & C273  |
|    | 442652   | AI005163   | Hs.201378  | Homo sapiens cDNA FLJ40427 fis   | Seq ID No. C59 & C274  |
|    | 450726   | AW204600   | Hs.355462  | HUMPSPBA Human pulmonary surfactant-asso   | Seq ID No. C60 & C275  |
|    | 416965   | N26223   | Hs.160436  | MDAC1  | Seq ID No. C61 & C276  |
|    | 442275   | AW449467   | Hs.54795   | Homo sapiens secretoglobin, family 3A, m   | Seq ID No. C62 & C277  |
| 75 | 431745   | AW972448   | Hs.163425  | Novel FGENESH predicted cadherin repeat  | Seq ID No. C63 & C278  |
|    | 431745   | AW972448   | Hs.163425  | Novel FGENESH predicted cadherin repeat  | Seq ID No. C64 & C279  |
|    | 453142   | AA033648   | Hs.7473  | Homo sapiens gap junction protein, alpha   | Seq ID No. C65 & C280  |
|    | 421659   | NM_014459  | Hs.106511  | protocadherin 17   | Seq ID No. C66 & C281  |
|    | 444090   | S69115   | Hs.10306   | natural killer cell group 7 sequence   | Seq ID No. C67 & C282  |
| 80 | 421563<br>430413<br>414991<br>419833<br>424943                     | NM_006433<br>AW842182<br>C17898<br>AA251131<br>AU077260                        | Hs.105806<br>Hs.241392<br>Hs.220697<br>Hs.153924                                 | granulysin<br>small inducible cytokine A5 (RANTES)<br>Homo sapiens up-regulated by BCG-CWS (LO<br>Homo sapiens tryptophanyl-IRNA synthetas<br>death-associated protein kinase 1  | Seq ID No. C68 & C283<br>Seq ID No. C69 & C284<br>Seq ID No. C70 & C285<br>Seq ID No. C71 & C286<br>Seq ID No. C72 & C287  |

|    |        |           |           |   | 0 10 11 000 0 0000     |
|----|--------|-----------|-----------|---|------------------------|
|    | 430890 | X54232    | Hs.2699   | glypican 1                                | Seq ID No. C73 & C288  |
|    | 452401 | NM_007115 | Hs.29352  | tumor necrosis factor, alpha-induced pro  | Seq ID No. C74 & C289  |
|    | 439180 | Al393742  | Hs.199057 | v-erb-b2 avian erythroblastic leukemia v  | Seq ID No. C75 & C290  |
|    | 410407 | X66839    | Hs.63287  | carbonic anhydrase IX                     | Seq ID No. C76 & C291  |
| 5  | 418526 | BE019020  | Hs.85838  | solute carrier family 16 (monocarboxylic  | Seq ID No. C77 & C292  |
| -  | 422627 | BE336857  | Hs.118787 | transforming growth factor, beta-induced  | Seq 1D No. C78 & C293  |
|    | 430486 | BE062109  | Hs.241551 | chloride channel, calcium activated, fam  | Seq ID No. C79 & C294  |
|    |        |           |           |   | Seq ID No. C80 & C295  |
|    | 423673 | BE003054  | Hs.1695   | matrix metalloproteinase 12 (macrophage   |                        |
| 10 | 423673 | BE003054  | Hs.1695   | matrix metalloproteinase 12 (macrophage   | Seq ID No. C81 & C296  |
| 10 | 431846 | BE019924  | Hs.271580 | uroplakin 1B                              | Seq ID No. C82 & C297  |
|    | 431958 | X63629    | Hs.2877   | cadherin 3, type 1, P-cadherin (placenta  | Seq ID No. C83 & C298  |
|    | 448733 | NM_005629 | Hs.187958 | solute carrier family 6 (neurotransmitte  | Seq ID No. C84 & C299  |
|    | 426440 | BE382756  | Hs,169902 | solute carrier family 2 (facilitated glu  | Seq ID No. C85 & C300  |
|    | 428484 | AF104032  | Hs.184601 | solute carrier family 7 (cationic amino   | Seq ID No. C86 & C301  |
| 15 | 429211 | AF052693  | Hs.198249 | gap junction protein, beta 5 (connexin 3  | Seq ID No. C87 & C302  |
| 13 |        |           |           | heparin-binding growth factor binding pr  | Seq ID No. C88 & C303  |
|    | 423634 | AW959908  | Hs.1690   |   | Seq ID No. C89 & C304  |
|    | 457819 | AA057484  | Hs.35406  | FLJ20522 Hypothetical protein FLJ20522    |                        |
|    | 424687 | J05070    | Hs.151738 | matrix metalloproteinase 9 (gelatinase B  | Seq ID No. C90 & C305  |
| 20 | 418462 | BE001596  | Hs.85266  | integrin, beta 4                          | Seq ID No. C91 & C306  |
| 20 | 439606 | W79123    | Hs.58561  | G protein-coupled receptor 87             | Seq ID No. C92 & C307  |
|    | 407720 | AB037776  | Hs.38002  | Immunoglobulin superfamily, member 9      | Seq ID No. C93 & C308  |
|    | 418543 | NM_005329 | Hs.85962  | hyaluronan synthase 3                     | Seq ID No. C94 & C309  |
|    | 417512 | X76534    | Hs.82226  | glycoprotein (transmembrane) nmb          | Seq ID No. C95 & C310  |
|    | 415817 | U88967    | Hs.78867  | protein tyrosine phosphatase, receptor-t  | Seq ID No. C96 & C311  |
| 25 |        |           |           |   | Seq ID No. C97 & C312  |
| 23 | 415817 | U88967    | Hs.78867  | protein tyrosine phosphalase, receptor-t  |                        |
|    | 415817 | U88967    | Hs.78867  | protein tyrosine phosphatase, receptor-t  | Seq ID No. C98 & C313  |
|    | 415817 | U88967    | Hs.78867  | protein tyrosine phosphatase, receptor-t  | Seq ID No. C99 & C314  |
|    | 415817 | U88967    | Hs.78867  | protein tyrosine phosphatase, receptor-t  | Seq ID No. C100 & C315 |
|    | 415817 | U88967    | Hs.78867  | protein tyrosine phosphatase, receptor-t  | Seq ID No. C101 & C316 |
| 30 | 415817 | U88967    | Hs.78867  | protein tyrosine phosphatase, receptor-t  | Seq ID No. C102 & C317 |
| 50 | 415817 | U88967    | Hs.78867  | protein tyrosine phosphatase, receptor-t  | Seg ID No. C103 & C318 |
|    |        |           |           | ATP-binding cassette, sub-family C (CFTR  | Seq ID No. C104 & C319 |
|    | 421817 | AF146074  | Hs.108660 |   |                        |
|    | 421817 | AF146074  | Hs.108660 | ATP-binding cassette, sub-family C (CFTR  | Seq ID No. C105 & C320 |
| 25 | 409420 | Z15008    | Hs.54451  | laminin, gamma 2 (nicein (100kD), kalini  | Seq ID No. C106 & C321 |
| 35 | 440659 | AF134160  | Hs.7327   | claudin 1                                 | Seq ID No. C107 & C322 |
|    | 408790 | AW580227  | Hs.47860  | neurotrophic tyrosine kinase, receptor,   | Seq ID No. C108 & C323 |
|    | 408790 | AW580227  | Hs.47860  | neurotrophic tyrosine kinase, receptor,   | Seq ID No. C109 & C324 |
|    | 408790 | AW580227  | Hs.47860  | neurotrophic tyrosine kinase, receptor,   | Seq ID No. C110 & C325 |
|    | 450701 | H39960    | Hs.288467 | hypothetical protein XP_098151 (leucine-  | Seq ID No. C111 & C326 |
| 40 |        |           |           |   | Seq ID No. C112 & C327 |
| 40 | 414774 | X02419    | Hs.77274  | plasminogen activator, urokinase          |                        |
|    | 413691 | AB023173  | Hs.75478  | ATPase, Class VI, type 11B                | Seq ID No. C113 & C328 |
|    | 453857 | AL080235  | Hs.35861  | Ras-Induced senescence 1 (RIS1)           | Seq ID No. C114 & C329 |
|    | 449101 | AA205847  | Hs.23016  | G protein-coupled receptor                | Seq ID No. C115 & C330 |
|    | 429263 | AA019004  | Hs.198396 | ATP-binding cassette, sub-family A (ABC1  | Seq ID No. C116 & C331 |
| 45 | 421474 | U76362    | Hs.104637 | solute carrier family 1 (glutarnate trans | Seq ID No. C117 & C332 |
|    | 421753 | BE314828  | Hs.107911 | ATP-binding cassette, sub-family B (MDR/  | Seq ID No. C118 & C333 |
|    | 408482 | NM_000676 | Hs.45743  | adenosine A2b receptor                    | Seq ID No. C119 & C334 |
|    |        |           |           |   | Seq ID No. C120 & C335 |
|    | 426761 | AI015709  | Hs.172089 | PORIMIN Pro-oncosis receptor inducing me  |                        |
| 50 | 429736 | AF125304  | Hs.212680 | turnor necrosis factor receptor superfami | Seq ID No. C121 & C336 |
| 50 | 430985 | AA490232  | Hs.27323  | ESTs, Weakly similar to 178885 serine/th  | Seq ID No. C122 & C337 |
|    | 431890 | X17033    | Hs.271986 | integrin, alpha 2 (CD49B, alpha 2 subuni  | Seq ID No. C123 & C338 |
|    | 432583 | AW023624  | Hs.162282 | potassium channel TASK-4; potassium chan  | Seq ID No. C124 & C339 |
|    | 446872 | X97058    | Hs.16362  | pyrimidinergic receptor P2Y, G-protein c  | Seq ID No. C125 & C340 |
|    | 453102 | NM_007197 | Hs.31664  | frizzled (Drosophila) homolog 10          | Seq ID No. C126 & C341 |
| 55 | 428513 | BE220806  | Hs.184697 | plexin C1                                 | Seq ID No. C127 & C342 |
|    | 430280 | AA361258  | Hs.237868 | interleukin 7 receptor                    | Seq ID No. C128 & C343 |
|    | 428486 | AW583497  | Hs.184604 | pancreatic polypeptide                    | Seq ID No. C129 & C344 |
|    | 457489 | Al693815  | Hs.127179 | cryptic gene                              | Seq ID No. C130 & C345 |
|    |        |           |           |   |                        |
| 60 | 432874 | W94322    | Hs.279651 | melanoma inhibitory activity              | Seq ID No. C131 & C346 |
| OU | 445891 | AW391342  | Hs.199460 | DPCR1 protein                             | Seq ID No. C132 & C347 |
|    | 445891 | AW391342  | Hs.199460 | DPCR1 protein                             | Seq ID No. C133 & C348 |
|    | 404682 |           |           | ortholog of mouse polydomain protein      | Seq ID No. C134 & C349 |
|    | 429547 | AW009166  | Hs.99376  | FGENESH predicted novel secreted protein  | Seq ID No. C135 & C350 |
|    | 404287 |           |           | FGENESH predicted novel CUB-domain conta  | Seq ID No. C136 & C351 |
| 65 | 404287 |           |           | FGENESH predicted novel CUB-domain conta  | Seq ID No. C137 & C352 |
|    | 404287 |           |           | FGENESH predicted novel CUB-domain conta  | Seq ID No. C138 & C353 |
|    | 418318 | U47732    | Hs.84072  | transmembrane 4 superfamily member 3      | Seq ID No. C139 & C354 |
|    |        |           |           |   | Seq ID No. C140 & C355 |
|    | 444754 | T83911    | Hs.11881  | transmembrane 4 superfamily member 4      |                        |
| 70 | 432596 | AJ224741  | Hs.278461 | matrilin 3                                | Seq ID No. C141 & C356 |
| 70 | 444006 | BE395085  | Hs.334762 |   | Seq ID No. C142 & C357 |
|    | 428505 | AL035461  | Hs.2281   | chromogranin B (secretogranin 1)          | Seq ID No. C143 & C358 |
|    | 448844 | Al581519  | Hs.177164 | FGENESH predicted novel cell surface pr   | Seq ID No. C144 & C359 |
|    | 448844 | AI581519  | Hs.177164 |   | Seg ID No. C145 & C360 |
|    | 428392 | H10233    | Hs.2265   | secretory granule, neuroendocrine protei  | Seq ID No. C146 & C361 |
| 75 |        |           |           |   | Seq ID No. C147 & C362 |
| 13 | 448030 | N30714    | Hs.325960 |   |                        |
|    | 422109 | S73265    | Hs.1473   | gastrin-releasing peptide                 | Seq ID No. C148 & C363 |
|    | 449048 | Z45051    | Hs.22920  | similar to S68401 (cattle) glucose induc  | Seq ID No. C149 & C364 |
|    | 417931 | W95642    | Hs.82961  | trefoil factor 3 (intestinal)             | Seq ID No. C150 & C365 |
|    | 419216 | AU076718  | Hs.164021 |   | Seq ID No. C151 & C366 |
| 80 | 426227 | U6705B    | Hs.154299 |   | Seq ID No. C152 & C367 |
|    | 413554 | AA319146  | Hs.75426  | secretogranin II (chromogranin C)         | Seq ID No. C153 & C368 |
|    | 445417 |           | Hs.12680  | a disintegrin-like and metalloprotease w  | Seq ID No. C154 & C369 |
|    |        |           |           |   |                        |
|    | 426322 | J05068    | Hs.2012   | transcobalamin I (vitamin B12 binding pr  | Seq ID No. C155 & C370 |
|    |        |           |           |   |                        |

|     | 443740           | DC 400500            | 11- 25400              | HALL SHALL A MAN AND A 10   |  |
|-----|------------------|----------------------|------------------------|---|--|
|     | 413719           | BE439580             | Hs.75498               | small inducible cytokine subfamily A (Cy  | Seq ID No. C156 & C371   |
|     | 431462<br>416498 | AW583672             | Hs.256311              | granin-like neuroendocrine peptide precu  | Seq ID No. C157 & C372   |
|     |                  | U33632               | Hs.79351               | potassium channel, subfamily K, member 1  | Seq ID No. C158 & C373   |
| 5   | 413095           | AA494359             | Hs.30715               | polassium voltage-gated channel, isk-rel  | Seq ID No. C159 & C374   |
| •   | 426125<br>436729 | X87241<br>BE621807   | Hs.166994              | FAT tumor suppressor (Drosophila) homolo  | Seq ID No. C160 & C375   |
|     | 437145           | AF007216             | Hs.351316<br>Hs.5462   | transmembrane 4 superfamily member 1 solute carrier family 4, sodium bicarbon                               | Seq ID No. C161 & C376   |
|     | 451820           | AW058357             | Hs.199248              | ESTs  | Seq ID No. C162 & C377   |
|     | 427557           | NM_002659            | Hs.179657              | plasminogen activator, urokinase recepto  | Seq ID No. C163 & C378   |
| 10  | 408308           | AL033377             | Hs.44197               | hypothetical protein DKFZp564D0462  | Seq ID No. C164 & C379<br>Seq ID No. C165 & C380   |
|     | 421340           | F07783               | Hs.1369                | decay accelerating factor for complement  | Seq ID No. C165 & C381   |
|     | 428187           | AI687303             | Hs.285529              | G protein-coupled receptor 49   | Seq ID No. C167 & C382   |
|     | 428187           | AI687303             | Hs.285529              | G protein-coupled receptor 49   | Seq ID No. C168 & C383   |
|     | 422278           | AF072873             | Hs.114218              | frizzled (Drosophila) homolog 6   | Seq ID No. C169 & C384   |
| 15  | 446619           | AU076643             | Hs.313                 | secreted phosphoprotein 1 (osteopontin,   | Seq ID No. C170 & C385   |
|     | 419452           | U33635               | Hs.90572               | PTK7 protein tyrosine kinase 7  | Seq ID No. C171 & C386   |
|     | 428242           | H55709               | Hs.2250                | leukemia inhibitory factor (cholinergic   | Seq ID No. C172 & C387   |
|     | 439659           | AW970780             | Hs.59483               | leucine-rich repeat-containing G protein  | Seq ID No. C173 & C388   |
| 20  | 411825           | AK000334             | Hs.352415              | solute carrier family 39 (zinc transport  | Seq ID No. C174 & C389   |
| 20  | 412314           | AA825247             | Hs.356084              | G protein-coupled receptor 27 (GPR27) (S  | Seq ID No. C175 & C390   |
|     | 429150           | AF120103             | Hs.197366              | smoothened (Drosophila) homolog   | Seq ID No. C176 & C391   |
|     | 419073           | AW372170             | Hs.183918              | transmembrane receptor Unc5H2 mRNA  | Seq ID No. C177 & C392   |
|     | 411828<br>419508 | AW161449<br>AW997938 | Hs.72290<br>Hs.90786   | wingless-type MMTV integration site fami  | Seq ID No. C178 & C393   |
| 25  | 421779           | AI879159             | Hs.108219              | ATP-binding cassette, sub-family C (CFTR wingless-type MMTV integration sile fami                           | Seq ID No. C179 & C394   |
|     | 439668           | AI091277             | Hs.302634              | frizzled (Drosophila) homolog 8   | Seq ID No. C180 & C395<br>Seq ID No. C181 & C396   |
|     | 433336           | AF017986             | Hs.31386               | secreted frizzled-related protein 2 (str  | Seq ID No. C182 & C397   |
|     | 436972           | AA284679             | Hs.25640               | claudin 3   | Seq ID No. C183 & C398   |
| •   | 410268           | AA316181             | Hs.61635               | six transmembrane epithelial antigen of   | Seq ID No. C184 & C399   |
| 30  | 416370           | N90470               | Hs.203697              | CD38 antigen (p45)  | Seq ID No. C185 & C400   |
|     | 437052           | AA861697             | Hs.120591              | ESTs  | Seq ID No. C186 & C401   |
|     | 421481           | AW391972             | Hs.104696              | KIAA1324 protein  | Seq ID No. C187 & C402   |
|     | 444151           | AW972917             | Hs.128749              | alpha-methylacyl-CoA racemase   | Seq ID No. C188 & C403   |
| 35  | 426174<br>410037 | AA547959<br>AB020725 | Hs.115838<br>Hs.58009  | Homo sapiens similar to Echinoidin (LOC1<br>KIAA0918 protein  | Seq ID No. C189 & C404   |
|     | 425071           | NM_013989            | Hs.154424              | deiodinase, iodothyronine, type II  | Seq ID No. C190 & C405<br>Seq ID No. C191 & C406   |
|     | 421829           | AB018330             | Hs.108708              | calcium/calmodulin-dependent protein kin  | Seq ID No. C192 & C407   |
|     | 418576           | AW968159             | Hs.302740              | Epithelial calcium channel 2, CaT-like A  | Seq ID No. C193 & C408   |
| 40  | 419693           | AA133749             | Hs.301350              | FXYD domain-containing ion transport reg  | Seq ID No. C194 & C409   |
| 40  | 419693           | AA133749             | Hs.301350              | FXYD domain-containing ion transport reg  | Seq ID No. C195 & C410   |
|     | 448988           | Y09763               | Hs.22785               | gamma-aminobutyric acid (GABA) A recepto  | Seq ID No. C196 & C411   |
|     | 448988<br>448988 | Y09763               | Hs.22785               | gamma-aminobutyric acid (GABA) A recepto  | Seq ID No. C197 & C412   |
|     | 448988           | Y09763<br>Y09763     | Hs.22785<br>Hs.22785   | gamma-aminobutyric acid (GABA) A recepto<br>gamma-aminobutyric acid (GABA) A recepto                        | Seq ID No. C198 & C413   |
| 45  | 430144           | A1732722             | Hs.98927               | ERGL protein; ERGIC-53-like protein   | Seq ID No. C199 & C414<br>Seq ID No. C200 & C415   |
|     | 408833           | AW612232             | Hs.254835              | ESTs  | Seq ID No. C201 & C416   |
|     | 452017           | AF109302             | Hs.27495               | prostate cancer associated protein 7  | Seq ID No. C202 & C417   |
|     | 415992           | C05837               | Hs.145807              | hypothetical protein FLJ13593   | Seq ID No. C203 & C418   |
| 50  | 415992           | C05837               | Hs.145807              | hypothetical protein FLJ13593   | Seq ID No. C204 & C419   |
| 50  | 443991           | NM_002250            | Hs.10082               | potassium intermediate/small conductance  | Seq ID No. C205 & C420   |
|     | 425976           | C75094               | Hs.334514              | NG22 protein  | Seq ID No. C206 & C421   |
|     | 432800<br>452955 | BE391046<br>AW390282 | Hs.278962              | AlM-1 protein   | Seq ID No. C207 & C422   |
|     | 424339           | BE257148             | Hs.31130<br>Hs.145416  | transmembrane 7 superfamily member 2<br>endoglycan  | Seq ID No. C208 & C423<br>Seq ID No. C209 & C424   |
| 55  | 425263           | NM_001197            | Hs.155419              | BCL2-interacting killer (apoptosis-induc  | Seq ID No. C210 & C425   |
|     | 421537           | BE383488             | Hs.105547              | neural proliferation, differentiation an  | Seq ID No. C211 & C426   |
|     | 434293           | NM_004445            | Hs.3796                | EphB6   | Seq ID No. C212 & C427   |
|     | 427715           | BE245274             | Hs.180428              | KIAA1181 protein  | Seq ID No. C213 & C428   |
| 60  | 413049           | NM_002151            | Hs.823                 | hepsin (transmembrane protease, serine 1  | Seq ID No. C214 & C429   |
| UU  | 414555           | N98569               | Hs.76422               | phospholipase A2, group IIA (platelets,   | Seq ID No. C215 & C430   |
|     | 422424<br>432378 | Al186431<br>Al493046 | Hs.296638<br>Hs.146133 | prostate differentiation factor<br>ESTs   | Seq ID No. C216 & C431   |
|     | 409041           | AB033025             | Hs.50081               | Hypothetical protein, XP_051860 (KIAA119  | Seq ID No. C432 & C433<br>Seq ID No. C434 & C435   |
|     | 100011           | 710000020            | 113.50001              | Libonence brotein' vi Too 1000 futvet 12  | 384 ID NO. C434 & C433   |
| 65  | TABLE 79         | В                    |                        |   |  |
|     |                  |                      |                        |   |  |
|     | Pkey:            |                      | probeset iden          | lifier number   |  |
|     |                  | er: Gene duste       |                        |   |  |
| 70  | Accession        | : Genbank ac         | cession numb           | ers   | •  |
| , 0 | Pkey             | CAT Numbe            | r Accession            |   |  |
|     | ,                | On Humbe             | A LINESCOSION          |   |  |
|     | 414991           | 1785136_1            | D78831 C1              | 7898 D78863   |  |
| 75  | TABLE 79         | С                    |                        |   |  |
|     |                  |                      |                        |   |  |
|     | Pkey:            | Unique num           | ber correspon          | ding to an Eos probeset   | (Official Annual Control of the Cont |
|     | Ref:             | Sequence of          | outce. The / i         | digit numbers in this column are Genbank Identifier (<br>nosome 22.° Dunham I. et al., Nature (1999) 402:48 | (GI) numbers. "Dunham I, et al." refers to the publication entitled "The DNA   |
| 80  | Strand:          | Indicates Of         | VA strand from         | nosome 22.  | 5 <del>-1</del> 50.  |
|     | Nt_position      | n: Indicates nu      | cleotide posifi        | ons of predicted exons.   |  |
|     | _                |                      |                        | •   |  |
|     | Pkey             | Ref                  | Strand                 | Nt_position   |  |

|   | 404682<br>404287 | 9797231<br>2326514 | Minus<br>Plus | 40977-41150<br>53134-53281 |
|---|------------------|--------------------|---------------|----------------------------|
|   | 404287           | 2326514            | Plus          | 53134-53281                |
| _ | 404287           | 2326514            | Plus          | 53134-53281                |

Table 80:

```
Seq ID NO: C1 DNA Sequence
Nucleic Acid Accession #: NM_005814
Coding sequence: 345..1304
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| 5  | Coding sequ | ence: 345                | 1304             |            |                 |            |              |
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|    | 1           | 11                       | 21               | 31         | 41              | 51         |              |
|    | CLYCCCCALLA | GTGAGCAGTC               | <br>  TACCACTETY | TACACTCTT  | A A COTA COCCAC | NACCONGCCC |              |
| 10 |             | TTTAAGGGGA               |                  |            |                 |            | 60<br>120    |
|    |             | ACATGAGCCC               |                  |            |                 |            | 180          |
|    | GCCAATCCAG  | CTGAGGCTGG               | CCAGAGGTGG       | GTGAGAAGAG | GCAAAATTGC      | AGGGACCTCC | 240          |
|    |             | GGCCAGAAGC               |                  |            |                 |            | 300          |
|    |             | CAGGTTAGGT               |                  |            |                 |            | 360          |
| 15 |             | GTGGACACTC               |                  |            |                 |            | 420          |
|    |             | CGTTCTTCGG               |                  |            |                 |            | 480          |
|    |             | CTCCAGTCGA               |                  |            |                 |            | 540          |
|    |             | GGTCATCTGG               |                  |            |                 |            | 600          |
|    |             | CAGCATATCC               |                  |            |                 |            | 660          |
| 20 |             | GGCTGACAAC               |                  |            |                 |            | 720          |
|    |             | CAAGTCACGT               |                  |            |                 |            | 780          |
|    |             | GGGAGAGACC               |                  |            |                 |            | 840          |
|    |             | AACCCCTCAG               |                  |            |                 |            | 900          |
|    |             | GCCAGCCTCA               |                  |            |                 |            | 960          |
| 25 |             | CATCTGTACC               |                  |            |                 |            | 1020         |
|    |             | ATCTCCCTCC               |                  |            |                 |            | 1080         |
|    |             | CATTATCATT               |                  |            |                 |            | 1140         |
|    | ACAACACTGA  | AGACAAGGAG               | GATGCAAGGC       | CGAACCGGGA | AGCCTATGAG      | GAGCCACCAG | 1200         |
| ~~ | AGCAGCTAAG  | AGAACTTTCC               | AGAGAGAGGG       | AGGAGGAGGA | TGACTACAGG      | CAAGAAGAGC | 1260         |
| 30 | AGAGGAGCAC  | TGGGCGTGAA               | TCCCCGGACC       | ACCTCGACCA | GTGACAGGCC      | AGCAGCAGAG | 1320         |
|    |             | GAAGGGTTAG               |                  |            |                 |            | 1380         |
|    |             | CTCCTGTCCC               |                  |            |                 |            | 1440         |
|    | CAGCTGTGGG  | GAACATGGCT               | GGCCTGGTAA       | GGGGGTCCCT | GTGCTGATCC      | TGCTGACCTC | 1500         |
| 25 |             | GAAGTAACCC               |                  |            |                 |            | 1560         |
| 35 |             | TGCAGCCTCC               |                  |            |                 |            | 1620         |
|    |             | GGCGCTCCCA               |                  |            |                 |            | 1680         |
|    |             | CTGCTCACCT               |                  |            |                 |            | 1740         |
|    |             | ATCTTTCTTG               |                  |            |                 |            | 1800         |
| 40 |             | TCCAGCTCCC               |                  |            |                 |            | 1860         |
| 40 |             | CCTGGGAAGG               |                  |            |                 |            | 1920         |
|    |             | TTTCCATCTC               |                  |            |                 |            | 1980         |
|    |             | ATTTCTCTAA               |                  |            |                 |            | 2040         |
|    |             | ACGTCCAATC               |                  |            |                 |            | 2100         |
| 45 |             | CGCCAGCTCC               |                  |            |                 |            | 2160         |
| 73 |             | AGCTGGCGCC               |                  |            |                 |            | 2220         |
|    |             | TGCCTTCCCT               |                  |            |                 |            | 2280         |
|    |             | ACCCACGTAT               |                  |            |                 |            | 2340         |
|    |             | AGCTTGCTTG<br>ATTGGCATGT |                  |            |                 |            | 2400         |
| 50 |             |                          |                  |            |                 |            | 2460         |
| 50 |             | GCCCTGGCCC               |                  |            |                 |            | 2520         |
|    |             | TAGGGCTGCT               |                  |            |                 |            | 2580         |
|    |             | CTATCTTTTC               |                  |            |                 |            | 2640         |
|    |             | TTAAAAAATG               |                  |            |                 |            | 2700         |
| 55 |             | AGTAATAATA               |                  |            | IMMICCIII       | GCTTCATTCC | 2760<br>2793 |
| 60 | Nucleic Ac  | C2 DNA Sequid Accession  | n #: Eos se      | quence     |                 |            |              |
|    | 1           | 11                       | 21               | 31         | 41              | 51         |              |
|    | 1           | 1                        |                  |            | 1               | 1          |              |
|    |             | GGACGCCAGA               |                  |            |                 |            | 60           |
| 65 |             | CGCTSSTGCC               |                  |            |                 |            | 120          |
| UJ |             | TAGACGCGGA               |                  |            |                 |            | 180          |
|    |             | TGGAGTTTTA               |                  |            |                 |            | 240          |
|    |             | ATACCAGCCA               |                  |            |                 |            | 300          |
|    | TGGGGTGCCA  | GCCCCACACA               | GTGCACCCCC       | ATTGAATTTG | ACAGCAAAGG      | CTCTCGGCTC | 360          |
| 70 | CTGGAGTCCT  | CACTGTCCAG               | CTCAGAGGGA       | GAGGAGCCTG | TGGAGTACAA      | GTCCTTGCAG | 420          |
| 70 |             |                          |                  |            |                 | TCCACTGTAC | 480          |
|    |             |                          |                  |            |                 | CCTCTCCACA | 540          |
|    |             |                          |                  |            |                 | CTGGGCAGCA | 600          |
|    |             |                          |                  |            |                 | CCGTGTGGTT | 660          |
| 75 |             |                          |                  |            |                 | TCAGGAGCAG | 720          |
| 13 |             |                          |                  |            |                 | GCTGCAGACT | 780          |
|    |             |                          |                  |            |                 | TGTTGGTGAA | 840          |
|    |             |                          |                  |            |                 | CCTCACTTAC |              |
|    |             |                          |                  |            |                 | CTCAGGGGAA | 960          |
| 80 |             |                          |                  |            |                 | GGACGGGCTG | 1020         |
| ou | GATGACTTGC  | TGGTGGGGGC               | ACCCCTGCTC       | ATGGATCGGA | CCCCTGACGG      | GCGGCCTCAG | 1080         |
|    |             |                          |                  |            |                 | CACGCCCACC | 1140         |
|    |             |                          |                  |            |                 | CCCCCTGGGG | 1200         |
|    | CACCAGGACC  | AGGATGGCTA               | CAATGATGTG       | GCCATCGGGG | CICCCTITGG      | TGGGGAGACC | 1260         |
|    | CAGCAGGAG   | IAGIGITIGT               | ATTTCCTGGG       | GGCCCAGGAG | GGCTGGGCTC      | TAAGCCTTCC | 1320         |

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                                                                                          2340
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                                                                                          3000
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         TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCAGTG
                                                                                          180
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                                                                                          360
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ATATCTTTTG TCAGGGGAGA TCATCGGACC AACTCTCCTT TTGATGGACC TGGAGGAAAT
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                                                                                          600
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                                                                                          720
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                                                                                          780
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                                                                                          840
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         TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC
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                                                                                          1020
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                                                                                          1080
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CTTTCTGAGG AAAACACTGG AAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT
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                                                                                          1200
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65
         Nucleic Acid Accession #: Bos sequence
         Coding sequence: 1..1410
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                                                31
                                                             41
                                                                          51
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                                                                                          60
         CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA
                                                                                          120
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         GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT
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                                                                                          300
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        CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT
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        GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT
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        GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT
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        Nucleic Acid Accession #: NM_014331.2
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                                              31
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                                                                                      180
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                                                                                      840
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|     | Nucleic Aci  | C10 DNA Sec<br>d Accession   | #: NM_0032  | 25   |  |  |  |
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|     | GCCCTCCCAG   | TGTGCAAATA<br>CCTAATACCA   | AGGGCTGCTG  | TTTCGACGAC   | ACCGTTCGTG   | GGGTCCCCTG   | 240<br>300   |
| 0.5 | TCTGCAGGGA   | TCTGCCTGCA<br>GCCACCTCCA   | TCCTGACGGG  | GTGCCGTCCC   | CAGCACGGTG   | ATTAGTCCCA   | 360<br>420   |
| 25  |  | ATTGACTGCT<br>AAAAAAAAAA   |   |  |  |  | 480<br>540   |
| •   |  | C11 DNA Sec  |   |  |  |  |  |
| 30  |  | id Accession<br>Lence: 184   |   | 119.1  |  |  |  |
|     | 1<br>1   | 11<br>   | 21<br>  | 31<br>!  | 41<br>   | 51<br>   |  |
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|     |  | TTATGATTCA<br>CTCTTCAGGT   |   |  |  |  | 300<br>360   |
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| 60  |  | AAGCTTCTGA<br>CCATGGATGA   |   |  |  | TGGCTCCATC   | 1560<br>1620   |
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| 70  |  |  |   |  |  | CAAGAAAGGG<br>TGTTGCAGAA   |  |
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|     | GAGCGCTGGG   | CTGATATTT  | AGCCAAAGTC  | CGTGGGAAAA   | ATCTCCCTAA   | GGGCACAGAA   | 2400   |
| 75  |  |  |   |  |  | CACACCACCT<br>TGCTGAAGAA   |  |
|     |  |  |   |  |  | CATTTCCTCA   |  |
|     | GCCAGCATGG   | GCTAGAACA  | CAACCACAAT  | GGAGTTATTC   | TTGTTGAACC   | TGAAGTAACA   | 2640   |
|     | AGCACACCTO   | TGGAGGAAGT   | TGTTGATGAC  | CTTTCTGAGA   | AGACTGAGGA   | GATAACTTCC<br>TTATGAACCA   | 2700   |
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|     | ACAGAGGGTT   | GGTCTGCAGC   | AGATGTTGGA  | TCGTCACCAC   | AGCCCACATO   | CAGTGAGTAT   | 2880   |
|     |  |  |   |  |  | CTTTGACCCA   |  |
|     |  |  |   |  |  | ATTTGAGGAT   |  |
|     |  |  |   |  | _  |  |  |

|     |              |                          |            |             |              | C1 C1 C1 C1 1 C | 3120         |
|-----|--------------|--------------------------|------------|-------------|--------------|-----------------|--------------|
|     | TCTACTATAG   |                          |            |             |              |                 |              |
|     | ATCCACCTTG   |                          |            |             |              |                 | 3180         |
|     | AAAGAGATGT   |                          |            |             |              |                 | 3240         |
| 5   | AGAAGTTCTG . | AGAGTGAGGG               | CCAAGAGAGC | AAATCCATCA  | CTTTGCCTGA   | CICCACACIG      | 3300         |
| 3   | GGTATAATGA   | GCAGTATGTC               | TCCAGTTAAG | AAGCCTGCGG  | AAACCACAGT   | TGGTACCCTC      | 3360         |
|     | CTAGACAAAG   | ACACCACAAC               | AGTAACAACA | ACACCAAGGC  | AAAAAGTIGC   | TCCGTCATCC      | 3420         |
|     | ACCATGAGCA   | CTCACCCTTC               | TCGAAGGAGA | CCCAACGGGA  | GAAGGAGATT   | ACGCCCCAAC      | 3480         |
|     | AAATTCCGCC   | ACCGGCACAA               | GCAAACCCCA | CCCACAACTT  | TTGCCCCATC   | AGAGACTTTT      | 3540         |
| 10  |              | CAACTCAAGC               |            |             |              |                 | 3600         |
| 10  |              | CTTGGGTGGA               |            |             |              |                 | 3660         |
|     |              | CCACATCCAA               |            |             |              |                 | 3720         |
|     | CATCGATATA   | CCCCTTCTAC               | AGTGAGCTCA | AGAGCGTCCG  | GATCCAAGCC   | CAGCCCTTCT      | 3780         |
|     | CCAGAAAATA   | AACATAGAAA               | CATTGTTACT | CCCAGTTCAG  | AAACTATACT   | TTTGCCTAGA      | 3840         |
|     | ACTGTTTCTC   | TGAAAACTGA               | GGGCCCTTAT | GATTCCTTAG  | ATTACATGAC   | AACCACCAGA      | 3900         |
| 15  | TTATATAAAA   | CATCTTACCC               | TAAAGTCCAA | GAGACACTTC  | CAGTCACATA   | TAAACCCACA      | 3960         |
|     | TCAGATGGAA   | AAGAAATTAA               | GGATGATGTT | GCCACAAATG  | TTGACAAACA   | TAAAAGTGAC      | 4020         |
|     |              | CTGGTGAATC               |            |             |              |                 | 4080         |
|     |              | AATTTAAGGA               |            |             |              |                 | 4140         |
|     | AATCCCTCAA   | GGACGGCCCA               | CCLACCINCO | CTACAGACAG  | ACATACCTGT   | TACCACTTCT      | 4200         |
| 20  | CCCCAAAATC   | TTACAGACCC               | ACCIGGGUOD | AAAGAGCTTG  | ACCATCTCCA   | TTTCACTTCC      | 4260         |
| 20  | CACTOROGOTO  | CCTCTTTGAC               | ICCCCIICII | CCNTTTCNC   | AGGRAGAGC    | TECTTETTE       | 4320         |
|     |              | CAAGCATAAA               |            |             |              |                 | 4380         |
|     |              |                          |            |             |              |                 | 4440         |
|     | GATCAAGATC   | ATCTTGAAAC<br>CTGCTGCCCG | CACIGIGGCI | ATTOTOTTT   | CIGAAACIAG   | ACCACAGAA1      | 4500         |
| 25  |              |                          |            |             |              |                 |              |
| 23  |              |                          |            |             |              | AATATCTCAA      | 4560         |
|     |              |                          |            |             |              | AGAAACAGAA      | 4620         |
|     |              |                          |            |             |              | ATTATCAACA      | 4680         |
|     | CCCTCTTCCG   | ACCGGGATGC               | ATTTAACTTG | TCTACAAAGC  | TGGAATTGGA   | AAAGCAAGTA      | 4740         |
| 20  |              |                          |            |             |              | AAGAGTTCAT      | 4800         |
| 30  |              |                          |            |             |              | AACAGTGAGG      | 4860         |
|     |              |                          |            |             |              | GTCACCTCGT      | 4920         |
|     |              |                          |            |             |              | AGAGAACAAA      | 4980         |
|     | CAGTTTACAA   | CTCCAAGATT               | ATCAAGTACA | ACAATTCCTC  | · TCCCATTGCA | CATGTCCAAA      | 5040         |
| 25  | CCCAGCATTC   | CTAGTAAGTT               | TACTGACCGA | AGAACTGACC  | AATTCAATGG   | TTACTCCAAA      | 5100         |
| 35  | GTGTTTGGAA   | ATAACAACAT               | CCCTGAGGCA | AGAAACCCAG  | TTGGAAAGCC   | TCCCAGTCCA      | 5160         |
|     |              |                          |            |             |              | TCTTTCTTTT      | 5220         |
|     | CCACAGTTGG   | GAGTCACCCG               | GAGACCCCAG | ATACCCACTT  | CTCCTGCCCC   | AGTAATGAGA      | 5280         |
|     |              |                          |            |             |              | CTTCCATCTG      | 5340         |
|     | GACTTTGGCC   | CTCCGGCACC               | TCCGTTGTTG | CACACTCCGC  | · AGACCACGGG | ATCACCCTCA      | 5400         |
| 40  | ACTAACTTAC   | AGAATATCCC               | TATGGTCTCT | TCCACCCAGA  | GTTCTATCTC   | CTTTATAACA      | 5460         |
|     |              |                          |            |             |              | TGCAGGAGGA      | 5520         |
|     |              |                          |            |             |              | CAAGTCCCCA      | 5580         |
|     |              |                          |            |             |              | AACAGGAAAA      | 5640         |
|     |              |                          |            |             |              | TCCGAATACC      | 5700         |
| 45  |              |                          |            |             |              | GGTTCAAGTA      | 5760         |
|     |              |                          |            |             |              | CAGGATGGTG      | 5820         |
|     |              |                          |            |             |              | CCAGGACGTC      | 5880         |
|     |              |                          |            |             |              | CCCAGCCCCC      | 5940         |
|     |              |                          |            |             |              | CGTGGAGAGC      | 6000         |
| 50  |              |                          |            |             |              | CTCAGACAGA      | 6060         |
| 50  |              |                          |            |             |              | CATCCGCCTG      | 6120         |
|     |              |                          |            |             |              |                 | 6180         |
|     |              |                          |            |             |              | CTCGCTGCCC      |              |
|     |              |                          |            |             |              | CAGCGTGCGC      | 6240<br>6300 |
| 55  |              |                          |            |             |              | GAACTTGTTT      |              |
| 33  |              |                          |            |             |              | CGGGCGCTAT      | 6360         |
|     |              |                          |            |             |              | GAACGTGCAG      | 6420         |
|     |              |                          |            |             |              | CGTCAGGTAC      | 6480         |
|     |              |                          |            |             |              | CATCCTCTGG      | 6540         |
| 60  |              |                          |            |             |              | AATCAAGGTG      | 6600         |
| 60  | TTTGCCAATG   | GGACCCTGGT               | GGTGAAATC  | GTGACGGAC   | AAGATGCCGG   | AGATTACCTG      | 6660         |
|     |              |                          |            |             |              | TGTGGTGATG      | 6720         |
|     |              |                          |            |             |              | CGGGGGTGAC      | 6780         |
|     |              |                          |            |             |              | GAGCCTCCCA      | 6840         |
| 15  |              |                          |            |             |              | CACCAAGCGC      | 6900         |
| 65  |              |                          |            |             |              | GGAGGAAGGA      | 6960         |
|     |              |                          |            |             |              | CAGAGTCAAG      | 7020         |
|     | GTGGTGACAC   | CGCCCGCCAC               | CATCCGGAAG | AAGACTTAC   | r tggcggttc/ | GGTGCCCTAT      | 7080         |
|     | GGAGACGTGG   | TCACTGTAGC               | CTGTGAGGC  | CAAAGGAGAA  | C CCATGCCCA  | GGTGACTTGG      | 7140         |
| =-  | TTGTCCCCA    | CCAACAAGGT               | GATCCCCAC  | C TCCTCTGAG | A AGTATCAGA  | r ataccaagat    | 7200         |
| 70  | GGCACTCTCC   | TTATTCAGA                | AGCCCAGCG  | TCTGACAGC   | G GCAACTACA  | CTGCCTGGTC      | 7260         |
|     |              |                          |            |             |              | CCAGCCACCC      | 7320         |
|     |              |                          |            |             |              | CGGGGGCAGT      | 7380         |
|     |              |                          |            |             |              | T ATGGGCTTTT    | 7440         |
| _   |              |                          |            |             |              | CCATGGCAAC      | 7500         |
| 75  |              |                          |            |             |              | 1 ATGCATGGCA    | 7560         |
| . • |              |                          |            |             |              | A GCCCATGGAG    | 7620         |
|     |              |                          |            |             |              | 3 CCACACCATC    | 7680         |
|     |              |                          |            |             |              | CCTTCCCAAT      | 7740         |
|     |              |                          |            |             |              | C TGACGGCATG    |              |
| 80  |              |                          |            |             |              | T GGCCCGCAAT    | 7860         |
| -   |              |                          |            |             |              | C AGAAGCAAAC    | 7920         |
|     |              |                          |            |             |              | T CCCCTGCACC    | 7980         |
|     |              |                          |            |             |              | T GCATCTGGAG    |              |
|     |              |                          |            |             |              |                 |              |
|     | GGCCCCAA     | - CCCIGGGACT             | - willtier | . CIGGACAAT | G GLACCICA   | C GGTTCGTGAG    | 9100         |
|     |              |                          |            |             | _            |                 |              |

```
GCCTCGGTGT TTGACAGGGG TACCTATGTA TGCAGGATGG AGACGGAGTA CGGCCCTTCG
                                                                                     8160
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                                                                                     8220
                                                                                     8280
        CCCAAAGCTG ACATCACGTG GGAGTTACCG GATAAGTCGC ATCTGAAGGC AGGGGTTCAG
                                                                                     8340
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        GCTCGTCTGT ATGGAAACAG ATTTCTTCAC CCCCAGGGAT CACTGACCAT CCAGCATGCC
                                                                                     8400
        ACACAGAGAG ATGCCGGCTT CTACAAGTGC ATGGCAAAAA ACATTCTCGG CAGTGACTCC
        AAAACAACTT ACATCCACGT CTTCTGAAAT GTGGATTCCA GAATGATTGC TTAGGAACTG
                                                                                     8520
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                                                                                     8580
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       ATTAAAATTA ATAAATTATT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA ATATAATTTT AAAAAATTTC TCTCCAACCT CCTTCAAATT CAGTCACCAC TGTTATATTA
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20
                                                                                     9300
        CCTTCTCCAG GAACCCTCCA GTGGGGAAGG CTGCGATATT AGATTTCCTT GTATGCAAAG
                                                                                     9360
        9420
        THITIGIES ANGUIGISCI CHORAGAGUI GAGAGAGAG GAAGAGAGAA ACTGCATCAT
AACTITACAG AATIGAATCI AGGICTICC COGAAAAGCC CAGAAACTIC TCTGCAGTAT
CTGGCTTGTC CATCTGGTCT AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC
                                                                                     9480
                                                                                     9540
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                                                                                     1140
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80
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                                                                                     300
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                                                                                     420
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                                                                                     480
        GTCTGTCTGC TGGACACAGG ACTGTTTTCA GTTTCCTCCT TCCAACCATC TGCCAAATCA
                                                                                     540
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|     | *******    | a. mmomme.a. | m1 00 00 00 00 00 |             | 1 mmmca 1 aa 1 |              |        |
|-----|------------|--------------|-------------------|-------------|----------------|--------------|--------|
|     | TTTCAGAATA | CATTCTTTCA   | TAUGUCCOGG        | CTCTCAAACC  | ATTIGGAGCA     | AAGTCCCTCA   | 600    |
|     |            | AGACACTACT   |                   |             |                |              | 660    |
|     |            | CCGGGCCACA   |                   |             |                |              | 720    |
| _   |            | AACAAGAATG   |                   |             |                |              | 780    |
| 5   | ATCGATATCC | AAACCAAACA   | AGTTAATAAA        | GATCCACAAC  | TGGAAGGGAG     | TGTTTTTGGA   | 840    |
|     | CCATGTTTTC | TITTCTACTT   | CCTCACATTT        | ATGCTGGATA  | TTGGCGGCTT     | TTCCTTCATT   | 900    |
|     | ATGTGCTATG | AAGACCCANN   | TGTTTCTTCT        | TTGACAGGCA  | ATTCTTTAAA     | ATCTGTTGCA   | 960    |
|     |            | CGGATGTTCA   |                   |             |                |              | 1020   |
|     |            | CTTCTCCCAG   |                   |             |                |              | 1080   |
| 10  |            |              |                   |             |                |              |        |
| 10  |            | GAAATGCCAA   |                   |             |                |              | 1140   |
|     |            | CCCGAAAACC   |                   |             |                |              | 1200   |
|     | TCGACAGAAA | TCACTGGGGA   | GGAGGAGCTG        | GGTTCCCGGG  | AGGACTCGCC     | CATGTCACCC   | 1260   |
|     | TCAGACACCC | AAGACCAGAA   | ACGGACCCTG        | AGGCCGCCAA  | GTAGACACGG     | CCACTCGGTG   | 1320   |
|     | GTTGCTCCCG | GCAGGACTGC   | AGTGAGGGCC        | CGGATGCCAG  | CGCTGCCCCG     | AAGGGAAGGC   | 1380   |
| 15  |            | CTGGCTTTTC   |                   |             |                |              | 1440   |
|     |            | CTGCCCACCA   |                   |             |                |              | 1500   |
|     |            | ATGACAACGA   |                   |             |                |              |        |
|     |            |              |                   |             |                |              | 1560   |
|     |            | AGGGCGCCTT   |                   |             |                |              | 1620   |
| 20  |            | TTCTCCGCGA   |                   |             |                |              | 1680   |
| 20  | GCGCGGAGGA | CCCCCCATTC   | AGGGGCCGCA        | GAGGAAGATT  | CCAGTGCCTC     | AGCCCCACCC   | 1740   |
|     | TCAAGACTTT | CTCCACCCCA   | TGGGGGATCA        | TCTCGGCTGC  | TGCCCACCCA     | GCCACACCTG   | 1800   |
|     |            | TTTCCAAGGG   |                   |             |                |              | 1860   |
|     |            | GGTCCACCAT   |                   |             |                |              | 1920   |
|     |            | GAGCGGAGGC   |                   |             |                |              | 1980   |
| 25  |            |              |                   |             |                | CTCTGGACAC   |        |
|     |            |              |                   |             |                |              | 2040   |
|     |            | TCAGACACAA   |                   |             |                |              | 2100   |
|     |            | GACCTCGGCT   |                   |             |                |              | 2160   |
|     |            | GGGTTCCCTC   |                   |             |                |              | 2220   |
| 20  | GGAGACGAGG | AGGATGAGAA   | GCCGCTTCCT        | GCCACCGTTG  | TCAATGACCA     | CGTGCCTTCC   | 2280   |
| 30  | TCCTCCAGGC | AGCCCATCTC   | CCGGGGCTGG        | GAGGACTTAA  | GGAGAAGCCC     | GCAGAGAGGG   | 2340   |
|     |            |              |                   |             |                | GGCAGATACA   | 2400   |
|     |            |              |                   |             |                | ACAGAGCACA   | 2460   |
|     |            |              |                   |             |                | CCGCCACGCG   |        |
|     |            |              |                   |             |                |              | 2520   |
| 35  |            | GTCCTCCCGC   |                   |             |                |              | 2580   |
| 22  | ACACCCGGCC | GGGCCCCAGA   | ACAGCAGCCC        | CCTCCTCCCG  | TCGCCACGTC     | CCAGCACCAC . | 2640   |
|     | CCGGGACCCC | AGAGCAGAGA   | CGCGGGTCGG        | TCACCTTCCC  | AGCCCAGGCT     | CTCACTGACC   | 2700   |
|     | CAGGCCGGGC | GGCCCCGCCC   | CACGTCGCAG        | GGCCGCTCCC  | ACTCCTCCTC     | GGACCCTTAC   | 2760   |
|     |            |              |                   |             |                |              | 2820   |
|     |            |              |                   |             |                | CCCCGCGCAC   | 2880   |
| 40  |            |              |                   |             |                | GGAGTCTCCC   |        |
| 40  |            |              |                   |             |                |              | . 2940 |
|     |            | GGGCAGGTGG   |                   |             |                |              | 3000   |
|     |            |              |                   |             |                | GGCAGCGCCG   | 3060   |
|     | GGGAAGTCGG | AGCCTCCTTC   | CAAGCGGCCC        | CTGTCCTCCA  | AGTCCCAGCA     | GTCGGTCTCA   | 3120   |
| 4.5 | GCCGAGGACG | AGGAGGAGGA   | GGACGCGGGG        | TTTTTTAAAG  | GCGGGAAAGA     | AGACCTTCTG   | 3180   |
| 45  | TCTTCCTCTG | TGCCAAAGTG   | GCCCTCTTCC        | TCCACTCCCA  | GGGGCGCAA      | AGACGCCGAT . | 3240   |
|     |            |              |                   |             |                | CGGAGGGAGC   |        |
|     |            |              |                   |             |                | GGCCTCCCAC   |        |
|     |            |              |                   |             |                |              |        |
|     |            |              |                   |             |                | GGGCACCCAC   | 3420   |
| 50  |            |              |                   |             |                | CCCGATGCTG   | 3480   |
| 50  |            |              |                   |             |                | ACAGCCTGCC   | 3540   |
|     | AGACCCTCTT | ACAGACAAGG   | TTATAATGGC        | AGACCAAATG  | TAGAAGGGAA     | AGTCCTTCCT   | 3600   |
|     | GGTAGTAATG | GAAAACCGAA   | TGGACAGAGA        | ATTATCAATG  | GCCCTCAAGG     | AACAAAGTGG   | 3660   |
|     | GTTGTGGACC | TTGATCGTGG   | GTTAGTATTG        | AATGCAGAAG  | GAAGGTACCT     | CCAAGATTCA   | 3720   |
|     |            |              |                   |             |                | AGATCTGGAA   | 3780   |
| 55  | GGGACCCCCG | TEGTGAGTCC   | TGACGCCCTC        | CCVCALCALAC | GGCAGGGGGG     | ACATGGCACA   |        |
|     |            |              |                   |             |                | GCTGGTGGGC . |        |
|     |            |              |                   |             |                |              |        |
|     |            |              |                   |             |                | CACCACTACT   | 3960   |
|     |            |              |                   |             |                | CATGCAGCCC   | 4020   |
| 60  |            |              |                   |             |                | CACCACCCCC   | 4080   |
| 60  |            |              |                   |             |                | AACCACCACC   | 4140   |
|     |            |              |                   |             |                | GGAACGGCAC   | 4200   |
|     |            |              |                   |             |                | CGCTGAAGAA   | 4260   |
|     | GATGAGTTCT | CAGGCTTGGA   | GACTGACACT        | GCAGTACCTA  | CGGAAGAGGC     | CTACGTTATA   | 4320   |
|     |            |              |                   |             |                | GCCTTCGACC   | 4380   |
| 65  |            |              |                   |             |                | TCCTGAAGAA   |        |
|     |            |              |                   |             |                |              | 4440   |
|     |            |              |                   |             |                | CCTAAATAAA   | 4500   |
|     |            |              |                   |             |                | GGACAGCCTG   | 4560   |
|     |            |              |                   |             |                | TGCTCCCCGC   | 4620   |
| 70  | AACATCACCG | TGGTGGCCGT   | GGAAGGTTGC        | CACTCATTIG  | TCATTGTGGA     | TTGGGACAAA   | 4680   |
| 70  |            |              |                   |             |                | TGAAGATTTC   | 4740   |
|     | ATCAGGAACA | AGTTTTCCAC   | TCAAGCTTCA        | TCAGTAACTC  | ACTTGCCCAT     | TGAGAACCTA   | 4800   |
|     |            |              |                   |             |                | CTACGGACCT   | 4860   |
|     |            |              |                   |             |                | TGTGAGGCCC   | 4920   |
|     |            |              |                   |             |                | TACACGGACT   |        |
| 75  |            |              |                   |             |                |              | 4980   |
|     |            |              |                   |             |                | GTTGTTCTTT   | 5040   |
|     |            |              |                   |             |                | TTCTACAGCA   | 5100   |
|     | TTGGAGACAG | CTGGGGAAGA   | GGTGAAGACC        | ATTGCCAATT  | TGTGGATTCA     | CACCTTGATG   | 5160   |
|     | GAAGAACAGG | GCCTCAGTCC   | TATGTAGAAG        | CCCTCCCTAC  | TATTCAAGGC     | TACTATCGCC   | 5220   |
| 00  |            |              |                   |             |                | TACTACTATG   | 5280   |
| 80  |            |              |                   |             |                | GACCGTCATG   | 5340   |
|     |            |              |                   |             |                | TGAGCAAAGA   | 5400   |
|     |            |              |                   |             |                |              |        |
|     |            |              |                   |             |                | GGACACTGGC   | 5460   |
|     |            |              |                   |             |                | ATGAACAGGA   | 5520   |
|     | TTCAGTTTTC | CIGITAACTI   | TGCTTCTCTA        | CTTTTTTTC   | TTTGTTTGTA     | ATAGCACATC   | 5580   |
|     |            |              |                   |             | _              |              |        |

|     | CCAGAGACAT    | CAGAAACCAG   | CAACTGATTC             | AGTGTGATTT     | CCCAGACTTT                              | TTAGGCATGA   | 5640 |
|-----|---------------|--------------|------------------------|----------------|---|--|------|
|     | AATTCGGACA    | CTTCAGTATT   | TCCAGGAATA             | GCATATGCAC     | CCTCTTCTTC                              | CTTCATCCAA   | 5700 |
|     |               |              |                        |                |   |  |      |
|     |               | TTTCTGTTTT   |                        |                |   |  | 5760 |
| 5   |               | TTGTATGCAG   |                        |                |   |  | 5820 |
| 3   | ATATCCTACT    | TGAAATTTAC   | TCTATGGACT             | TACCCACTGC     | TAGAATAAAT                              | GTATCAAATC   | 5880 |
|     | TTATTTGTAA    | ATTCTCAATT   | TTGATATATA             | TATGTATATA     | TGCATATACA                              | TATCCACACT   | 5940 |
|     |               | AATATTGATT   |                        |                |   |  | 6000 |
|     | AAAAAAA       |              | WEEK! TOCIN            | AMITIGIACI     | IGIICACCAA                              | ~~~~~~~  |      |
|     | AMAMMA        |              |                        |                |   |  | 6007 |
| 10  |               |              |                        |                |   |  |      |
| 10  | Seq ID NO:    | C14 DNA Sec  | ruence                 |                |   |  |      |
|     | Nucleic Aci   | d Accession  | #: NM 0030             | 14             |   |  |      |
|     |               | ence: 238    |                        |                |   |  |      |
|     | accuma code   | 250          | 2270                   |                |   |  |      |
|     |               | ••           |                        |                |   |  |      |
| 15  | 1             | 11           | 21                     | 31             | 41                                      | 51   |      |
| 13  |               | 1            | 1                      |                |   |  |      |
|     | GGCGGGTTCG    | CGCCCCGAAG   | GCTGAGAGCT             | GGCGCTGCTC     | GTGCCCTGTG                              | TGCCAGACGG   | 60   |
|     | CGGAGCTCCG    | CGGCCGGACC   | CCGCGGCCCC             | COTTOCTCC      | CGACTGGAGT                              | TTGGGGGAAG   | 120  |
|     |               | GCGCCCCAGA   |                        |                |   |  |      |
|     |               |              |                        |                |   |  | 180  |
| 20  |               | GAAGGCGCTT   |                        |                |   |  | 240  |
| 20  | TTCCTCTCCA    | TCCTAGTGGC   | GCTGTGCCTG             | TGGCTGCACC     | TGGCGCTGGG                              | CGTGCGCGGC   | 300  |
|     | GCGCCCTGCG    | AGGCGGTGCG   | CATCCCTATG             | TGCCGGCACA     | TGCCCTGGAA                              | CATCACGCGG   | 360  |
|     | ATGCCCAACC    | ACCTGCACCA   | CAGCACGCAG             | GAGAACGCCA     | TCCTGGCCAT                              | CGAGCAGTAC   | 420  |
|     |               | TGGACGTGAA   |                        |                |   |  | 480  |
|     |               | GCACCCTGGA   |                        |                |   |  |      |
| 25  | CARCCCCCCC    | GCGACGACTG   | COLCOCOCTO             | ADOLLO TOTAL   | AGCCGIGCAA                              | GICGGIGIGC   | 540  |
|     | AACGCGCGC     | GCGACGACIG   | CGAGCCCCTC             | MIGWAGAIGI     | ACAACCACAG                              | CIGGCCCGAA   | 600  |
|     | AGCCTGGCCT    | GCGACGAGCT   | GCCTGTCTAT             | GACCGTGGCG     | TGTGCATTTC                              | GCCTGAAGCC   | 660  |
|     |               | ACCTCCCGGA   |                        |                |   |  | 720  |
|     | CAGGAAAGGC    | CTCTTGATGT   | TGACTGTAAA             | CGCCTAAGCC     | CCGATCGGTG                              | CAAGTGTAAA   | 780  |
| 0.0 | AAGGTGAAGC    | CAACTTTGGC   | AACGTATCTC             | AGCAAAAACT     | ACAGCTATGT                              | TATTCATGCC   | 840  |
| 30  | DAAATAAAAG    | CTGTGCAGAG   | GAGTGGCTGC             | AATGAGGTCA     | CAACCCTCCT                              | CCATCTAAAA   | 900  |
|     | CACATOTO      | AGTCCTCATC   | Y COCKETOR             | CONTRACTOR     |   | CONTRACTOR AND A STATE OF THE S |      |
|     | GAGAICTICA    | MOTOCICATO   | ACCCATCCCT             | CGAACTCAAG     | TCCCGCTCAT                              | TACAAATTCT   | 960  |
|     | TCTTGCCAGT    | GTCCACACAT   | CCTGCCCCAT             | CAAGATGTTC     | TCATCATGTG                              | TTACGAGTGG   | 1020 |
|     |               | TGATGCTTCT   |                        |                |   |  | 1080 |
| 25  | AAAAGATCCA    | TACAGTGGGA   | AGAGAGGCTG             | CAGGAACAGC     | GGAGAACAGT                              | TCAGGACAAG   | 1140 |
| 35  | AAGAAAACAG    | CCGGGCGCAC   | CAGTCGTAGT             | AATCCCCCCA     | AACCAAAGGG                              | AAAGCCTCCT   | 1200 |
|     | CCTCCCAAAC    | CAGCCAGTCC   | CAAGAAGAAC             | ATTABABOTA     | CCACTCCCCA                              | CARCACARCA   | 1260 |
|     | AACCCCAAAA    | GAGTGTGAGC   | The same               | ATTAMACTA      | CONGIGCCCA                              | GAAGAGAACA   |      |
|     |               |              |                        |                |   |  | 1320 |
|     |               | GGCATTGCCT   |                        |                |   |  | 1380 |
| 40  |               | GTGCTCTTCA   |                        |                |   |  | 1440 |
| 40  | GTTTTTCTTT    | GTAAGCCATC   | <b>ACAAGCCATA</b>      | GTGGTAGGTT     | TGCCCTTTGG                              | TACAGAAGGT   | 1500 |
|     | GAGTTAAAGC    | TGGTGGAAAA   | GGCTTATTGC             | ATTGCATTCA     | GAGTAACCTG                              | TOTOCATACT   | 1560 |
|     | CTAGAAGAGT    | AGGGAAAATA   | מיויייביציייים באיני מ | CAATTCCACC     | TAATATOTO                               | A TOTAL CONTRACT   | 1620 |
|     | AAATGCCATA    | TTTCAAACAA   | AACACCTAAT             | THE TENTE      | TATIOTOC .                              | MIGIMMI  |      |
|     |               |              |                        |                |   |  | 1680 |
| 45  |               | TGCAATGTTA   |                        |                |   |  | 1740 |
| 43  |               | AGTGGAATGA   |                        |                |   |  | 1800 |
|     | TTTTTGTGAT    | GAAAGGGGAT   | TTTTTGAAAA             | ATTAGAGAAG     | TAGCATATGG                              | AAAATTATAA   | 1860 |
|     | TGTGTTTTTT    | TACCAATGAC   | TTCAGTTTCT             | GTTTTTAGCT     | AGAAACTTAA                              | AAACAAAAAT .   | 1920 |
|     | AATAATAAAG    | AAAAATAAAT   | AAAAAGGAGA             | CCCAGACAAT     | CTCTCCATTTC                             | CTCTTTTTTTC  | 1980 |
|     | CTTACTCAT     | TTCCATGATC   | ATCATCCTTC             | TTCTCAACAC     | COLCIOCHIAC                             | 200100111110   |      |
| 50  | POPULACIONI   | TGTCTGTACC   | ATOMICCITC             | 1101CAACAC     | CCICITAAGC                              | AGCACCAGAA   | 2040 |
| 20  |               |              |                        |                |   |  | 2100 |
|     |               | CACAAGAGAG   |                        |                |   |  | 2160 |
|     | AATAATTTGA    | CAAGCTTAAA   | AATGGCCTTC             | ATGTGAGTGC     | CAAATTTTGT                              | TTTTCTTCAT   | 2220 |
|     | TTAAAATATTT   | TCTTTGCCTA   | AATACATGTG             | AGAGGAGTTA     | <b>DTAAAATG</b>                         | TACAGAGAGG   | 2280 |
|     | AAAGTTGAGT    | TCCACCTCTG   | AAATGAGAAT             | TACTTGACAG     | TTGGGATACT                              | TTAATCAGAA   | 2340 |
| 55  | AAAAAGAACT    | TATTTGCAGC   | ATTTTATCAA             | CAAATTTCAT     | AATTGTGGAC                              | AATTGGAGGC   | 2400 |
|     | ATTTATTTA     | AAAAACAATT   | TALE DATE OF THE       | TTTCCTAACA     | CACTAACCAT                              | Carsacanana  |      |
|     | ACCCA TENCA A | TAAATGCACA   | 1141100001             | TIIOCIAACA     | CHGIMAGCAI                              | GIAITTIAIA   | 2460 |
|     | AGGCATICAL    | IMMIGCACA    | ACGCCCAAAG             | GAAATAAAAT     | CCTATCTAAT                              | CCTACTCTCC   | 2520 |
|     |               | GGTAATCACT   |                        |                |   |  | 2580 |
| 60  | GCACTTATAA    | AATGATTTGA   | ACAAATAAAA             | CTAGGAACCT     | GTATACATGT                              | GTTTCATAAC   | 2640 |
| UU  | CTGCCTCCTT    | TGCTTGGCCC   | TTTATTGAGA             | TAAGTTTTCC     | TGTCAAGAAA                              | GCAGAAACCA   | 2700 |
|     | TCTCATTTCT    | AACAGCTGTG   | TTATATTCCA             | TAGTATGCAT     | TACTCAACAA                              | ACTGTTGTGC   | 2760 |
|     |               |              |                        |                |   | ACCGGAATTC   | 2820 |
|     |               |              |                        |                |   |  | 2020 |
|     | Sea ID NO.    | C15 DNA Sec  | 710700                 |                |   |  |      |
| 65  |               |              |                        |                |   |  |      |
| 05  |               | ld Accession |                        | 940            |   |  |      |
|     | Coding sequ   | uence: 23    | 1489                   |                |   |  |      |
|     |               |              |                        |                |   |  |      |
|     | 1             | 11           | 21                     | 31             | 41                                      | 51   |      |
|     | 1             | 1            | 1                      | 1              | 1                                       | ī  |      |
| 70  | AAGCCCAGCA    | GCCCCGGGGC   | CONTROCTOR             |                | 000000000000000000000000000000000000000 | 000000000  |      |
| . • |               | 000000000    | AGE TOOCICE            | CONTRACTOR COL | CICCGCAGCG                              |  | 60   |
|     | Coccercing    | CCCCCGATGC   | TGCTGCTGCT             | GCTCCAGCCG     | CCGCCGCTGC                              | TGGCCCGGGC   | 120  |
|     | * CIGCCGCCG   | GAUGTCCACC   | ACCTCCATGC             | CGAGAGGAGG     | GGGCCACAGC                              | CCTGGCATGC   | 180  |
|     | AGCCCTGCCC    | AGTAGCCCGG   | CACCTGCCCC             | TGCCACGCAG     | GAAGCCCCCC                              | GGCCTGCCAG   | 240  |
| 7.  | CAGCCTCAGG    | CCTCCCCGCT   | GTGGCGTGCC             | CGACCCATCT     | GATGGGCTGA                              | GTGCCCGCAA   | 300  |
| 75  | CCGACAGAAG    | AGGTTCTTTCC  | TTTCTCCCC              | GCGCTCCCAC     | AAGACCCACC                              | TCACCTACAG   |      |
| -   | CATCCPTCC     | THUCKATUC    | PCALCOCCO.             | CCACAGOGAG     | ACCOUNTE                                | TGGCAGAGGC   | 360  |
|     |               |              |                        |                |   |  | 420  |
|     | CCTAAAGGTA    | IGGAGCGATG   | TGACGCCACT             | CACCITTACT     | GAGGTGCACG                              | AGGGCCGTGC   | 480  |
|     | IGACATCATG    | ATCGACTTCG   | CCAGGTACTG             | GCATGGGGAC     | GACCTGCCGT                              | TTGATGGGCC   | 540  |
| 00  | TGGGGGCATC    | CTGGCCCCATG  | CCTTCTTCCC             | CAAGACTCAC     | CGAGAAGGGG                              | ATGTCCACTT   | 600  |
| 80  | CGACTATGAT    | GAGACCTGGA   | CTATCGGGGA             | TGACCAGGGC     | ACAGACCTCC                              | TGCAGGTGGC   | 660  |
|     | AGCCCATGAA    | TTTGGCCACC   | TGCTGGGGG              | GCAGCACACA     | ACAGCACCCA                              | AGGCCCTGAT   |      |
|     |               |              |                        |                |   |  | 720  |
|     |               |              |                        |                |   | GCAGGGGCGT   | 780  |
|     | CAACACCTA     | TATGGCCAGC   | CCTGGCCCAC             | TGTCACCTCC     | AGGACCCCAG                              | CCCTGGGCCC   | 840  |
|     | CAGGCTGGG     | ATAGACACCA   | ATGAGATTGC             | ACCGCTGGAG     | CCAGACGCCC                              | CGCCAGATGC   | 900  |
|     |               |              |                        |                |   |  |      |

|     |             |             |                       |            | GAGCTCTTTT               |                          | 960          |
|-----|-------------|-------------|-----------------------|------------|--------------------------|--------------------------|--------------|
|     |             |             |                       |            | GGCTACCCAG<br>TTCGAGGATG |                          | 1020         |
| _   |             |             |                       |            | GGTGAAAAGC               |                          | 1080<br>1140 |
| 5   |             |             |                       |            | GTCCATGCTG               |                          | 1200         |
|     |             |             |                       |            | GACTACTGGC               |                          | 1260         |
|     |             |             |                       |            | ACTGACTGGA               |                          | 1320         |
|     |             |             |                       |            | GCCTACTTCC               |                          | 1380         |
| 10  |             |             |                       |            | GAAGGCTTCC               |                          | 1440         |
| 10  |             |             |                       |            | TTCCTCTGAC<br>CAGGCTAGAG |                          | 1500         |
|     |             |             |                       |            | TGTCTCCTGC               |                          | 1560<br>1620 |
|     |             |             |                       |            | GCAGGTCGTG               |                          | 1680         |
| 1.5 |             |             |                       |            | TTAAGAGGAA               |                          | 1740         |
| 15  |             |             |                       |            | TCTCATCCCT               |                          | 1800         |
|     |             |             |                       |            | CTGTATCCCT               |                          | 1860         |
|     | TCACCAGG    | GGCTGGCACT  | CARGCAAGGG            | TGCTGGGGCC | CCATGGCCTT<br>AGGTCTTGGT | CAGCCCTGGC               | 1920         |
|     | ATCTGTCTGC  | CTTCTGGCTG  | ACAATCCTGG            | AAATCTGTTC | TCCAGAATCC               | AGGCCAAAAA               | 1980<br>2040 |
| 20  |             |             |                       |            | ACCCCAGGCC               |                          | 2100         |
|     |             |             |                       |            | GCCCTTTTCG               |                          | 2160         |
|     |             |             |                       |            | AACCTTCTTC               | TTCTTTTTT                | 2220         |
|     | TTTTTAAACT  | GAGGATTGTC  | ATTAAACACA            | GTTGTTTTCT |                          |                          | 2260         |
| 25  | Sec ID NO.  | C16 DNA Sec |                       |            |                          |                          |              |
| 23  |             |             | uence<br>1 #: NM_0240 | 122        |                          |                          |              |
|     | Coding sequ |             |                       |            |                          |                          |              |
|     |             |             |                       |            |                          |                          |              |
| 30  | 1           | 11          | 21                    | 31         | 41                       | 51                       |              |
| 20  | 1           | 1           |                       |            | 1                        |                          |              |
|     | GGAAAGGGCT  | CTCTTTATCC  | GAAGCCAGTA            | ACACTETECC | GGTCATGCCC<br>CTACTATCTC | TTCCCTCCTC               | 60<br>120    |
|     |             |             |                       |            | TGGAGGCGGA               |                          | 180          |
| ~ - |             |             |                       |            | CTGCTGTTGA               |                          | 240          |
| 35  | TCATTCCGAT  | CGCTTTTTGG  | CCTTGATGAT            | TTGAAAATAA | GTCCTGTTGC               | ACCAGATGCA               | 300          |
|     |             |             |                       |            | AGTTTTTTCC               |                          | 360          |
|     |             |             |                       |            | TGGGCATCCA               |                          | 420          |
|     |             |             |                       |            | AGCTGATAGC<br>GTGTCCGGGT |                          | 480          |
| 40  |             |             |                       |            | CCATGTGCTC               |                          | 540<br>600   |
|     |             |             |                       |            | TCCCAAGCTA               |                          | 660          |
|     | GATAACCTCA  | GAGTGAGCTC  | GCTGGAGGGG            | CAGTTCCGGG | AGGAGTTTGT               | GTCCATCGAT               | 720          |
|     | CACCTCTTGC  | CAGATGACAA  | GGTGACTGCA            | TTACACCACT | CAGTATATGT               | GAGGGAGGGA               | 7B0          |
| 45  |             |             |                       |            | GTGGTCATAG               |                          | 840          |
| 43  |             |             |                       |            | AGTGGCCCTG               |                          | 900          |
|     |             |             |                       |            | TCACGCCCCT               |                          | 960          |
|     |             |             |                       |            | TGGAGAAGAT               |                          | 1020<br>1080 |
| 50  |             |             |                       |            | TTATGAAGCT               |                          | 1140         |
| 50  |             |             |                       |            | ACTCTGAAGA               |                          | 1200         |
|     |             |             |                       |            | AGGATGGAGG               |                          | 1260         |
|     | CCTGTCCTGA  | ACCACGCGGC  | CGTCCCTTTG            | ATTTCCAACA | AGATCTGCAA               | CCACAGGGAC               | 1320         |
|     | GREACCTCCC  | ACCCCCATCAC | CCCCTCCATG            | CTCTGCGCGG | GCTACCTGAC               | GGGTGGCGTG<br>GCTGTGGAAG | 1380         |
| 55  | TTAGTGGGAG  | CGACCAGCTT  | TGGCATCGGC            | TGCGCAGAGG | TGAACAAGCC               | TGGGGTGTAC               | 1440<br>1500 |
|     | ACCCGTGTCA  | CCTCCTTCCT  | GGACTGGATC            | CACGAGCAGA | TGGAGAGAGA               | CCTAAAAACC               | 1560         |
|     | TGAAGAGGAA  | GGGGACAAGT  | AGCCACCTGA            | GTTCCTGAGG | TGATGAAGAC               | AGCCCGATCC '             | 1620         |
|     | TCCCCTGGAC  | TCCCGTGTAG  | GAACCIGCAC            | ACGAGCAGAC | ACCCTTGGAG               | CTCTGAGTTC               | 1680         |
| 60  |             |             |                       |            |                          | CAACCTTCAA               | 1740         |
| 00  |             |             |                       |            |                          | AGGCTGGAGT<br>GATTCTCTTG | 1800<br>1860 |
|     |             |             |                       |            | CCACACCCAA               |                          | 1920         |
|     | TATTTTTAGT  | AGAGACAGGG  | TTTCACCATG            | TTGGCCAGGC | TGCTCTCAAA               | CCCCTGACCT               | 1980         |
| 65  | CAAATGATGT  | GCCTGCTTCA  | GCCTCCCACA            | GTGCTGGGAT | TACAGGCATG               | GGCCACCACG               | 2040         |
| 65  |             |             |                       |            |                          | ACTTGCAAGG               | 2100         |
|     | GCGGCCTTTC  | CCACTGGTCC  | ATCTGGTTTT            | CTCTCCAGGG | GTCTTGCAAA               | ATTCCTGACG               | 2160         |
|     | CCAGCCCAG   | ACTOCAGAAC  | TCACGTGCAA            | AGCCACCAAC | AGCCACTCAG               | AAAAGACGCA<br>ACCAGAACCA | 2220         |
|     | AACCCACCCT  | TTCTACTTCC  | AAGACTTATT            | TTCACATGTG | GCCDCCTTAA               | TCTAGGAACCA              | 2280<br>2340 |
| 70  | ACTCGTTTAA  | GGCCTATTTT  | CATGATTTCT            | TTGTAGCATT | TGGTGCTTGA               | CGTATTATTG               | 2400         |
|     |             |             |                       |            |                          | AAAAAAAAA                | 2460         |
|     | ААААА       |             |                       |            |                          |                          | 2465         |
|     |             |             |                       |            |                          |                          |              |
| 75  |             | C17 DNA Se  | quence<br>n #: NM 003 | 222        |                          |                          |              |
| ,,, |             | uence: 63   |                       | 220        |                          |                          |              |
|     |             | 03          |                       |            |                          |                          |              |
|     | 1           | 11          | 21                    | 31         | 41                       | 51                       |              |
| 80  | 1           |             | 1                     | 1          | 1                        | 1                        |              |
| 0U  | GAATTCCGGC  | TCTCTGGGTG  | AGAGACCGAG            | AGGGGCATAT | CCGTTCACGC               | CGATCCATGA               | 60           |
|     |             |             |                       |            |                          | CGTCACGACG               | 120          |
|     | CGAGCGCCCC  | GCCGCTCTCC  | CACACCCCC             | AGCIGGCAC  | TGTAGGTCAA               | TCTCCCTACA               | 180          |
|     | CACCCTACCA  | GCCTATCTAC  | CCCCAGTCGC            | AAGATCCTTA | CTCCCACCTC               | AACGACCCCT               | 240<br>300   |
|     |             |             |                       |            |                          |                          | -00          |

|   | ACAGCCTGAA   | CCCCTGCAC  | GCCCAGCCGC   | AGCCGCAGCA   | CCCAGGCTGG   | CCCGGCCAGA   | 360  |
|---|--|--|--|--|--|--|--|
|   | GGCAGAGCCA   |  |  |  |  |  | 420  |
|   | GCCTGGATCC   |  |  |  |  |  | 480  |
| 5   | TCAGCTCAGG   |  |  |  |  |  | 540  |
| 3   | CGCATGTAGA   |  |  |  |  |  | 600  |
|   | TGTCCCTGTC   |  |  |  |  |  | 660  |
|   | TCTTCGGCGG   |  |  |  |  |  | 720<br>780   |
|   | CACCCGAGTG   |  |  |  |  |  | 840  |
| 10  | ATGGAGGAAG   |  |  |  |  |  | 900  |
|   | GACGTAAAGC   |  |  |  |  |  | 960  |
|   | TAGCCAGGGA   |  |  |  |  |  | 1020   |
|   |  |  |  | AGCAAGTGAC   |  |  | 1080   |
| 15  |  |  |  | ACCTGCTGGC   |  |  | 1140   |
| 13  | GGAACTCACG   |  |  |  |  |  | 1200   |
|   |  |  |  | CGGTGTGTGC<br>ACAAAATGTA   |  |  | 1260<br>1320   |
|   |  |  |  | ACAAAGAGGA   |  |  | 1380   |
|   |  |  |  | CCAGCCCCCC   |  |  | 1440   |
| 20  |  |  |  | GCTGCTGCTA   |  |  | 1500   |
|   | GCCGCCGCCG   | CCGCTGCCCT   | TGGGTCCCCC   | CGAGTCTCCG   | GGACTGCCCT   | CTCGACTGTC   | 1560   |
|   |  |  | TCTGCACCCG   | CCTCGACCTC   | CCCACCCGCT   | CCCACACCCC   | 1620   |
|   | TGTGCCCCCG   | GAATTC   |  |  |  |  | 1636   |
| 25  | Sea ID NO.   | C18 DNA Sec  | monco  |  |  |  |  |
|   |  | d Accession  | •  | 886  |  |  |  |
|   |  | ence: 713  |  | ر  |  |  |  |
|   |  |  |  |  |  |  |  |
| 30  | 1  | 11   | 21   | 31   | 41 .   | 51   |  |
| 50  | CCCCCACCAC   | I CONCERCENCE  | ACTOTOCO AC  | CCCCAGCTCA   | CTCTCACCAC   | Tall Call Call   | 60   |
|   |  |  |  | CCTCCTTGTC   |  |  | 120  |
|   |  |  |  | AGAGCTCTGC   |  |  | 180  |
| 0.5   |  |  |  | TTCTGAAACC   |  |  | 240  |
| 35  |  |  |  | GCAGATCTGT   |  |  | 300  |
|   |  |  |  | GAATGCCTGA   |  |  | 360  |
|   |  |  |  | ACAGGAGCCT   |  |  | 420  |
|   |  |  |  | CCATCTGCTA   |  |  | 480<br>540   |
| 40  |  |  |  | CATGACATTG   |  |  | 600  |
|   |  |  |  | TGGATCAATC   |  |  | 660  |
|   |  |  |  | AATCTTTATT   |  |  | 720  |
|   |  |  |  |  |  |  |  |
|   |  |  |  | ATAAAAGGTA   | AACCAGCATT   | CTCACTGTGA   | 780  |
| 45  |  | ATATTGGCAG<br>AAAAAAAAAA   |  | ATAAAAGGTA   | AACCAGCATT   | CTCACTGTGA   | 780<br>803   |
| 45  | АЛАЛАЛАЛА  | AAAAAAAA   | AAA  | ATAAAAGGTA   | AACCAGCATT   | CTCACTGTGA   |  |
| 45  | Seq ID NO:   | C19 DNA Se   | AAA<br>quence  |  | AACCAGCATT   | CTCACTGTGA   |  |
| 45  | Seq ID NO:<br>Nucleic Ac:  | AAAAAAAA   | AAA<br>quence<br>n #: NM_004   |  | AACCAGCATT   | CTCACTGTGA   |  |
|   | Seq ID NO:<br>Nucleic Ac:<br>Coding seq  | C19 DNA Serid Accession<br>uence: 121.   | AAA<br>quence<br>n #: NM_004<br>.2619  | 063  |  |  |  |
| 45<br>50  | Seq ID NO:<br>Nucleic Ac:  | AAAAAAAAAA<br>C19 DNA Se<br>id Accessio  | AAA<br>quence<br>n #: NM_004   |  | AACCAGCATT   | CTCACTGTGA   |  |
|   | AAAAAAAAAA<br>Seq ID NO:<br>Nucleic Ac:<br>Coding sequ   | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   | AAA<br>quence<br>n #: NM_004<br>.2619<br>21  | 063<br>31<br>]   | 41<br>   | 51<br>   | 803  |
|   | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  1   AGGGAGTGTT   | AAAAAAAAAAAA C19 DNA Sedid Accession Lence: 121.  11   | AAA quence n #: NM_004 .2619 21   ATACTCCAGT   | 063<br>31<br> <br>  CGTAGCAAGA   | 41<br> <br>GTCTCGACCA  | 51<br> <br>CTGAATGGAA  | 803<br>60  |
| 50  | AAAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  AGGGAGTGTT GAAAAGGACT   | AAAAAAAAAA C19 DNA Seid Accession uence: 121.  11         CCCGGGGGAG TTTAACCACC  | AAA quence n #: NM_004 .2619 21   ATACTCCAGT ATTTTGTGAC  | 063<br>31<br>]   | 41<br> <br>GTCTCGACCA<br>GAATTTGAAT  | 51<br> <br> -<br>  CTGAATGGAA<br>AAAGAAAACT  | 803  |
|   | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG  | AAAAAAAAAA  C19 DNA Seid Accessionence: 121.  11   | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGGAC TCACTCCCT  | 31<br> <br>  CGTAGCAAGA<br>TTACAGAAAG<br>TGTCTTCTTA<br>CTGAAACCCA  | 41<br> <br>GTCTCGACCA<br>GAATTTGAATT<br>TGCTTTATTT<br>TGACATTTTC   | 51<br> <br>CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA  | 60<br>120  |
| 50  | AAAAAAAAA<br>Seq ID NO:<br>Nucleic Ac:<br>Coding sequ<br>1<br> <br>AGGGAGTGTT<br>GAAAAGGACT<br>ATGATACTTC<br>TATGGCCAAG  | AAAAAAAAAA C19 DNA Seid Accession uence: 121.  11   CCCGGGGGAG TTTAACCACC AGGCCCATC AGGGGAAGTT CGAGTCAAAT  | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGGAC TCACTCCCT TAGTGGACCC TATATTCCAG  | 31<br> <br>  CGTAGCAAGA<br>TTACAGAAG<br>TGTCTTCTTA<br>CTGAAACCCA<br>TTTAAGGCCA   | 41<br> <br>GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATT<br>TGACATTTTC<br>ATCCTCCTGC   | 51<br> <br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATITATGAA<br>TGTGACTTTT  | 60<br>120<br>180<br>240<br>300   |
| 50  | AAAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG   | AAAAAAAAAA  C19 DNA Sedid Accession Lence: 121.  11  CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAAGTT AGGGGAAAT GGGAGACAGA  | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TAGTGGACCC TATATTCCAG TAATATTCCAG TCACATATTT  | 31<br>CGTAGCAAGA<br>TTACAGAAAG<br>TGTCTTCTTA<br>CTGAAACCCA<br>TTTAAGGCCA<br>GTGATAGAAC   | 41<br> <br>GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATTT<br>TGACATTTTC<br>ATCCTCCTG<br>GGGAGGGACT   | 51<br> <br>CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TGTGACTTTT<br>TCTGTATTAC  | 60<br>120<br>180<br>240<br>300<br>360  |
| 50  | AAAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG AACAGAGCCT  | AAAAAAAAAA  C19 DNA Sedid Accession Lence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGAAGTT CGAGTCAAAT GGGAGACAAG TGGACAGGGA   | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCCTG TAGTGGACCC TATATTCCAG CAACATATTT AACAAGATCT  | 31<br>  CGTAGCAAGA<br>TTACAGAAAG<br>TGTCTTCTTA<br>CTGAAACCCA<br>TTTAGGCCA<br>GTGATAGAAC<br>ACTCACAATC  | 41<br>  GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATTT<br>TGACATTTCC<br>ATCCTCCTGC<br>GGGAGGGACT<br>TCCAGGTTGC   | 51<br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TGTGACTTTT<br>TCTGTATTAC<br>AGCCCTGGAC   | 60<br>120<br>180<br>240<br>300<br>360<br>420   |
| 50  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG AACAGAGCT GCTAATGGAA   | AAAAAAAAAA  C19 DNA Seid Accessionence: 121.  11   | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGGAC TCACTCCCTG TAGTGGACCC TATATTCCAG CAACATATTT AACAAGATCT GGGTCCAGTC  | 31<br> <br>  CGTAGCAAGA<br>TTACAGAAAG<br>TGTCTTCTTA<br>CTGAAACCCA<br>TTTAAGGCCA<br>GTGATAGAAC<br>ACTCACAATC<br>CCTATCACCA  | 41<br> <br>GTCTCGACCA<br>GAATTIGAAT<br>TGCTTATTT<br>TGACATTTTC<br>ATCCTCCTGC<br>GGGAGGACT<br>TCCAGGTTGC<br>TAGAAGTGAA  | 51<br> <br>CTGAATGGAA<br>AAAGAAAACT<br>GCAACTGGA<br>TATITATGAA<br>TGTGACTTT<br>TCTGTATTAC<br>AGCCCTGGAC<br>GGACATCAAC  | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480  |
| 50  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG AACAGAGCC GCTAATGGAA GACAATCGAC GAAATCGAC  | AAAAAAAAAA  C19 DNA Sedid Accession Lence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAAGTT CGAGTCAAAT GGGACAGGA TTATAGTGGA TCATAGTGGA CCACGTTTCT   | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TAGTGGACCC TATATTCCAG CAACATATTT AACAAGATCT GGGTCCAGTCCCAGG   | 31<br>CGTAGCAAGA<br>TTACAGAAAG<br>TGTCTTCTTA<br>CTGAAACCCA<br>TTTAAGGCA<br>GTGATAGAAC<br>ACTCACAATC<br>CCTATCACCA<br>TACCAAGGCT  | 41<br>  GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATTT<br>TGACATTTTC<br>GGGAGGACT<br>TCCAGGTTGC<br>TCCAGGTTGC<br>TCAGGAGTGAA<br>TCAGTAAGGCA  | 51<br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TGTGACTTTT<br>TCTGTATTAC<br>AGCCCTGGAC<br>GGACATCAAC<br>GGACTCAAC  | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540  |
| 50  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  I GAAAGGACTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCTAAGAAC GAACTAACTG AACAGAGCCT GCTAATGGAA GACAATCGAA CCCAGGAAAGGC CCAGGAAAGGC   | AAAAAAAAAA  C19 DNA Secid Accession Hence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAAGTT CGAGTCAAAT CGGAGACAGA TGGACAGGA TTATAGTGGA CCACGTTTCT CCTTCTTGTA  | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTGTGAC TCACTCCCTG TAGTGGACCC TATATTCCAG CAACATATTT AACAAGATCT GGGTCCAGTC CCAGTCAAAG TGTCAATGCC  | 31<br> <br>  CGTAGCAAGA<br>TTACAGAAAG<br>TGTCTTCTTA<br>CTGAAACCCA<br>TTTAAGGCCA<br>GTGATAGAAC<br>ACTCACAATC<br>CCTATCACCA  | 41<br>  GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATTT<br>TGACATTTTC<br>ATCCTCCTGC<br>TGGAGGGACT<br>TCCAGGTTGC<br>TAGAAGTGAA<br>CAGTAAGGCA<br>ATGATCCGGC   | 51<br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TGTGACTTTT<br>TCTGTATTAC<br>AGCCCTGGAC<br>GGACATCAAC<br>GAACTCTCGC<br>CACTCCCAAT   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480  |
| 50  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequ  1   AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG AACAGAGACT GCTAATGGAAAGC CCAGGAAAGC GGCCAGCTTT CAGATCAACA  | AAAAAAAAAA  C19 DNA Sedid Accession Lence: 121.  11    CCCGGGGGAG TITAACCACC AGGCCATCT AGGGGAACAGA TGGACAGGGA TGTAATGGA CCACGTTTCT CCTTCTTGTA ATTACCAGAT ACAAAACGGG  | AAA quence n #: NM_004 .2619  21   ATACTCCAGT AATTTTGTGAC TCACTCCCTG TAGTGGACC TATATTCCAG CAACATATTT AACAAGATCT AACAAGATCT CCAGTCAAAG TGTCAATCCAG AGCCATTCTCT  | 31 COTAGCAAGA TTACAGAAAG TGTCTTCTTA CTGAAACCCA GTGATAGAAC GTGATAGAAC CCTATCACAATC CCTATCACCA TACGAAGGCT ACAGACCTGG CTTCCCATGA  | 41<br>  GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATTT<br>TGACATTTIC<br>TCGAGGTGC<br>TCAAGGTTGC<br>TCAAGGTAG<br>ATGATCAGGC<br>TCAACAATGT<br>AGGGATCTCA   | 51<br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TGTGACTTTT<br>TCTGTATTAC<br>AGCCCTGGAC<br>GGACATCAAC<br>GAACTCTCGC<br>CACTCCCAAT<br>CATGTACTTT<br>GGAATTGAAT   | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>600<br>720  |
| 50<br>55<br>60  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding seq  1   AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTGA ACAGAGCCT ACAGAGACC CCAGGAAAGC GGCCAGCTTT CAGATCACA CCTGCTAAGAA CCTGCTAAGAA  | AAAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAAGTT CGAGTCAAAT GGGAACAGGA TGACAGGGA TTATAGTGGA CCACGTTTCT CCTTCTTGTA ATTACCAGAT ACAAAAACGGA ATCCTTCCTA   | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TATATTCCAG CAACATATTT AACAAGATCT GCGTCCAGT CCAGTCCAAG TGTCAATGC TGTCATCCAG AGCCATCTCT AACCACCATCTCT TATCTCGGG AGCCATCTCT  | 31 CGTAGCAAGA TTACAGAAGA TGTCTTCTTA CTGAAACCCA GTGATAGGAA ACTCACAATC CCTATCACCA TACGAAGGCT ACAGACCTGG CTTCCCATGA CTTACCCGAG ATCTACCAGAG ATCTCAGTGA   | 41<br>  GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATTT<br>TGACATTTTC<br>ATCCTCGC<br>GGGAGGGACT<br>TCCAGGTTGC<br>TAGAAGTGAA<br>ATGATCCGCC<br>TCACAATGT<br>AGGAATTCA<br>AGGACATGGA   | 51<br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TGTGACTTTT<br>TCTGTAATTAC<br>AGCCCTGGAC<br>GGACTCAAC<br>GAACTCTGC<br>CACTCCCAAT<br>CATGTACTTT<br>GGGAATTGAAT<br>AGGCCAGAGT   | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>660<br>660<br>720<br>780   |
| 50  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG AACAGAGCCT GCTAATGGAA GACAATCGAC CCAGGAAAGC GGCCAGCTTT CAGATCAACA CCTGCTAAGA GAGAATTCCT  | AAAAAAAAAA  C19 DNA Sedid Accession Lence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCATCT AGGGAAGTT CGAGTCAAAT TGGACAGGA TTATAGTGGA CCACGTTTCT CCTTCTTGTA ATTACCAGAT ACAAAACGGGA TCATCATACT ACTACTACAT ACTACAGAT ACAAAACGGGA TCACTGCATA   | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCCTG TAGTGGACCC TATATTCCAG CAACATATT AACAAGATCT GGGTCCAGTC CCAGTCAAG TGTCAATGCC TGTCAATCCGG AGCCATCTCAG AGCCATCTCAG CACATCTCAG CACATCTCAG CACATCTCAG CACATCTCAG CACATCTCAG CACATCTCAG CACATCTGTG  | 31   CGTAGCAAGA TTACAGAAAG TTTACAGAAAG CTGAAACCCA TTTAAGGCCA ACTCACAATC CCTATCACCA TACAGAAGGCT ACAGACCTGG CTTCCCATGA CTTACCCGAG ATCTCAGGAG ATCTCAGGAG ATCTCAGGAG   | 41<br>  GTCTCGACCA<br>GAATTTGAAT<br>TGCTTTATTT<br>TGACATTTCC<br>ATCCTCCTGC<br>TCCAGGTTGC<br>TCAGGTTGC<br>TAGAAGTGA<br>ATGATCCGGC<br>TCACAATGT<br>AGGACATGGG<br>TGACAGAGAA<br>TGACAGAGAA  | 51<br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TCTGTATTAC<br>AGCCTGGAC<br>GGACATCAAC<br>GAACTCTAC<br>CACTCCCAAT<br>CATGTACTTT<br>GGAATTGAAT<br>AGGCCAGAGT<br>TATTTGGAAA   | 60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>660<br>720<br>780<br>840  |
| 50<br>55<br>60  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequ  I AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG GCTAATGGAA GACAATCGAC CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCTGCTAAGA GAGAATCACA CCTGCTAAGA GAGAATTCCT GCACCAAAAAC   | AAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGGAG TITAACCACC AGGCCATCT AGGGGAAGTT CGAGTCAAAT GGGAGACAGA TGGACAGGGA TTATATGGA CCACGTTTCT CCTTCTTGTA ACAAAACGGG ATCCTTCCTA ACAAAACGGG ATCCTTCCTA CCATGATAC CCTGTGAAAC CTGTGAAAAC  | Quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCCTG TAGTTCCAG CAACATATTT AACAAGATCT AACAAGATCT CCAGTCAAAG TGTCAATCCAG CGATCTAATCCAG AGCCATCTCT TAATCTGGTG CACATCTGTG CACATCTGTG CACATCTGTG CACATCTGTG CACATCTGTG CACATCTGTG CACATCTGTG CGGTGAAAAA  | 31  CONTROL OF THE CO | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC GGGAGGGACT TCAGGTTGC TAGAAGTTGC TAGAAGTAC CAGTAAGGCA ATGATCCGGG TCAACAATGT AGGGATCTCA AGGACATGGG TGACAGAGAA TGACAGAGAA  | 51  CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TCTGACTTTT TCTGTATTAC AGCCCTGGAC GAACTCCCAAT CAGTACTTT GGAATTGAAT AGGCCAGAGT TATTTGGAAT AAGCCAGAGT TATTTGGAAAA CAAAATCACT  | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900   |
| 50<br>55<br>60  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  1  | AAAAAAAAAA  C19 DNA Sedid Accession Lence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCATCT AGGGGAAGTT CGAGTCAAAT GGGACAGGA TTATAGTGGA CCACGTTTCT CCTTCTTGTA ATTACCAGAT ACTAAAACGGG ATCCTTCCTA TCAGTGATAC CCTGTGGAGAT GGAATGATCC  | AAA quence n #: NM_004 .2619  21   ATACTCCAGT AATTTTGTGAC TCACTCCTG TAGTGGACCC CAACATATTT AACAAGATCT AACAAGATCT CCAGTCAAAG TGTCATCCAG AGCCATCTCT AACTCATCCG CGGTGCAACAC CGGTGCAACAC CGGTGCAACAC CGGTGCAACAC  | 31 CGTAGCAAGA TTACAGAAGA TGTCTTCTTA CTGAAACCCA GTGATAGAAC CCTATCACCA TACCAATC CCTATCACCA TACCAAGCCTGG CTTCCCATGG CTTCCCATGG ATTCCCTGAG TTCACAGGCT TATCACTGAC TATCACTGAC TATCACTGAC TATCACTGAC TATCATTAC  | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC GGGAGGGACT TCCAGGTTGC TAGAAGTGAA ATGATCAGGC TCAACAATGT TCACACATGGT TCACACATGGT TCACACAGGA TGACAGAGAA ATGACAGAGAA TGACAGAGAA TTTGACAAAGAT  | 51<br>  CTGAATGGAA<br>AAAGAAAACT<br>GGCAACTGGA<br>TATTTATGAA<br>TGTGACTTTT<br>TCTGTATTAC<br>AGCCCTGGAC<br>GGACATCAAC<br>GAACTCTCGC<br>CACTCCCAAT<br>CATGTACTTT<br>GGAATTGAAT<br>AGGCCAGAGT<br>TATTTGGAAA<br>CAAAATCACT<br>GAAGCTGCCA   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>660<br>660<br>720<br>780<br>840<br>900<br>960   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  1   GAAAGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG AACAGAGCCT ACAGGAAAC CCAGGAAAGC CCAGGAAAGC CCAGGTAATGAA CCTGCTAAGA GAGAATTCCT GCACCAAAAC CAGGTGCGGT AGATTCCCAT   | AAAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAAGTT CGAGTCAAAT GGGAACAGA TGACAGGGA TTATAGTGGA ATTACCAGAT ACTACAGAT ACAAAACGG ATCCTTCCTGTA ATTACCAGAT CCTTCTGTA TCAGTGATAC CTGTGAGAGT TCAGTGATAC CTGTGAGAGT TCAGTGATAC CTGTGAGAGT TTACAATTGA  | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTGTGAC TCACTCCCTG TAGTGGACCC TATATTCCAGT CAACACATATTT AACAAGATCT GGGTCCAATG TGTCATCCAG AGCATCTT TAATTCTGG AGCATCTT TAATTCTGG CACATCTGTG CACATCTG CACATCTGTG CACATCTG CACATC | 31 CGTAGCAAGA TTACAGAAAG TTACAGAAAG TTTAAGGCA TTTAAGGCA TTTAAGGCA ACTCACAATC CCTATCACCA ACAGACTGG CTTCCCATGA CTTACCCGAG ATCTCAGTGA ATCTACTAGCA TTACCCGAG TTACCCGAG ATCTCAGTGA GATATCATAG GATATTCATTAG  | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTC TGGGAGGGACT AGGGATGCA ATGATCCGGC TCACCATTT AGGGATCTCA AGGACATGGT TGACACATGT TGACACACATGT TGACACACATGT TGACACACATGT TGACACACATGT TGACACACATGT TGACACACACATGT TGACACACACATGT TGACACACACA   | 51  CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TCTGACTTTT TCTGTATTAC AGCCCTGGAC GAACTCCCAAT CAGTACTTT GGAATTGAAT AGGCCAGAGT TATTTGGAAT AAGCCAGAGT TATTTGGAAAA CAAAATCACT  | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900   |
| 50<br>55<br>60  | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  1  | AAAAAAAAAA  C19 DNA Sedid Accession Lence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCATCT AGGGGAAGTT CGAGTCAAAT GGGACAGGA TTATAGTGGA CCACGTTTCT CCTTCTTGTA ATTACCAGAT ACAAAAACGGG ATCCTTCCTA TCAGTGATAC CGGGAGATGATCC TTTCAATTGA ATTCAATGAT ATGCATATTCA TGGAAAATTCA   | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TAGTGGACCC CAACATATTT AACAAGATCT AACAAGATCT TGGGTCCAGT GGGTCCATCC TGTCATCCAG AGCCATCTCT TAATCTGGG GGTGGAAAA CCAGGAAGAA TTTTTATGCA TTTTATGCA TTTTATGCA  | 31 CGTAGCAAGA TTACAGAAAG TGTCTTCTTA CTGAAACCCA GTGATAGAAC CCTATCACCA TACCAAGC CCTATCACCA TACCAAGC CTTCCCATG CTTCCCATG CTTCCCATG CTTACCCGAG TACCAGTGA TACCAGTGA CTTACCTGAG ATCTCATGAC TATCCTTAG ATCTCATTAG TATTCCTTAG ATATTTACG ATATTTACG ATATTTACA   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC GGGAGGGACT TCCAGGTTGC TAGAAGTGAA CAGTAAGGCA ATGATCCGGC TGACACAATGT TGACACAATGT TGACACAAGGT TGACACAAGGA ATGATCAGGC ATGATCAGGC ATGATCAGCC ATGATCAGCC ATGATCAAGCA ATGATCAAGCA ATGATCAAGCA ATGATCAAGCA ATGATCAAGCC ATGATCAACC ATGATCAACC ATGATCAACC ATGATCAACC ATGATCAACC ATGATCACC ATGAT | 51  CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTT TCTGTATTAC AGCCCTGGAC GGACATCAAC GAACTCTCGC CACTCCCAAT CATGTACTTT AGGCCAGAGT TATTTGGAAA CAAAATCACT GAAGCTGCCA AAAACCACTT ACCTACACTT  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>840<br>900<br>960<br>1020   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding seq  I GAAAAGGACTGTT GAAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTGA ACAGAGCCT ACAGAAAAGGACC CCAGGAAAAG GGCCAGCTTT CAGATCACA CCTGCTAAGA GAGAATCCCA GCACCAAAAA CCTGCTAAGA GAGAAAAGG CAGGTGCGGT AGATTCCCAT GAAGAAAAAGG CAGGTACCAAT CCCGTCACCAG  | AAAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAACAGG TGGACAGGA TGGACAGGA TTATAGTGGA ATTACCAGAT ACTACAGAT ACTACAGAT ACTACAGAT TCAGTGATAC CCTTCTTCTA TCAGTGATAC TCAGTGATAC TCAGTGATAC TCAGTGATAC TTTCAATTGA ATTCAATTGA ATGCATATGT TGGAATTCA TTTCAATTGA ATGCATATGT TGGAATTCA TGGAATTCA  | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TAGTGGACCCC TATATTCCAG CACATATTT AACAAGATCT AGGTCCAATG TGTCATCCAG TGTCATCTGTG CACATCTTTG CGGTGCACAA CCAGGAAGGA TTTTTTATCAG TGTAAAAAGTT TGAGGTCCAG   | 31 CGTAGCAAGA TTACAGAAGA TGTCTTCTTA CTGAAACCCA GTGATAGGCA ACTCACAATC CCTATCACCA ACTCACCAGG ACTCACCAGG ATCTCCATGA ATCTACCGAG ATCTACCGAG ATCTCAGTGA GGTATTCATGA GATATTTACG GATATTTACG AAAGGATATTA  | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC ATCCTCGGC GGGAGGACT TCCAGGATTGC ATGATCACAATTT AGGGATCTCA AGGACATCGGC TCAACAATGT TGACAGAGAA TGACTCACCCAT TTGACAAAGA TGACTCAGCC ATGACTACGC ATGACTACGG ATGATTAATCC GACTGGGTAA  | 51  CTGAATGGAA AAGGAAACT GGCACTGGA TATTTATGAA TGTGACTTTT TCTGTATTAC AGCCTGGAC GGACTCCAC CACTCCCAAT CATGTACTTG GGAATTGAAT AGGCAGAGT TATTTGGAAA CAAATCACT GAGGTGCCA CTTGGACCGA AAAACCACTT ACTTACATG  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1180  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GACTAATGGAA GACTAATGGAA GACAATGGAC GACAAGAGCT CAGGAAGAG GGCCAAGATC CAGGAAGAT CAGGACTTT CAGATCAACA CCTGCTAAGA GAGAATTCCT GCACCAAAAC CAGGTGCGGT AGATTCCCAT GAAGAAAAG CAGGTGCGGT AGATTCCCAT AGATTCCCAT AGATTCCCAT AGATTCCCAT AGATTCCATACACACACACACACACACACACACACACACA   | AAAAAAAAA  C19 DNA Seid Accession Hence: 121.  11    CCCCGGGGGAG TITTAACCACC AGGCCATCT AGGGGAATCAAA TGGACAGGA TTATAGTGGA CCACGTTCT CCTTCTTGTA ACTATACCAGAT ACAAAACGGG ATCCTTCCTA TCATGATAC CTGTGGAGAT CTGTGGAGAT CTGTGGAGAT ACAAAACGGG ATCCTTCCTAT TCATGATAC TTGTGGAGAT TCATGATACC TTTCAATTGA ATGCATATTGT TGGAAATTGT TGGAAATTGT TGAAATTGT TAACCGTTATT  | AAA quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTTGGAC TCACTCCCTG TAGTGGACCC TATATTTCAG CAACATATTT AACAGATCT CCGGTCCAGTG GGCACTAG CACATCTCT TAATCTGGTG CACATCTCT TAATCTGGTG CCACGTGCACAA TTTTTATGCA CCAGGAAGGA TTTTTATGCA TGTAAAAGTT TGAGGGTCCAGG GGGACGAA TTTTTATGCA GGGTGCACAA TGTAAAAGTT TGAGGGTCCAGG GGGGACGAA TTTTTATGCA GGGTGACAAA CCAGGGAAGGAA TTTTTATGCA GGGTGCACAA GCAGTGCACAA TGTAAAAGTT TGAGAGGTCCAGG GGATGAAGGAA   | 31  CGTAGCAAGA TTACAGAAAG TTACAGAAAG TTTAAGCCA TTTAAGCCA TTTAAGCCA ACTCACAATC CCTATCACCA TACGAAGGCT ACAGACCTGG CTTCCCATGA CTTACCCAGG ATCTCACAGG TACTCAGGAG TCAACTGATCA CGTATCACAGG GGTATTACTGAGG TCAACTGATCA GGTATTACGAGG AATACTGACAGG AAAGATTACAG AAAGATTAACAGAACGAACAAAAACACAAAAAAAAAA   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC ATCCTCCTGC GGGAGGGACT TCACAGTTGC TCACCAATCT AGGGATCCAC AGGACCATCCA AGGACCATCCA AGGACCATCCA AGGACCATCCA AGGACCATCCA AGGACCATCCA AGGACCATCCA ATCACACCCCAT TTGACAAACA ATCACTCACCC ATGACTACCC ATGACTACCC ATGACTACCC ATGACTACCC ATGACTACCC ATGACTACCC ATGACTACCC ATCACTCACCC ATGACTACCC ATCACTCACCC ATCACTCACCC ATCACTCAC  | 51   CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTTT TCTGTATTAC AGCCCTGGAC GGACATCAAC GAACTCTOGC CACTCCCAAT ACGCCAGAT TATTTGGAAA CAGATTGAAT AGGCCAGAGT TATTTGGAAA CAAAATCACT GAAGCTGCCA AAAACCACTT ACCTACATGT ACGTACATGT CAGTATCAGG AAAATCACG   | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>840<br>900<br>1020<br>1080<br>1140<br>1260  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity I AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG CAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCTGCTAAGA GAGATTCCT GCACCAAAAC CAGGTGCGGT AGATTCCT GCACCAAAAC CAGGTGCGGT AGATTCCT CAGATACCA CCTCTTACTG ACCTTACTG ACCTTACTG ACTTACTG  | AAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAGAGTTTAACCACC AGGCCATCT AGGGGAACAGA TGGACAGGGA ATTATAGTGGA CCACGTTTCT CCTTCTTGTA ACTACAGAT ACAAAACGGG ATCCTTCCTA ACTAGTGATAC CTGTGATAC CTGTGATAGT GGAATGATCC TTCAATTGGA ATGCATATTGT TGGAAATTCA TGAAATTCA TAACCGTATTC TCACTGATAGT TCACTGATAGT TGGAAATTCA ATGCATATGT TGAACTGACAG AAACTCCCAA  | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATITITGTGAC TCACTCCAGT TAGTTGACC TATATTCCAG CAACATATIT AACAAGATCT AACAAGATCT TATCATCCAG GGTCCAGTC CAGTCATAG CACATCTCT TAATCTGGT CACATCTGTG GGTGGAAAAC TGTTAATCGGT CACAGAAGGA TTTTTTATGCA TGTAAAAGTT TGAGGTCCAG GGGTGCACAA CGGAGGAGAAA ACTTCCCATG  | 31  COTAGCAAGA TTACAGAAAG TTACAGAAAG TTACAGAAAC CTACAATC CCTATCACA TACGAAGCCTA CTCACAATC CTACACATC CTACACATC TACGAAGCT ACAGACTGA CTTACCAGA GATATCATAG GATATTACAG GATATTACAG GATATTACC GATATTACAG AATACTGCAAG AATACTGCAC GATACACC   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC TGACATTTTC TCGGGTTGC TGAGAGTTGC TCACAGTTGC TCACACATGG TGACAATGT TGACAAAGA TGACTCCACA TGACAAGAGAA TGACTCACCCCAT TTGACAAAGA TGACTCACCC ATGATTACC ATGATTACCA ATGATTACCA TCCCTATCACT TCCTAATCCA   | 51  CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTT TCTGTATTAC AGCCCTGGAC GGACATCCCAAT CATGTACTTC GGAATTGAAT AGGCCAGAGT TATTTGGAAT AGGCCAGAGT TATTTGGAAA CAAAATCACT GAAGCTGCCA CTTGGACCGA AAAACCACTT ACCTACATGT CAGTATCGGG AAACTACAGG AACTACAGG  | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200<br>1320                                   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding seq  1   AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG ACAGAGCGT ACCAGAAAC CCAGGAAAGC CCAGGAAAGC GGCCAGCTTT CAGATCAACA CCTGCTAAGA GACAAAAAC CCAGGTGCGGT AGATTCCCAT GCACCAAAAAC CAGGTGCGGT TCATATCGAC CCAGTAACAC ACCCTTACTG ATTGTGGAGC GGAATGTTACC  | AAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAAGTT CGAGTCAAAT GGGACAGGA TTATAGTGGA TTATAGTGGA ATCATCTCT CCTTCTTGTA ATTACCAGAT TCAGTGATACC CTTCTGTA TCAGTGATAC CTGGGAGAT GGAATGATCC TTTCAATTGA ATGCATATGC ATGCATATCA TGAAATTCA TGAAATTCA TGAAAATTCA TGACATATCA TAACCGTATTC CACATGACAAC AAACTCCCAA AAGTTAGCTAA   | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGGAC TCACTCCTG TAGTGGACCC CAGTCAAAG TGTCAATCC AGGTCCAATG TGTCATCCAG TGTAAAACTT TGAGGTCCAC TGGAAAACT TGAAAACTT TGAGGTCCAC TGGAAAACT TGAAAACTT TGAGGTCCAC ACAGTCCTTC   | 31 CGTAGCAAGA TTACAGAAGA TGTCTTCTTA CTGAAACCCA GTGATAGGAAC ACTCACAATC CCTATCACCA TACGAAGCCT ACAGACCTGG CTTCCCATGA CTTCCCATGA GATATCATAG GATATCATAG GATATCATAG GATATCATAG GATATTTACG GATATTTACG GATATTTACG GATATCATAG GATATTTACG GATATTTACG GATATTTACG GATAGATCACAGA AATACTCCCAG AAAGATATTA   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC ATCCTCCTGC GGGAGGACT TCCAGGTTGC TAGAAGTGAA AGGATCTCA AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCCCAT TTGACCAAGAA TAGATCAGCC ATGATCAGC GACTGGGTAA ACAGTTTTCT GACTAATCCA ACAGTTTTCT ACAGTCCCCAT ATCATCCCCA ATTACTCCTCA  | 51  CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTTT TCTGTATTAC AGCCTGGAC GAACTCTGGC CACTCCCAAT CATGTACTTT AGGCATGAAT AGGCCAGAGT TATTTGGAAA ACAAATCACT GAAGCTGCCA CTTGGACCGA AAAACCACTT ACCTACATGT CAGTATCAGG AAACTACTG CAGTATCAGG AACTACAGG AACCTACTG GTACAACTTA  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>660<br>660<br>720<br>780<br>840<br>900<br>900<br>1020<br>1020<br>1140<br>1260<br>1380  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequence  1  | AAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAG TITAACCACC AGGCCCATCT AGGGGAAGTT TGGAATCAGA TGACAGGGA TTATAGTGGA ATTATACTGAA ATTACCAGAT ACAAAACGG ATCCTTCCTA TCAGTGATAC TGAATTGAAT   | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCCTG TAGTGGACCC TATATTCCAGT CACACCAGTCAATC CCAGTCAAAG TGTCAATCCCAGT GGGTCCAATC TGTCATCCAG AGCCATCTCT CAGTGGAACAA CCAGGAACGA TTTTATCCAG CCGGTGCACAA CCAGGAACGA TTTTATACCA CGGTCCACA CCAGGAACGA TGTAAAAGTT TGAAGACT TGAAAAGTT TGAAGACTAA ACTTCCCATC ACAGTCCTCAA  | 31 CGTAGCAAGA TTACAGAAAG TGTCTTCTTA CTGAAACCCA GTGATAGGCA GTGATAGGCA ACTCACAATC CCTATCACCA ACAGACCTGG CTTCCCATGA ACTCACTGAG ATTCCATGAG ATTCCATGAG ATTCCATGAG ATTCCATGAG ATTCCATGAG ATTCCATGAG GATATTTACG GATATTTACG AAAGAATTAAG AAAAGAACAAG  | 41    GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTCC ATCCTCCTGG GGGAGGGACT TCCAGGTTGC TAGAAAGTGAA ATGATCCGGC TCAACAATGT AGGGATTGCG AGGACATGGG TGACACAGAGAA TGACTCAGCC ATGACTACGG ATGATTACCG ATGATTACCG ATGATTACCG ATGATTACCT TCTAATCCA ATACTCCTCCA ATGATCCACAT TTGTGCAAAT TTGTGCAAT TTGTGCAAAT TTGTGCAAAT TT | 51    CTGAATGGAA AAAGAAAACT GGCACTGGA TATTTATGAA TGTGACTTT TCTGTATTAC AGCCCTGGAC GGACTCCAAT CATGTACTTT GGAATTGAAT AGGCCAGAGT TATTTGGAAA CAAATCACT CAAGGTCGCA CTTGGACCGA AAAACCACTT ACCTACATGT CACTACATGT CACTACATGT CAGACTGAC AAACTACAGG AACCTATGCT GTACAACTTA CAACGTTATT CACACTTAT CACACTTAT  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>840<br>900<br>1020<br>1080<br>1140<br>1260<br>1320<br>1320   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity I AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTG GCAAATGGAC GCAAATGGAC GGCCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCTGCTAAGA GAGAATTCCT GCACCAAAAAC CAGGTGCGGT AGATTCCTG AATTCCTG AATTCCTG ATTGTGGAGC GGAATGTTAAC ACGATAGAGG GGAATGTTAAC ACGATAGAGG GGAATGTTAAC ACGATAGAGG GGATATCAATG   | AAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAGATTTAACCACC AGGCCATCT AGGGGAACAGA TGGACAGGGA ATTATAGTGGA CCACGTTCTTGTA ATTACAGAT ACAAAACGGG ATCCTTCCTA ATCAGTATC CTTCAATTGA ATGACATAGT TGAAATTCA TAACCGTATT TCACATTGA ATGACATAGT CACATAGCAG AAACTCCCAA AGGTAACCAA AGGTAACCAA AGGTAACCAA AGGTAACCAA AGGTAACACAA AGGTAACACAA AGGTAACACAA AGTTAGCTAAA ATGACTACAA ATGACACACAA AGTTAGCTAAA ATGACTACAA AGTTAGCTAAA ATGACTACAA   | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCAGT TAGTTCCAG CAACATATTT AACAGGATCT CCAGTCAAAG TGTCAATCCAG AGCATCTCT TAATCTGTGAC CCAGTACAAG TGTCAATCCAG AGCATCTCT TAATCTGTG CCAGGAAGAA TTTTTATCGAG TGTAAAAGTT TGAAGTCCAG GGATCAAAG TGTAAAAGTT TGAAGTCCAG GGATGAAAAG ACTTCCCATC ACAGTCCTTG ACAGTTCCAG AGATTCCAG AGATCCTTTGAA   | 31  COTAGCAAGA TTACAGAAAG TTACAGAAAG TTTAAGGCA GTGATAGAACC CCTATCACA TACGAAGC TACGAAGC TACGAAGC TACGAAGC TACGAAGC TACGAAGC TACCAAGA CTTACCAGA CTTACCAGA GATATCATGA GATATTACG GATATTACG GATATTACG AATACTGCA AATACTGCA AATACTGCA GATGGCAC GATGGCACC AAGACGCAG AATACTGCCA GATGGCACC AAGACGCAG AACCTTGTT AAATCAGATT  | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC TGACATTTTC TGGGGGGGGACT TCAGGGTTGAC ATGATCCGGC TCAACAATGT AGGGATCTCA AGGACATGAC TGACCAGAAA TGACCAGACA TGACCAGACA TGACTAGCC ATGATCAGCC ATGATCAGCC ATGATCAGCC ATGATCAGCC ATGATCAGCC ATGATCAGCA ATGATCAGCC TCCTCAATCCC ATACTCCTCA ATACTCCTCA ATGCTCAAAACA ATGGGAAAACA ATGGGAAAACA ATGACTCACCA ATACTCCTCA TTGTGCAAAT ATGGAAAACCT  | 51    CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTATGGAA TGTGACTTT TCTGTATTAC AGCCCTGGAC GGACATCCCAAT CAGTCACC GAACTCTCGC CACTCCCAAT AGGCCAGAGT TATTTGGAAAA CAAATCACT GAAGCTGCCA CTTGGACCGA AAACACCATT ACCTACATGT CAGTATCGGG AACCTACAGGT AACCTACAGGT AACCTACAGGT AACCTACAGGT CAGGTATTTG GAACTTATCAGGT CAACGTTATT GACTCTTGCT GACCTTTGT CAACGTTATTT GACTCTTGCT  | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1080<br>1140<br>1260<br>1320<br>1380<br>1480                          |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity I AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAC GAACTAACTG ACAGAGAC CCAGGAAAGC CCAGGAAAGC GGCCAGCTT CAGATCAACA CCTGCTAAGA CCAGGTCGGT AGAATCCCAT GAACAAAAC CAGGTCGGT AGATTCCCAT GAACAAAAC CAGGTGCGGT AGATTCCCAT GAACAAAAC CAGGTGCGGT AGATTCCACAAAAC CAGGTGCGGT AGATTCCACAAAAC CAGGTGCGGT AGATTCCACAAAAC CCGTCACCAG ACCCTTACTG GGAATGTTAC ACGATACAAGG GGAATGTTAC ACGATACAAGG GAATACAAAGG GAATACAAAGG GAATACAAAGG GAAAAACG ACACAAAAC ACGATACAAGG GGAATGTTAC ACGATACAAGG GAAAAACCAAA   | AAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCATCT AGGGGAAGTT CGAGTCAAAT GGGACAGGA TTATAGTGA CCACGTTCT CCTTCTTGTA ATTACCAGAT ACTACAGAA ACCATATCA TGGAATGATAC CTTCATTATAGA ATCATATGA TGGAAATTCA TAACCGTATT CACATGACAG AAACTCCCAA AGTTAGCTAA AGTTAGCTAA AGTTAGCTAA ATCAGATCCCAA ATTAGATACA ATCAGATCCCAA ATTAGGTACA ACATTGGGTCA   | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TAGTGGACCC CAACATATTT AACAAGATCT AACAAGATCT TGGGTCCAGT GGGTCCAGT CCAGTAAAG TGTCATCAG CACATCTTC CGGTGCACAA CCAGAAGAA TTTTTATGCA TGTAAAAGT TGAGAAGAA ACTTCCATC ACAGTCCAG ACAGTCTTG ACAGTCTTTG ACACTCTTTG ACACTCTTTG CACCATCTTTG CACCATCTTT CACCATCTTT CACCATCTTT CACCATCTTT CACCATCTT CACCATCTT CACCATCTT CACCATCTT CACCATCTT CACCATCTT CACCATCTT CACCATCTT CACCATCT CACCATC CA | 31 CGTAGCAAGA TTACAGAAGA TGTCTTCTTA CTGAAACCCA GTGATAGAAC ACTCACAATC CCTATCACCA TACGAAGCCT ACAGACCTGG CTTCCCATGA CTTACACGAG ATTCACAGA ATTCACTGAG ATTCACTGAG ATTCACTGAG ATTCACTGAG ATTCCTTAG GATATTACG GATATTTACG AAAAGCAAGG AAAGAATGAAC AATACTGCCA GATGGACTCTTGTTG AAGAAGCAAGG ACCTTTGTT AAACCGATT AAATCAGATT AAATCAGATT AAACCAGATT AAACCAGATT AAACTAGATT AACCTCCAGG   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC ATCCTCCTGC GGGAGGACT TCACAGTTTG CAGTAGACAATGAT AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCA ATGACAAGAGA ACAGTTATCC GACTGGGTAA ACAGTTTCC TCCTAATCCC ATACCCCAT TTGCCAAATC ATACCCCCAC TTGTGCAAAT ACAGTTTCCC ATACCCCCAC TTGTGCAAAT ATGACACCCCAC TTGTGCAAAT ATGACACCCCAC ATACCCCCAC ATACCCCCACTGATCCC CCACTGATCCC CCACTGATCC CCACTGATCC   | 51    CTGAATGGAA AAAGAAAACT GGCACTGGA TATTTATGAA TGTGACTTT TCTGTATTAC AGCCCTGGAC GGACTCCAAT CATGTACTTT GGAATTGAAT AGGCCAGAGT TATTTGGAAA CAAATCACT CAAGGTCGCA CTTGGACCGA AAAACCACTT ACCTACATGT CACTACATGT CACTACATGT CAGACTGAC AAACTACAGG AACCTATGCT GTACAACTTA CAACGTTATT CACACTTAT CACACTTAT  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>840<br>900<br>1020<br>1080<br>1140<br>1260<br>1320<br>1320   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity I   AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GACTAACTG GACAAGAAC GAACTAACTG GCCAAGAAGC CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCAGGAAGC CCAGGAAGC CCTGCTAAGA GAGATTCCAT GAAGAAAAC CAGGTGGGT AGATTCCCAT GAAGAAAAGG TCATATCCGC ACCTTACTG ATTGTGGAGC GGAATGTTACC GAAGACACAA TTTACTGGGA TTTACTGGGAC GGGGTTGACA GGGGTTGACA GGGGTTGACA GGGGTTGACAG GGGTTGACAG GGGGTTGACAG G | AAAAAAAAA  C19 DNA Seid Accession  lence: 121.  11    CCCGGGGGGAG  TITTAACCACC  AGGCCATCT  AGGGGAACAT  TCGAGTCAAAT  GGAACAGGA  ATTATCAGTGA  ACCAGATT  ACAAAACGGG  ATCCTTCCTA  ATGACAGAT  ACAAAATCCAGAT  TAACCGTATT  TCACATGATAC  TAACCGTATT  CACATGACAG  ATGTCACAGAT  AGAAATCCCAA  AGTTAGCTAA  TAACCGTATC  TAACCGTATC  AGTTAGCTAA  TATCCTACAG  AGTTAGCTAA  TGTCTGACAA  TGTCTGACAA  TGTCTGACAA  TGTCTGACAA  CGTTCTAAAAAI  CCGGTTCTAAAAAI  CCGGTTCTAAAAAI  CCGGTTCTAAAAAI  CCGGTTCTAAAAAI  CCGGTTCTAAAAAI  CCAGATCCCCCC  | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGGAC TCACTCCAG TAGTTCCAG TAGTTCCAG CAACATATTT AACAGACATCT CCAGTCAAAG TGTCATCCAG AGCATCTCT TAATCTGGAC CAGTCAAAG TGTTAATCGAG CACGTACAAA TGTTAATCGAG CAACATCTT TGAGTCCAG GGTGCACAA ACTTCTCAG AGCATCTTT TGAGGTCCAG ACATCTTT TGAGTTCCAG ACATCTTT AACAGTCCTT AACAGTCCTT CACGCACAC ACATCTTT AGCACACACC CCACATCTTT TTCTTATCCAG CCACCATCTTT TTCTTATCCAC   | 31  CGTAGCAAGA TTACAGAAAG TTACAGAAAG TTTAAGCCA TTTAAGCCA GTGATAGAAC CCTATCACA TACGAAGC TACGAAGC TACGAAGC TACGAAGC TACGAAGC TACCAAGA CTTACCAAGA CTTACCAAGA CTTACCAAGA CTTACCAAGA CTTACCAAGA CATTACAGAG GATATTACG GATATTACG GATATTACG GATAGATCAAG AATACTGCAA GATGACTCT AAAGACCAAG ACCATCTTGTT AAATCAGATT ACCATCCAGG ACCATCTAGT AAATCAGATT ACCATCCAGG CACCATCAGG CA | 41   GTCTCGACCA GAATTTGAAT TGCTTTATT TGACATTTTC ATCCTCGG GGGAGGACT TCACAGTTGA CAGTAGC CAGTAGC ATGATCCGC ATGATCCGC ATGATCCGC ATGATCAGC TGACAAGA TGACAAGA TGACAAGA ATGATAACC ATGATCAGCC ATGATTACCA ATGATTACC ATGATTACCA ATGATTACC ATTACTCCTC ATTACTCAATC ATGACAAGA ACAGTTTTCI TCCTAATCCA ATGATACCC ATGACTCAGC ATGACTACC ATGACAACA TGACACACC CCACTGATCC GAGACAGTCG TAATTAAAAA   | 51    CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTT TCTGTATTAC AGCCCTGGAC GGACATCCCAAT CAGTACTTT GGAATTGAAT AGGCCAGAGT TATTTGGAAA CAAATCACT GAAGCTGCCA AAAACCACTT ACCTACACG AAAACCACTT CAGTATCAGG AAAACCACTT CAGTATCAGG AACTTACAGG AACTTACAGG AACTTACAGG AACTTACAGG CAACGTTATT GACTCTTGCT TGATGACCCT TGATGACCTA CAAGGTTATT GACTCTTGCT TGATGACCCTA GGGACGCCTG GGCACGCCTGAT  | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>660<br>660<br>720<br>780<br>840<br>960<br>1020<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560                         |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity I AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAC GAACTAACTG ACAGAAACG CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCTGCTAAGAA CCTGCTAAGA ACAAAACC CAGGTCGGT AGAATCCCAT GAACAAAAC CAGGTCGGT AGATTCCAT GAACAAAAC CCGTCACCAG ACCCTTACTG ACCGTACCAG ACCTTACTGGACACAC ACCTTACTGGACACACAC ACTTTTGGGAGC GGAATGTTAC ACGATAGAGG GGATATCAGG GATATCCAGT TTTGGAACACAC TTTACTGGAAC CTTTGGAACACAC TTTGAAACAG   | AAAAAAAAA  C19 DNA Sedid Accession  lence: 121.  11    CCCGGGGGAG TITAACCACC AGGCCATCT AGGGGAAGTT CGAGTCAAAT GGGACAGGA ATTATAGTGAA CCACGTTTCT CCTTCTTGTA ATTACCAGAT ACAAAACGGG ATCCTTCCTA TCAGTGATACC CTGTGGAGAT GGAATGATCC TTTCAATTGA ATTACATGATACC ACATGACAC AAACTCCCAA AGTTAGCTAAT CAGATCACCAA AGTTAGCTAAT CAGATCACCAA CAGATCACCAA CACTTGACCAC ACATTGACCCCAC CAGCTGTTTCC CCAGCTGTTTCC CCCCCCC CCAGCTGTTTCC CCCCCCC CCAGCTGTTTCC CCCCCCC CCCCCC CCCCCC CCCCCCC CCCCCC   | Quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TAGTGGACCC TATATTCCAG CAACATATTT AACAAGATCT TAGTGATGCC TGTCAATCG AGCCATCTCT TAATCTGGG CGTGGAAAGA TTTTTATGCA CGGTGCACAA CGGTGCACAA CGGTGCACAA CGGTGCACAA CGGTGCACAA CGGTGCACAA CCAGGAAGGA CTGTACAACCC CAACATCTTG CGGTGCACAA CCAGGAAGGA CCAGGAAGGA CCAGGATCACAC CCAGGATCACAC CGGTGCACAA CCTGTGCACAA CCTGTTGAAAGTT TGTAAAAGTT TGTAAAAGTT TGTAAAAGTT CGGTGCACAC CGACTCTTGA CACCTTTGAA CCTCTTTGAAACCC CAACATCTTT   | 31  CGTAGCAAGA TTACAGAAAG TGTCTTCTTA CTGAAACCCA GTGATAGAAC GTGATAGAAC CCTATCACAA TACCAAGC TACCAAGC TACCAGGC TAATACTGCC TATTCCTTAG GATATTTACG GATATTTACG GATATTTACG GATATTTACG TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCATCAGGC TACCATCAGGC TACCATCAGGC TACCATCAGGC TACCATCAGGC TACCAGGC TACCATCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TACCAGGC TTCAAAGCCAGC TTCAAAGCCAGC TTCAAAGCCAGC TTCAAAAGCAGC TTCAAAAGCCAGC TTCAAAAGCCAGC TTCAAAAGCCAGC TTCAAAAGCCAGC TTCAAAGCCAGC TTCAAAAGCCAGC TTCAAAAGCAAGCAAGC TTCAAAAGCCAGC TTCAAAAGCAAGCAAGC TTCAAAAGCAAGCAAGCAAGC TTCAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC ATCCTCCTGC GGGAGGGACT TCCAGGTTGC TCAACAATGT AGGCATCCCAC AGGACATCGG TGACAGAGAA ACACTCAGC ATGATCAGCC ATGATAATCC GACTGGTAA ACAGTTTCT TCCTAATCCCA TTGCAAATGT TCCTAATCCCA TTGCAAATGT TCCTAATCCC ATTATCCAGC ATTATCAGC ATTATCAG | 51  CTGAATGGAA AAGGAAAACT GGCAACTGGA TATTTATGAA TGGACTTTT TCTGTATTAC AGCCCTGGAC GGACATCAC GGACATCAC GAACTCTGGC CACTCCCAAT AGGCCAGAGT TATTTGGAAA CAAATCACT GAAGCTGCCA CTTGGACCGA AAAACCACTT ACCTACATGT CAGTATCGG AACTACACT GAACTACTC GAACGTTATT CGACTTTCCC GTACACTTT CAGTATCGGG AACTACTCC TGATGACCCA TTGACCCA TTGGACCCA TTGGACCCA TTGGACCCA TTGGACCTC TCGTACACTTT CACTTTCCT TGATGACCCA GGCACCCTC TGATGACCCA GGCCTCTGGT GCCTCTTGGT   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>660<br>660<br>660<br>1020<br>1080<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560<br>1620<br>1620                              |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | AAAAAAAAA  Seq ID NO: Nucleic Ac: Coding seq  1   AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAAC GAACTAACTGA ACAGAGCGT CCAGGAAAC CCAGGAAAC CCAGGAAAC CCAGGAAAC CCAGGAAAC CCAGGAAAC CCAGGAAAC CCAGCTATC GCACCAAAAC CCAGTTACTGG ACCATTACTGG ATTGTGGAGC ACCTTACTGG ATTGTGGAGC GGAATGTTAC ACGATAGAGG GGAATGTTAC ACGATAGAGG GTAATCACA TTTACTGGGAC GGAATGTTAC TATGTGGAGC GGAATGTTAC TATGTGGAGC GGAATGTTAC TATGTGGAGC GTAACACA TTTGAACAG TTTGGTGTGA   | AAAAAAAAA  C19 DNA Seid Accessionence: 121.  11    CCCGGGGGAG TTTAACCACC AGGCCCATCT AGGGGAAGTT CGAGTCAAAT GGGAAAGGA TTATAGTGGA TTATAGTGGA ATTATAGTGGA ATTACTAGTATAC CTTCTTCTA ATTACTAGTATAC CTTCTTCTA TCAGTATAC CTGGAAAT GGAAATGATCC TTCAATTGA ATGCATATGA ATGCATATGA TGAAAATCACAGAT CACATGACAG TGACATGACA  | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCTG TAGTGGACCCC GAACATATT AACAAGATCT AGGTCCAGT AGGTCCAGT TGTCATCCAG TGTCAATGCC TGTCAATGCC TGTCAATCCC TAATCTCTCC TGGTGCACAA CCGGTGCACAA CCGGTGCACCAA CCGGTGCACCAA CCGTCCTTC TGGTTCCCTC TGCACCTCC TCCCATCTTC TCTCTTTCCTTCC TCTCTTTTTTTCTCTTTTTT   | 31  CGTAGCAAGA TTACAGAAGA TGTCTTCTTA CTGAAACCCA GTGATAGGAA ACTCACAATC CCTATCACCA ACAGACCTGG ACAGACCTGG ACTCACCAGG ATTTCATAGGCA ACTTACCGAG ATTTCATAGG ATTTCATAGG ATTTCATAGG ATATTTACG AAATGATTTACG AAAAGCAAG AAATCACATT AACAATGATC AAATCACATT AACAATGATC AAATCACTT AAGAAGCAAG ACCTTTCTTAG ACCTTTCTTAG AAATCACATT AACAATGATC AAATCACATT AACAATGATC AAATCACATT AACATGATC AACTCAGG ACCTTTCTAAAGGCAG TTCAAAGGCAG GCCAAGTTCA   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC TGACATTTTC GAGGGGACT TCCAGGTTGC TAGAAGTGAA AGGACTCCA AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCA AGGACATCCA ATGACTCAGCC ATGACTCAGCC ATGACTCAGCC ATGACTCAGCC ATGACTCAGC ATGATTCCT TCCTAATCCA ATGACACCT TTGTGCAAAT ATGGAAACCT CCCACTGATGC GAGAACCT TATTTAAACAA AAAATCCTCA CCACTGATGC GAGAACATTAAACAA AAAATCCTCA CGCTTATTCI C | 51    CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTTT TCTGTATTAC AGCCTGGAC GGACTCTGGC CACTCCCAAT CATGTACTTT GGGAATTGAAT AGGCCAGAGT TATTTGGAAA AGGCCAGAGT TATTTGGAAA ACTACTC CAGTATCACT CAGTATCACT CAGTATCACG AAACTACACT CAGTATCACG AACTACACG CTTGGACCGA CACTATCCC CAGTATCACG CAGTATCCG CACTCTTCAT CACTCTTCAT CACTCTTCACTTT GACCTCTTCAT CACGTCTTCAT CAGGACCCT GGCCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCCTCTTGAT   | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>660<br>660<br>6720<br>780<br>840<br>900<br>900<br>1020<br>1140<br>1200<br>1380<br>1440<br>1560<br>1560<br>1620<br>1680<br>1780 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity I AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GACTAACTG GACAAGAGCCT GCTAATGGAA GACAATCGAC CCAGGAAAGC CCAGGAAAGC CCAGGAAGC CCAGGAAGC CCTGCTAAGA AGATTCCCAT GAAGAAACC CCGCTACCAG AGATTCCCAT GAAGAAAAG TCATATCGGC GCACTTACGA ATTGTGGAGG GTAATTCATG ATTGTGGAGC GTAATTCATG ATTGTGGAGC GTAATCAGC CTTACTG ATTGTGGAGC GTATCTGAATTCAGC ACGATACAGG GAATTTCAGC CGGGTTGACA TTTGGTGGACA TTTGGTGGACA TTTGGTGGACA TTTGGTGGACA TTTGGTGGTGA AATGAAGCCAC   | AAAAAAAAA  C19 DNA Seid Accession  lence: 121.  11    CCCGGGGGGAG  TITAACACC  AGGCCATCT  AGGGGAACAGA  TGAACAGGA  TGACAGGGA  CCACGTTCTGTA  ATTACCAGAT  ACAAAACGGG  ATCCTTCCTGTA  ACAAAACGGG  ATCCTTCCTA  TCAGTGATAC  CTGTGGAGAT  CTGTGGAGAT  CTGTGGAGAT  CTGTGAATTCA  TAACCGTATTC  CACATGACAG  AGTTAGCAA  TGCTGACAA  TGCTGACAA  CTGTGGACAC  CGTTCTAAAAT  CAGATCCCCA  AGTTACCCCCC  CAGTTTTTC  CAGTTCCCCCC  CAGTTCTTTCC  CCCCAATTTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTTCC  CCCCAATTCC  CCCCCAATTCC  CCCCCAATTCC  CCCCCAATTCC  CCCCCAATTCC  CCCCCAATTCC  CCCCCAATTCC  CCCCCAATTCC  CCCCCC  CCCCAATTCC  CCCCCC  CCCCAATTCC  CCCCCC  CCCCAATTCC  CCCCCC  CCCCAATTCC  CCCCCC  CCCCC  CCCCC  CCCCCC  CCCCC  CCCC  | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTTGGAC TCACTCCAGT TAGTTCCAG TAGTTCCAG CAACATATTT AACAGATCT CCAGTCCAAG GGATCCAG AGCATCTCT TAATCTGGG CACATCTTT TGAGCACAG CACATCTTT TGAGCTCCAG GGAGAAAAC CCAGGAAGGA TTTTTATCCAG GGATGACAGA CCAGGACAGT TATTTCAG CACATCTTT TGAGGTTCCAG AGATTCTT AACAGTCTTT TGAGTTCCAG AGATTCTT TTAGCAACACC CAACATCTTT TTAGCAACACC CAACACGTT TTAGCAACACC CAACACGTT TTAGCAACACC CAACACGTT TTAGCAACACC CAACACGTT TTCCCAACACCGTT CCCAACACGTT CCCAACACGTT CCCAACACGTT CCCAACACGTT CCCAACACGTT CCCAACACCGTT CCCAACACGTT CCCAACACCGTT CCCAACACCCT CCCAACACCGTT CCCAACCT CCCACCT CCCAACCT CCCAACCT CCCAACCT CCCAACCT CCCAACCT CCCAACCT CCCAACC CCCACCT CCCAACCT CCCACCC CCCACCT CCCACCT CCCACCT CCCACCT CCCACC CCCACCT | 31  CGTAGCAAGA TTACAGAAAG TTACAGAAAG TTACAGAAAG TTAAGCCA GTGATAGAAC CCTATCACA TACGAAGGCT ACAGACCTGG CTTCCCATGA CTTACCAGAG CTTACCAAGA CTTACCAAGA CTTACCAAGA CTTACCAAGA CTTACCAAGA CTTACCAAGA CTTACCATGA CATACTCAAGA GATATTACAG GATATTTACG AATACTGCAAG AATACTGCAAG ACCTTTGTT AAATCAGATT AACTCAAGG CACCATCTAGT AAATCAGATT AACTCAAGC CACCAAGTTCAAG CACCAAGTTCAAGG CACCAAGTTCAAGC CACCAAGTTCAAGC CACCAAGTTCAAGC CACCAAGTTCAAGC CACCAAGTTCAAGC CACCAAGTTCAAGC CACCAAGTTCAAGCCAAGTTCAACCAAGTTCAAGCCAAGTTCAAGCCAAGTTCAACCAAGTTCAACCAAGCCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGCCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCAACCAAGTTCCAAGTTCCAAGTTCCAAGCCAAGTTCCAAGTTCCAAGCCAAGTTCCAAGTTCCAAGTTCCAAGTTCCAAGTTCCAAGTTCAAGCCAAGTTCAAGCAAG  | 41   GTCTCGACCA GAATTTGAAT TGCTTTATT TGACATTTTC ATCCTCGGGGGGGCT TCACGGTTGC ATGATCCGGC ATGATCCGCC ATGATCCGCC ATGATCAGCC ATGATCACCC ATGATCACCC ATGATCACCC ATATCCCTCATCC ATACTCCTCAATCCC ATACTCCTCAATCCC ATACTCCTCAATCCC ATACTCCTCAATCCC ATACTCCTCAATCCC ATACTCCTCAATCCC ATACTCCTCAATCCC CCACTGATCC CCACTGATCC CACCTGATCC TACTTATTGT AAATCCTCTC CCCTTATTGT AAATCCTCTC CCCTTATTGT AAATCCTCTCC CCCTTATTGT AAATCCTCCC CCCTTATTGT AAATCCTCTCC CCCTTATTGT AAATCCTCCC CCCTTCTCC CCCTTCC CCCTTCTCC CCCTTCC CCCTT | 51    CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTT TCTGTATTAC AGCCCTGGAC GGACATCCCAAT CAGTACTAT AGGCCAGAGT TATTTGGAA CAGATCACT GAACTCCCA AAAATCACT GAAGCTGCCA AAAACCACTT ACCTACAGT ACCTACAGG AAACTACAGG AACTACAGG AACTACAGG AACTACAGG CAGATTATT GGCTACACTT TGATGACCT TGATGACCT TGATGACCT TGATGACCT TGATGACT CAGGGACCT TGATGACCT TGATGACT TGATGACCT TGATGACCT TGATGACT TGATGACCT TGATGACCT TGATGACCT TGATGACCT TGATGACT TGATGACCT TGATGACT TGATGACCT TGATGACT TGATGACT TGATGACCT TGATGACT TGATGACCT TGATGACT TGATGACCT TGATGACT TGATGACT TGATGACCT TGATGACT TGATGACCT TGATGACT TGATGACCT TGATGACT TGATGACT TGATGACCT TGATGACT TGATC TGATGAC | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>900<br>1080<br>1140<br>1200<br>1320<br>1340<br>1500<br>1560<br>1620<br>1680<br>1740<br>1880 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | AAAAAAAAA Seq ID NO: Nucleic Ac: Coding sequity I AGGGAGTGTT GAAAAGGACT ATGATACTTC TATGGCCAAG GGCCAAGAC GAACTAACTG AACAGAGCTT CAGATAGACA CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCAGGAAAGC CCTGCTAAGA GAGATTCCT GCACCAAAAC CAGGTCCGGT AGATTCCCAT AATGAGAAAAGG ACCTTACTG AACACAAAAC CCGTCACCAG ACCTTACTG AATGTGGAGC GGAATGTTAC ACGATAGAGA CCTTACTG ATGTGGAGC GAATTCATG GAAGACCAA TTTACTGGGAC TTTGTGTGGAC ATTGGTTGAA AATGAAGCAC ATAGGCACTA   | AAAAAAAAA  C19 DNA Sedid Accession  lence: 121.  11    CCCGGGGGAG TITAACCACC AGGCCATCT AGGGGAACAGA TGGACAGGGA ATGATCAAAT GGAATCGATTCT CCTTCTTGTA ATTACAGAT ACAAAACGGG ATCCTTCCTA TCAGTGATAC CTGTGATATCA TCAGTGATAC GGAATGATCC TTTCAATTGA ATGACATATGT TGGAAATTCA TAACCGTATTC TAACCGTATTC TAACCGTATTC CACATGACAG AAACTCCCAA AGTTAGGTACAC CACATGACAC CACATGACCCC CACATGACAC CACATGACCCC CACATGACCC CACATGACCC CACATGACCC CACATGACCC CACATGACCC CACATGACCC CACATGACCC CACATGACC CACATGAC CACATGACC CACATGACC CACATGACC | AAA  quence n #: NM_004 .2619  21   ATACTCCAGT ATTTTGTGAC TCACTCCAGT TAAGTGGACC CAACATATTT AACAGGATCT CAGTCAAGA GGTCAAGA AGCATCTCT TAATCTGGG CACACTCTGTG GGTGGAAAA CCAGGAAGA TTTTTATGGA TGTAAAAGTT TGAGGTCCAG GGATGAAAAGT TGTAAAAGTT TGAGGTCCAG ACATCTTG CAACACCTCT AAGTTCTCAG AGATTCATCAG CAACACTCTTG CACACACTCTTG CACACACTCTTG CACACACCT CAACACCGT CAACACCGT CAACACCGT CAACACCGT CAACACCGT TGTGACTCCCC CAACACTCTCC CAACACCGT TGTGACTCCC TGTGACACCCC CAACACTCTCC TGTGACTCCC TGTGACACCCC TGTGACACCCC TGTGACTCCCC TTTTGACTCCCC TTTTTTTTTT   | 31  COTAGCAAGA TTACAGAAAG TTACAGAAAG TGTCTTCTTA CTGAAACCCA GTGATAGAAC CACTCACAATC CCTATCACA TACGAAGGCT ACAGACCTGG CTTCCCATGA CTTACCAGAG TCAAGACTGAT CAGAACTGATC TATTCCTTAG GATATTACAGA GATATTACAGA GATATTACAG GATACTCAAG GATACTCAG AAAGATTACAG AACATCTCT AAATCAGACT AAATCAGCAG CGGATATGTCA CGGATATGTCAGG CACCATCTGTT AAATCAGACT CACCATCAGG CACCATCAGG CACCATCAGG CACCAAGGCAAG CGCAAGTTCAG TTCAAAGCAG CACCACCAGG CACCAAGGATCCAG CACCAAGAAAGAACAACAAAAAAAAAA   | 41   GTCTCGACCA GAATTTGAAT TGCTTTATTT TGACATTTTC ATCCTCCTGC GGGAGGGACT TCCAGGTTGC ATGACAATGT AGGACATGGG TGACAATGT TGACAAGGA ATGATCAGGC ATGACTAGGGACATCGG ATGACTAGGGACATCGG ATGACTAGCG ATGACTACCG ATGACTACCG ATGACTACCG ATGACTACCG ATGACTACCG ATGACTACCG ATGACTACCC ATGACTACCG ATGACTCCG ATGACTACCG ATGACTACCC ATGACTACC ATGACTACCC ATGACTACC ATGACTACCC ATGACTACC ATGACTACCC ATGACTACC | 51    CTGAATGGAA AAAGAAAACT GGCAACTGGA TATTTATGAA TGTGACTTTT TCTGTATTAC AGCCTGGAC GGACTCTGGC CACTCCCAAT CATGTACTTT GGGAATTGAAT AGGCCAGAGT TATTTGGAAA AGGCCAGAGT TATTTGGAAA ACTACTC CAGTATCACT CAGTATCACT CAGTATCACG AAACTACACT CAGTATCACG AACTACACG CTTGGACCGA CACTATCCC CAGTATCACG CAGTATCCG CACTCTTCAT CACTCTTCAT CACTCTTCACTTT GACCTCTTCAT CACGTCTTCAT CAGGACCCT GGCCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCTCTTGAT GCCCTCTTGAT   | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>660<br>660<br>6720<br>780<br>840<br>900<br>900<br>1020<br>1140<br>1200<br>1380<br>1440<br>1560<br>1560<br>1620<br>1680<br>1780 |

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|            | GTTGGCATCG  | AAGGGCAAAA               | CCATGGCAGA  | CAGCTCCTAC | CAGCCAGAGG  | TCCTCAACAT               | 1560         |
| 20         | CCTTTCATTT  | CTGAGGATGA               | AAAACAGGAA  | CTCTGCATCT | CAGGTGGCTT  | CCAGTCTCGA               | 1620         |
| 20         | CAAACATGGAT | ATGAACCCAG<br>GCCGCCCGGA | AATGTTTTGT  | GTCACCACGG | TGTGCAAAAA  | GACACAAATC               | 1680         |
|            | CGAAGCCAAG  | CTGCGGTTCA               | TCCAGGCGTG  | GCAGTCACTG | CCTGAGTTTG  | GCCTCACCTA               | 1740<br>1800 |
|            | CTACCTTGTC  | AGATTTAAAG               | GAAGCAAAAA  | AGATGACATT | CTGGGAGTTT  | CATATAACAG               | 1860         |
| 25         | GTTGATTAAA  | ATTGATGCAG               | CCACCGGGAT  | TCCAGTGACA | ACATGGAGAT  | TCACAAATAT               | 1920         |
| 23         | CAAACAGIGG  | AATGTAAACT<br>TTCACCTGCC | GGGAAACCCG  | GCAGGTGGTC | ATCGAGTTTG  | ACCAAAACGT               | 1980         |
|            | CTACATTTTC  | TTGTCCACCC               | GCTCCAAGGA  | CCAGAATGAA | ACACTCGATG  | ACATTGGCGG               | 2040 °       |
|            | CCACAAATTG  | ACCGGCGGTC               | AGGATTGAAA  | CAAGCACGCG | TGCTCGGCTC  | ACACCAACAA               | 2160         |
| 30         | GGCAAGCCAA  | AGGCGCCCCT               | CCCCAGAGGG  | ATCCCTAACG | TGCCCAGCAT  | GTAGATTCTG               | 2220         |
| 50         | GACTAACAGA  | CAACATACAT               | TCACCGCTGG  | TCACCCAGAT | CCTCATTCAA  | ACCCACTGCT               | 2280         |
|            | TTTTCTATAA  | TTTCCTTACT<br>AATGGGTAGG | CAGGAGAAAA  | GCAGGTGCCC | TARGATTCCT  | CTCTCTTGTT               | 2340<br>2400 |
| -          | GCATGTGGTT  | ACAGTTCTCT               | GACTTGCAGA  | ACCTGCCAGG | TGTATGGCTA  | CAAGTTATCC               | 2460         |
| 35         | TCGTGCTGAT  | CTGTCTCATT               | ACTAAGTCAA  | TGGAGAAGAC | AGAAAGGTAA  | AAATCACGTG               | 2520         |
| 33         | TAGCAAGAAC  | AACTCTTATT               | TCACAAACTC  | AGGTATGAAA | CGAAACGCCT  | GTCCTTCATG               | 2580         |
|            | CCCTGGAGGC  | TAGCTCCTGT<br>CAAGGTCTAG | CCCTAGAAA   | TGGCAGAGGG | AGTTCCTACA  | CACACTTTTT               | 2640         |
|            | ACAACCCAAG  | GTCAGAGGAG               | TGGCCCTCAG  | TGTCATCTGT | CCACAGTGAT  | ACCTGCCAAG               | 2700<br>2760 |
| 40         | ATGACCACTG  | ACCCACATCT               | GGTCTTAGTC  | ATTGGTCTCC | TCAGATTTCT  | GGGGCCACCT               | 2820         |
| 40         | GCAAGCCCCA  | TTCCATTCCT               | ACAGATCTCT  | CAGCCACCTG | TAAGTCCTTT  | GTGAAGATGT               | 2880         |
|            | CTACTCTGGG  | GGGGGACAGG<br>TTGGGATTCA | AAAACCCATT  | CACACCCCA  | GATCCATGTC  | TCCACTGCTT               | 2940         |
|            | CCAGTGTCAA  | GGATTCCAGT               | CAGGTGTCTA  | TCCCAACTGG | TCAGGGAGAG  | AAGGGCAGAC               | 3000<br>3060 |
| 15         | CCATTCTCAA  | AGACCACCAT               | GTCCAAGGTC  | TGACAGCTCC | CCACTGGCTG  | CCCCCACAGG               | 3120         |
| 45         | GGCTTTAGGC  | TGGTCTGGGT               | CATGGGGAAG  | CGTCCCTCTT | ATCGCTGGTC  | TGTGTTCTCC               | 3180         |
|            | GTADATCACA  | ATCTATGTTG               | GTACGACTCC  | TGGCCTTTTA | TCTAAAGGAC  | TTTGGCTTTT               | 3240         |
|            | TGCCTTGAGA  | AGCCAATAAT<br>CTGCCTTGAG | ACACTITITI  | CCTTGAGAGA | GTGAGCCAAT  | TAACAGCTCC               | 3300<br>3360 |
| 50         | CTGAATTGTC  | ATTTTCCATT               | TTGGTTTGTT  | AGAGGTGGGA | GGGGTGGGTT  | TTGAGAAGGT               | 3420         |
| 50         | CAAAAGCAAT  | ACCAGAAGTA               | AAGGGAAATA  | TCAGACAATA | TTTTATTATT  | TTTTCATAGA               | 3480         |
| ,          | TCACTTCTCC  | CACAAAGAAC<br>TAGGATGCAC | TTGGGGTGTA  | AGGATAAGGC | AAAAGCTCCA  | ATCCCATTTT               | 3540         |
|            | TCAGCTGTTG  | CTTTATTTTC               | CATCAAAGCC  | CTCTGAGAAG | TGAGACCTCA  | CCCGTGAGCG               | 3600         |
| <i></i>    | GAGCCACATA  | GAGACAGACT               | TGGCAAGGGA  | CCCCCTGGTT | CTGAGCCAGT  | ACCTCCCATC               | 3660<br>3720 |
| 55         | TGGAAATTCC  | TCTTTTAGCC               | TCTCCTTAGA  | GGTGAATGTG | AATGAAGCCT  | CCCAGGCACC               | 3780         |
|            | CGCTGAATTT  | CTGAGGCCTT               | GCTTAAAGCT  | CAGAAGTGGT | TTAGGCATTT  | GGAAAATCTG               | 3840         |
|            | CGTATTATAC  | TAAAGAACTT<br>TTGATGTTGG | TCATTTCTCA  | GTCCTATTTC | TCACTTCTAT  | CTAAGTGTAC               | 3900<br>3960 |
| <b>C</b> O | CCTAGTCAGT  | TCTTTAAGAT               | TATAACTGGT  | CCTACATTAA | AATAATGCTT  | CTCCATCTCA               | 4020         |
| 60         | GATTTTACCT  | GTTTGCTGCT               | GAGAACATCT  | CTGCCTAATT | TACCAAAGCC  | AGACCTTCAG               | 4080         |
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| 65         | AATGCTACTG  | TTCCAAAGAG               | CAACTTGATG  | GTTTTTTTTA | ATACTGAGTG  | CAAAAGGTCA               | 4260<br>4320 |
| 65         | CCCAAATTCC  | TATGATGAAA               | TTTTAAATTA  | ATGGGCACCT | TTCAACATCA  | Talable Calabilities     | 4380         |
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|            | GAITTATATG  | GRITIGARAA               | MAAAAAAA    | A          |             |                          | 4471         |
| <b>7</b> 0 | Seq ID NO:  | C27 Proteir              | Sequence    |            |             |                          |              |
| 70         | Protein Acc | ession #: 1              | IP_005161.1 |            |             |                          |              |
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| 95         | MDGGTLPRSA  | PPAPPVPVGC               | AARRRPASPE  | LLRCSRRRRP | ATAETGGGAA  | AVADRNEDED               | 60           |
| 75         | NRVKLVNLGF  | QALRQHVPHG               | GASKKLSKVE  | TLRSAVEYIR | ALORLLAEHD  | AVRNALAGGI.              | 120          |
|            | RPQAVRPSAP  | RGPPGTTPVA               | aspsrasssp  | GRGGSSEPGS | PRSAYSSDDS  | GCEGALSPAE               | 180          |
|            | RELLDFSSWL  | GGY                      |             |            |             |                          | 193          |
| 00         | Seq ID NO:  | C28 DNA Sec              | mence       |            |             |                          |              |
| 80         | Nucleic Aci | id Accession             | #: NM_0177  | 763        |             |                          |              |
|            | coding sequ | uence: 169               | 2520        |            |             |                          |              |
|            | 1           | 11                       | 21          | 31         | 41          | 51                       |              |
|            | Ī           | 1                        | Ī           | Ī          | Ī           | l                        |              |
|            |             |                          |             |            |             | •                        |              |
|            |             |                          |             |            | 12          | 214                      |              |

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|     | CTGCTCGCCG | CCGTGGAAGA               | AACGCTAATG | GACTCCACTA | CAGCGACTGC | TGAGCTGGGC               | 120          |
| 5   |            | ATCCTCCATC               |            |            |            |                          | 180          |
| ,   |            | TCCGGCGCCG               |            |            |            | CTGGCTACGG               | 240          |
|     |            | GCAGCATCCC               |            |            |            |                          | 300<br>360   |
|     |            |                          |            |            |            | GGAGAATCCA               | 420          |
| 10  |            |                          |            |            |            | CCTGGGTGGC               | 480          |
| 10  |            | AAATCAACAC               |            |            |            |                          | 540          |
|     |            |                          |            |            |            | TGTCTTCTAC               | 600          |
|     |            | CCCGCATCAT               |            |            |            |                          | 660<br>720   |
|     |            |                          |            |            |            | CGGGCGCTGC               | 780          |
| 15  |            | CAGGCTTCGA               |            |            |            |                          | 840          |
|     |            | AGGCCAACCA               |            |            |            |                          | 900          |
|     |            |                          |            |            |            | AGCAGACCTG               | 960          |
|     |            | ACATGCCCTCAT             |            |            |            | AGGCCGAGAG               | 1020<br>1080 |
| 20  |            |                          |            |            |            | CTGCACCCGC               | 1140         |
|     |            |                          |            |            |            | ACGCATTTAC               | 1200         |
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| 25  |            |                          |            |            |            | CATTACCCTG<br>GCAGTACTAT | 1380<br>1440 |
|     |            |                          |            |            |            | CACGGTCACC               | 1500         |
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| 50  |            |                          |            |            |            | CCCAGGCATG               | 1740<br>1800 |
|     |            |                          |            |            |            | GGAGTTTGCC               | 1860         |
|     |            |                          |            |            |            | GGAGTTTGGC               | 1920         |
| 25  |            |                          |            |            |            | GGCCATCAAG               | 1980         |
| 35  |            |                          |            |            |            | AGCCTCCATC               | 2040         |
|     |            |                          |            |            |            | CAAGAGCACA<br>TCTCCGGCAA | 2100<br>2160 |
|     |            |                          |            |            |            | CGCAGCTGGC               | 2220         |
| 40  |            |                          |            |            |            | CAACATCCTC               | 2280         |
| 40  |            |                          |            |            |            | TCTAGAGGAC               | 2340         |
|     |            |                          |            |            |            | CCGCTGGACA<br>GAGCTACGGC | 2400         |
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| 45  |            |                          |            |            |            | GCCCAAGTTC               | 2640         |
|     |            |                          |            |            |            | CAAAGCCATG               | 2700         |
|     |            |                          |            |            |            | CGACTACACC<br>CAAGGAGAGC | 2760<br>2820 |
|     |            |                          |            |            |            | GGAGGACATT               | 2880         |
| 50  |            |                          |            |            |            | TATCCAGGTG               | 2940         |
| •   |            |                          |            |            |            | TGCCTCGGCT               | 3000         |
|     |            |                          |            |            |            | GGTGCTCTAT               | 3060         |
|     |            |                          |            |            |            | CAAGCGGTGC<br>AAAGGGAATG | 3120<br>3180 |
| 55  |            |                          |            |            |            | TTTTAAAGAG               | 3240         |
|     |            |                          |            |            |            | TTGGGAGATT               | 3300         |
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| 60  |            |                          |            |            |            | CTATTCCTGC               | 3540         |
|     |            |                          |            |            |            | AACTCCAATG               | 3600         |
|     |            |                          |            |            |            | CTCCTGGGTC               | 3660         |
|     |            |                          |            |            |            | CCCCAGGTCT               | 3720         |
| 65  |            |                          |            |            |            | CGACTGCCGC               | 3780<br>3840 |
|     |            |                          |            |            |            | CGGGGGTATT               | 3900         |
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|     |            |                          |            |            |            | GGACTTGATC               | 4020         |
| 70  |            |                          |            |            |            | AGGGCGANAT               | 4080         |
| , 0 |            |                          |            |            |            | ATTCAGAGAC               | 4140<br>4200 |
|     |            |                          |            |            |            |                          | 4260         |
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| 75  |            |                          |            |            |            | GCAAATAGGC               | 4380         |
| , , |            |                          |            |            |            | CTGGGAGCCT<br>TGCCCTCCAG | 4440         |
|     |            |                          |            |            |            | GAAAGTGTGT               | 4500<br>4560 |
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| 80  | ACCCAAGCAG | AGCAATCAGT               | TAGTGAATTG | GAATTCCCCA | AGTCTTTGCT | ATTGTGAATA               | 4740         |
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|     |            |                          |            |            |            | CAACAGTGTA               | 4860<br>4920 |
| _   |            |                          |            |            |            | TTTTTAATGA               | 4980         |
| -   |            |                          |            |            |            |                          |              |

| 5 10 | TTGCCATTCT TGACCAGTGA TGAGAAGTGT TAAACTTAAT ACAAAGCCTC GCTGAAAATG GAGAACTTCT CCCAAAGATA TTGAAATGAA GGAGCCCAT GGGGACCAAT CCAAACTTAG GAGATTTTGT AAAGAAAAA ATGAAGAAAA ATGAAGAAAA AGGATTTCACAC ACGCAGACTG CCATCTCACG Seq ID NO¹ | AGATGAGCTT CTGTTCATAA GAAATAAAGC CAAGAAATAT ACAGGGAGAA CCAACCTAGC TTTCTCGAGA GGAAAAAATG CAGACTAACA ATTCAACAATT CTTCATAAGC CACCACCAGG CTGGTGCCAG GGTGTCAACT ATAACAATAT GCAAAATTAGC | TTTTCATAT CCTTCACCAA ATGAAGACAA GGGACTATGT TGAAACCAAG AAGACAAACCC CTAAGGGCAG GCAGATCTCT CACAAAGAAA AAAGGAGAAA CCTGCCTTAC CCACTGCAAA AAAGAAA AATGGGCAAA TAACCTTATA TAAAGAGTCA CACATAGGCT | GTTTGTTGGC<br>TTTTTGATGA<br>GATTAGAAGA<br>GACAAGAACA<br>TTGGAAAACA<br>ACGTTCAAA<br>GAAGACACAT<br>CCAGAGAGAA<br>CTGCAGAAAC<br>AGAATTTTCA<br>AAGACATCCT<br>AAATACCAGC<br>TCTAAATGCG<br>AGACTCATTG | CACATGTTTG GGTTGTTTTT AAAAGAATGA AACTTACGTT CTCTTCAGGA TTCAGGAAAT AATTGTCAGA AGGTCAGGTT CCTACAACCT ATCCAGAATT TACAGACAAG GAAGGAAGCA TTGTAGAGAC TTGTAGAGAC AGTATCATAA AGTAATCCCC GTGTGCCGTA | TTGTTTCTTT TCTTTTTCTTG AAAGGAACAA TGACTGGTGT TATTATCCAG ACAGAACA TTCACCAAGG ACTCACAAAA AGAAGAGAGT TCATATCCAG CAAATCCTGG CTAAATATGG CATTGACACT TGACAGGATC CAATTAAAAG TTCAGGAGAC | \$040<br>\$100<br>\$160<br>\$220<br>\$280<br>\$340<br>\$460<br>\$520<br>\$520<br>\$580<br>\$760<br>\$760<br>\$820<br>\$8820<br>\$940<br>6000<br>6057 |
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| 30   | TCAGTTCGGG<br>GCGATGAAGT<br>CAGCCCTCAG  | ACAGTTGTGA<br>AAGGCTGTAG<br>TTCCAGCGCG<br>AGAATTCTGT  | CAGCTTTGCT<br>GACCCGCAGC<br>GAGTACCAGG<br>GACTGATTCC  | GTGAAGTTGA<br>TCTGATAATT<br>CAGTGCAGGC<br>GGAGCAACCA<br>AACTCCGATT<br>AAGCAAAACA  | TTGCAAACAC<br>ACTCTGGACC<br>ACAAAAAAGC<br>CAGAAGATGA   | GAGGCTGCAG<br>TCTCAGGGTG<br>AGAGTCCCGC<br>AAGTGGAATG   | 240<br>300<br>360<br>420<br>480  |
| 35   | ATGTCTGAAT<br>GACTCACAAT<br>CCTGAACGGA<br>GCTCTACCCA  | TAGAAAGCTT<br>CAAGGAGACC<br>GAGCTCGTCC<br>TGGAGGAGGA  | CCCTGGCTCG<br>GCGAAGGCGT<br>TCTTACCAGG<br>GGAGGAAGAG  | TTCCGTGGAA<br>ACATTCCCGG<br>TCAAGGTCCC<br>GATAAGTACA  | GACATCCCCT<br>GTGTTGCTTC<br>GGATCCTCGG<br>TGTTGGTGAG   | CCCAGGCTCC<br>CAGGAGAAAC<br>GTCCCTTGAC<br>AAAGAGGAAG   | 540<br>600<br>660<br>720<br>780  |
| 40   | GTGACCCTTC<br>GTCTGCAGCA<br>TGCCGTCAGA<br>CGAGGCCAGT  | CGCATATAAT<br>ATTCTCGAGA<br>AGACTATTGA<br>TCTGTGGCCC  | TCGCCCAGTG<br>GAAGATATAT<br>TACCAAAACA<br>CTGCCTTCGA  | CTGCCCAGAA<br>GAAGAAATTA<br>AACCGTTCAC<br>AACTGCAGAA<br>AACCGTTATG  | CAGAGGAGGA<br>TGGGCTCTAC<br>ACCCAGACTG<br>GTGAAGAGGT   | GTTGGAGAAC<br>TTGTCATCAA<br>CTGGGGCGTT<br>CAGGGATGCT   | 940<br>960<br>1020<br>1080   |
| 45   | CGGCAGCGAG<br>TTTGGGAATG<br>TATCTGGAAA  | ATGGACGGTG<br>TGCATGCCTA<br>ATTTGCTGCC  | TGCGACTGGG<br>CTTGAAAAGC<br>TGCCTTCTAC  | TGTCGAGGAA<br>GTCCTTGTGT<br>CTGAAACAGG<br>TTCTCAAATC<br>TGATGATCAG  | ATTTAGCCAA<br>AATTTGAAAT<br>TTTCTTGTAA   | ATATCATGGC<br>GCAAGCATAA<br>AAGTTTCCAA   | 1140<br>1200<br>1260<br>1320<br>1380   |
| 50   | AATCAAGTTA<br>TACACTTTGC<br>TCTATTTCCA<br>TATGAAAGCA  | ATCTTAGCAG<br>CCTCCTGCAG<br>ATGCTCCTCT<br>TATTTTATTT  | ACATGTGTTT<br>TTTCTTCTCT<br>CCAACCGCTT<br>ACTTGGTGTT  | CTGGAGCATC<br>GCTCCCAACC<br>AGTTTCTGAA<br>GAAATAGCCC<br>TCTATTGAAT  | ACAGAAGGTA<br>CCCATCTCAT<br>TTTCTTTTAA<br>TCATAAAACC   | TATTGCTAGT<br>AGCATCCCCC<br>ATTACAGTTT<br>TAAGCACTTG   | 1440<br>1500<br>1560<br>1620<br>1680   |
| 55   | TCAAGGCACA<br>CTCTCAATCC<br>CTCCTAATTT<br>AAGGTTGGTG  | AAAGTCTTAA<br>CATGTATTGC<br>CTTCTGCCCG<br>GGCAATGTAA  | AACCATGTGG<br>GCTTATGTTA<br>AAGGGTAAGT<br>TACTTAATTA  | CACTCATACT AAAAATTAGG CAAGTTGTTG GGTGCGTCCA AAATAATGAT  | TAATTATTGC<br>TCACAGTTGA<br>GCTTACACGA<br>GGAAGAGCTA   | AGATTGATGT<br>GACTTAATTT<br>TCATAATTCA<br>TCTGGAGATT   | 1740<br>1800<br>1860<br>1920<br>1980   |
| 60   | TTATTTCAGT<br>TTGATATTAA<br>CAAGGTTCAA<br>GTAACTTTTA  | TCACATGTAA<br>AAACTAGTCT<br>GTTTAGATTT<br>GCAGTTTGTT  | GGTATTGCAA<br>GTGGTTCTTT<br>TAAGCACTTT<br>AACCTGACAT  | AAACTTTAGT<br>ATAAATTCTT<br>GCAGTTTCTT<br>TATAACAATG<br>CTCTGCCAGT  | GGACAATTTT<br>GTAAATTTAT<br>ATAAGTGCCT<br>CTAGTTTCTG   | GTATGGAAAC<br>AAACCAGGCA<br>TTTTGGAGAT<br>GGCAGGTTTC   | 2040<br>2100<br>2160<br>2220<br>2280   |
| 65   | AAGTGTTTGT<br>GATGCATAAT  | ATGTCCAATT<br>TGGACCTTGA  | TACTTGCATA<br>ATCGATAAGT  |   | TGCTGTGCCA   | TTCAATGTTT<br>GTAATGCTTT   | 2340<br>2400<br>2460<br>2510   |
| 70   | Nucleic Act   | C32 DNA Serid Accession   | .1271   |   |  |  |  |
| 75   | GCGGCAGCCC<br>TCTCGCTGGA  | CCGCCGCCCC  | CGCAGCCCCT<br>TGCAGCATCG  |   | TCTCCCACGT<br>GAACTGGAGC   |  | 60<br>120<br>180<br>240  |
| 80   | GCTGCCGCC<br>CCCTGGGCAA<br>TTGGGGGAGA<br>GCAAGTGGAG<br>GGTCTTCGCT   | GCGCTCCGC<br>GGCCCTCTGC<br>GTCCATCTGT<br>CCAGACGCC<br>GCTGGGGGCC  | TGCTCCTGCC<br>GCTCTCCTCC<br>TCCGCCAGAG<br>TTCCCCAAGC<br>GCGCATAGCT  | GGGTGATGGA<br>TGGCCACTCT<br>CCCCGGCCAA<br>AGTACCCCCT<br>CCGACTACAG  | AAACCCCAGC<br>CGGCGCCGCC<br>ATACAGCATC<br>GTTCCGCCCC<br>CATGTGGAGG   | CCGGCCGCG<br>GGCCAGCCTC<br>ACCTTCACGG<br>CCTGCGCAGT<br>AAGAACCAGT<br>CTGATGAAGG  | 300<br>360<br>420<br>480<br>540<br>600   |

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|     |            | CCCCAGGTTA |            |            |            |            | 1140 |
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|     | GCACATTCCA | ACTACCGGGC | TGGCATGATC | ATAGACAACG | GAGTCAAAAC | CACCGAGGCC | 1200 |
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| 5   | AACCAGGACC | ACGGGGCCTG | GCTGCGCGGC | GGGGATGTGT | GGCTGGACAG | CTGCCGGTTT | 1380 |
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|     |            | AGATAAAGAA |            |            |            |            | 1500 |
|     |            | ATAGGATCTG |            |            |            |            | 1560 |
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| 15  |            | ACCTCACGAA |            |            |            |            | 1920 |
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|     |            | GTAACCTGCG |            |            |            |            | 2040 |
|     |            | GGGCGCTCAC |            |            |            |            | 2100 |
|     |            | GCTACACCAT |            |            |            |            | 2160 |
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| ~~  | CCAAAGAACG | CAGGCGTCAG | TGACTGCACA | GCCACAGCTT | ACCCCAAGTT | CACCGAGAGG | 2520 |
| 25  | GCTGTCGTAG | ACGTGCCGAT | GCCCAAGAAG | CTCTTTGGTT | CTCAGCTGAA | AACAAAGGAC | 2580 |
|     | CATTTCTTGG | AGGTGAAGAT | GGAGAGTTCC | AAGCAGCACT | TCTTCCACCT | CTGGAACGAC | 2640 |
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|     |            |            |            |            |            | AGAAATAAAG | 5760 |
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Seq ID NO: C39 DNA Sequence Nucleic Acid Accession #: NM\_014373 Coding sequence: 322.1338

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|            | Î          | ī                           | î           | ĩ <sup>*</sup> | ĩ          | 1                        |              |
|            |            | GGTGGTGGCA                  |             |                |            |                          | 60           |
| 5          |            | GCAGGTTCGG                  |             |                |            |                          | 120          |
| ,          |            | GCTTACTCAC<br>ATTGAAGGCA    |             |                |            |                          | 180<br>240   |
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| 13         |            | TATTTTATTT ACCCAGCCAT       |             |                |            |                          | 780<br>840   |
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| 20         |            | TGAATGAAAC                  |             |                |            |                          | 1020         |
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|            |            | TAGCATTTCA                  |             |                |            |                          | 1500         |
|            |            | AAAAACAAAA                  |             |                |            |                          | 1560         |
| 30         |            | TACTTTGTTA<br>TTACTCAAAA    |             |                |            |                          | 1620         |
|            |            | TTAAGATATC                  |             |                |            |                          | 1680<br>1740 |
|            | алалалал   | •                           |             |                |            | 011110011011             | 1749         |
|            |            |                             |             |                |            |                          |              |
| 35         | •          | C40 DNA Sec<br>id Accession | •           | 19             |            |                          |              |
|            |            | uence: 12                   |             |                |            |                          |              |
|            | _          |                             |             |                |            |                          |              |
|            | 1          | 11                          | 21          | 31             | 41         | 51                       |              |
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|            |            | CATCCACAGA                  |             |                |            |                          | 120          |
|            |            | AAGACTCCCA                  |             |                |            |                          | 180          |
|            |            | ATGTGGTACA<br>ATGAATCCAA    |             |                |            |                          | 240          |
| 45         |            | GTGTCCTGGG                  |             |                |            |                          | 300<br>360   |
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| 50         |            | AATATATATT                  |             |                |            |                          | 600<br>660   |
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|            | GGTTCAGATA | TCGACAATGT                  | AACTCAGCGT  | CTTCCTATTC     | AGGATATACT | CTCAGCATTC               | 1140<br>1200 |
| 60         | TCTGTTTATG | TTAATAACAC                  | TGAAAGTTAC  | ATCCACAGAA     | ATTTACCTAC | ATTGGAAGAG               | 1260         |
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|            |            |                             |             |                |            | ATTTAATAAA               | 1620         |
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| 70         | TTGGGTGCAG | CAGGAAGAAA                  | AAACCTTCAG  | GATTTTGCTG     | CTTGTGGAAT | AGACAGAATG               | 1860         |
|            | AATTATGACA | GCTACTTGGC                  | TCAGACTGGT  | AAATCCCCCG     | CAGGAGTGAA | TCTTTTATCA .             |              |
|            |            |                             |             |                |            | GAGGAACTCC ` TCCTATAGAA  | 1980<br>2040 |
| 75         | CAATCACTGA | GCACTCTATA                  | CCAAAGCGTC  | AAGATACTTC     | AACGCACAGG | GAATGGATTG               | 2100         |
| 75         | TTGGAGAGAG | TAACTAGGAT                  | TCTAGCTTCT  | CTGGATTTTG     | CTCAGAACTT | CATCACAAAC               | 2160         |
|            | AATACTTCCT | CTGTTATTAT                  | TGAGGAAACT  | AAGAAGTATG     | GGAGAACAAT | AATAGGATAT               | 2220         |
|            | CCTGTGGCCA | ATCIGCAGIG<br>ADATTTTCCCC   | TACTGCTGTTC | GATGTCTTTC     | HGAAAGTGGC | ATCGTGCAAA<br>CATTATCGAC | 2280         |
| 00         | CCCTTGAATT | TGTTTTGGTT                  | TGGCATAGGA  | AAAGCTACTG     | TATTTTTACT | TCCGGCTCTA               | 2400         |
| 80         | ATTTTTGCGG | TAAAACTGGC                  | TAAGTACTAT  | CGTCGAATGG     | ATTCGGAGGA | CGTGTACGAT               | 2460         |
|            |            |                             |             |                |            | TCATAAAGAT               |              |
|            | CALGIAIAIG | GTATTCACAA                  | recigitate  | ACANGCCCAT     | CACAACATTG | A                        | 2571         |

Nucleic Acid Accession #: NM\_033049 Coding sequence: 28..1566

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|            |                |                               | GGATCACAGC    |   |  |  |      |
|            |                |                               |               |   |  |  | 1440 |
| 5          |                |                               | AGTCTTAGGA    |   |  |  | 1500 |
| 3          | GGCTGCCATA     | TAACCTGACA                    | GGAACATGCT    | ACTGAAGTTT  | ATTTTACCAT                             | TGACTGCTGC                             | 1560 |
|            | CCTCAATCTA     | GAACGCTACA                    | CAAGAAATAT    | TANK TANK TANK TANK   | CAGCAGGTGT                             | CCCTTAACCT                             | 1620 |
|            | CCCTATTCAC     | AAACCCCCAC                    | ATCAATAAAC    | ATCACACACT  | CAACTCCAAAC                            | mrccareca                              |      |
|            | CCCIATICAG     | MAGCICCAC                     | ATCANTANAC    | MIGACACICI  | GAAGIGAAAG                             | TAGCCACGAG                             | 1680 |
|            | AATIGTGCTA     | CTTATACTGG                    | TTCATAATCT    | GGAGGCAAGG  | TTCGACTGCA                             | GCCGCCCCGT                             | 1740 |
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| 10         | AGTGACCACT     | CTCCCCTCAC                    | CCCGATCAGT    | TANCCACCTY  | TOCANTANCE                             | TTCCTACTAC                             | 1860 |
|            |                |                               |               |   |  |  |      |
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|            |                |                               | AAATAAAGAT    |   |  |  | 1980 |
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|            | TAGTCCTCCT     | TABCCACTTA                    | TCTCCCATAT    | CACACTOTO   | BABATACCAA                             | CACCACCACA                             | 2100 |
| 15         | N COTTON TOTAL | ************                  | TCTCCCATAT    | CAGAGIGIGA  | AMANIAGGAA                             | CACGIGCICI                             |      |
| 15         | ACCICCATII     | AGGGATTIGC                    | TTGGGATACA    | GAAGAGGCCA  | TGTGTCTCAG                             | AGCTGTTAAG                             | 2160 |
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|            | AATAAGTATC     | TATGTCTAAA                    | АЛЛАЛАЛАЛА    | AAA   |  |  | 2253 |
|            |                |                               |               |   |  |  |      |
|            | Sea ID NO:     | C44 DNA Sec                   | 710700        |   |  |  |      |
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| 20         |                |                               | #: NM_013     | 372   |  |  |      |
|            | Coding sequ    | ence: 636                     | 517           |   |  |  |      |
|            |                |                               |               |   |  |  |      |
|            | 1              | 11                            | 21            | 31  | 41                                     | 51                                     |      |
|            | 1              | 1                             | 1             | 1   | 1                                      | Ĭ.                                     |      |
| 25         | 0000000000     | MONOGOGON O                   |               | 1   | 1                                      | L                                      |      |
| 25         | GCGGCCGCAC     | TCAGCGCCAC                    | GCGTCGAAAG    | CGCAGGCCCC  | GAGGACCCGC                             | CGCACTGACA                             | 60   |
|            | GTATGAGCCG     | CACAGCCTAC                    | ACGGTGGGAG    | CCCTGCTTCT  | CCTCTTGGGG                             | ACCCTGCTGC                             | 120  |
|            | CGGCTGCTGA     | AGGGAAAAAG                    | AAAGGGTCCC    | AAGGTGCCAT  | CCCCCCCCCCA                            | GACAAGGCCC                             | 180  |
|            | AGCACAATGA     | CTCAGAGCAG                    | ACTCAGTCGC    | CCCAGCAGCC  | TERETTOTAGE                            | AACCGGGGGG                             | 240  |
|            | GCGGCCAACC     | GCGGGGGGG                     | GCCATGCCCG    | CCCACCAGCC  |  | ***********                            |      |
| 30         | COMPOST TO     | COOCCACT                      | GCCW1GCCCG    | GGGAGGAGGT  | GCTGGAGTCC                             | AGCCAAGAGG                             | 300  |
| JU         | CCCTGCATGT     | GACGGAGCGC                    | AAATACCTGA    | AGCGAGACTG  | GTGCAAAACC                             | CAGCCGCTTA                             | 360  |
|            | AGCAGACCAT     | CCACGAGGAA                    | GGCTGCAACA    | GTCGCACCAT  | CATCAACCGC                             | TTCTGTTACG                             | 420  |
|            | GCCAGTGCAA     | CTCTTTCTAC                    | ATCCCCAGGC    | ACATOGGAA   | GCAGGAAGGT                             | TOTTTO                                 | 480  |
|            | CONTROL OF THE | CTCCAACCCC                    | 33C3330000    | CONTRACTOR OF THE PARTY OF THE |  | recrirence                             |      |
|            | 220010011      | CIGCAMGULU                    | AAGAAATTCA    | CTACCATGAT  | GGTCACACTC                             | AACTGCCCTG                             | 540  |
| 25         |                |                               | AAGAAGAGAG    |   |  |  | 600  |
| 35         | CCATCGATTT     | GGATTAAGCC                    | AAATCCAGGT    | GCACCCAGCA  | TGTCCTAGGA                             | ATGCAGCCCC                             | 660  |
|            | AGGAAGTCCC     | AGACCTAAAA                    | CAACCAGATT    | CTTACTTCCC  | TTABACCTAG                             | ACCCCAGAAC                             | 720  |
|            | AACCCCCACC     | TOCTOTO                       | CAGGAGCCTG    | OTTO OTTO   |  | A BOA CROWNO                           |      |
|            | AGCCCCCAGC     | 1000100100                    | CAGGAGCCIG    | CITGIGCGIA  | GITCGIGIGC                             | ATGAGTGTGG                             | 780  |
|            | AIGGGIGCCI     | GIGGGIGITT                    | TTAGACACCA    | GAGAAAACAC  | AGTCTCTGCT                             | AGAGAGCACT                             | 840  |
| 40         | CCCTATTTTG     | TAAACATATC                    | TGCTTTAATG    | GGGATGTACC  | AGAAACCCAC                             | CTCACCCCGG                             | 900  |
| 40         | CTCACATCTA     | AAGGGGCGGG                    | GCCGTGGTCT    | GGTTCTGACT  | THETETETT                              | GTGCCCTCCT                             | 960  |
|            | GGGGACCAGA     | ATCTCCTTTC                    | GGAATGAATG    | TTCATCCAAC  | *CCCMCCMC                              | CACCCCACCA                             |      |
|            | Choomeman      | ATCTCCTTTC                    | GGAATGAATG    | TICATGGAAG  | AGGCICCICI                             | GAGGGCAAGA                             | 1020 |
|            | GACCIGITIT     | AGIGCIGCAT                    | TCGACATGGA    | AAAGTCCTTT  | TAACCTGTGC                             | TTGCATCCTC                             | 1080 |
|            | CTTTCCTCCT     | CCTCCTCACA                    | ATCCATCTCT    | TCTTAAGTTG  | ATAGTGACTA                             | TGTCAGTCTA                             | 1140 |
|            | ATCTCTTGTT     | TGCCAAGGTT                    | CCTAAATTAA    | TTCACTTAAC  | CATGATGCAA                             | ATGTTTTTCA                             | 1200 |
| 45         | TTTTGTGAAG     | ACCUTCUAGA                    | CTCTGGGAGA    | CONTRATOR   | CCCNACCACA                             | ACCACCATAC                             |      |
|            | TOGROTORON     | AACCCACCC                     | GGAGGGTGAG    | 0001001010  | GGCAMGGACA                             | MOCMOGATAG                             | 1260 |
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|            | TTTTCCTAGT     | ATTTAACAGA                    | ACCCAAGTGA    | ACAGAGGAGA  | AATGAGATTG                             | CCAGAAAGTG                             | 1440 |
|            | ATTAACTTTG     | GCCGTTGCAA                    | TCTGCTCAAA    | CCTAACACCA  | AACTGAAAAC                             | STOATAAATA                             | 1500 |
| 50         | ACCACTCCTA     | TGTTCGGACC                    | CAAGCAAGTT    | ACCTABACCA  | AACCAACTCC                             | TOTAL CONTROL                          |      |
|            | CCCTCACCTC     | CARARCACAC                    | CONCOUNTS I   | AGCIMARCCA  | TACCANCICC                             | 1CIGCIIIGI                             | 1560 |
|            | CCCICNOGIG     | GAAAAGAGAG                    | GTAGTTTAGA    | ACTUTUTGUA  | TAGGGGTGGG                             | AATTAATCAA                             | 1620 |
|            | AAACCKCAGA     | GGCTGAAATT                    | CCTAATACCT    | TTCCTTTATC  | GTGGTTATAG                             | TCAGCTCATT                             | 1680 |
|            | TCCATTCCAC     | TATTTCCCAT                    | AATGCTTCTG    | AGAGCCACTA  | ACTTGATTGA                             | TAAAGATCCT                             | 1740 |
|            | GCCTCTGCTG     | AGTGTACCTG                    | ACAGTAAGTC    | TAAAGATGAR  | AGAGTTTAGG                             | GACTACTCTG                             | 1800 |
| 55         | TTTTAGCAAG     | ARATATTETC                    | GGGGTCTTTT    | TOTTOTAL  | ATTOTOTOTO                             | Chrecocoma                             |      |
|            | RAGAGAAGAG     | GACCACACT                     | DCCARAMET-    | COUD I MOSSO  | ************************************** | CALL TOOCIN                            | 1860 |
|            |                |                               | AGGAAATAAA    |   |  |  | 1920 |
|            | COLCTTAATA     | CUIGGTAGAA                    | ATGTAAGGGA    | TATGACCTCC  | CTTTCTTTAT                             | GTGCTCACTG                             | 1980 |
|            | AGGATCTGAG     | GGGACCCTGT                    | TAGGAGAGCA    | TAGCATCATG  | ATGTATTAGC                             | TGTTCATCTG                             | 2040 |
| <i>c</i> o | CTACTGGTTG     | GATGGACATA                    | ACTATTGTAA    | CTATTCAGTA  | TTTACTGGTA                             | GGCACTGTCC                             | 2100 |
| 60         | TCTGATTAAA     | CTTGGCCTAC                    | TGGCAATGGC    | TACTTACCAT  | TEATOTARCO                             | CCCDDDCCC                              | 2160 |
|            | ACCOMMO        | V Chunky unc                  | dil Canadacco | **************************************  | TOTAL CAMOU                            | 2 2 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC |      |
|            |                | AACIITATTU                    | TACTTTGGAT    | TIGGITAACC  | IGITITETTE                             | AAGCCTGAGG                             | 2220 |
|            | IIITATATAC     | MAACTCCCTG                    | AATACTCTTT    | TTGCCTTGTA  | TCTTCTCAGC                             | CTCCTAGCCA                             | 2280 |
|            | AGTCCTATGT     | AATATGGAAA                    | ACAAACACTG    | CAGACTTGAG  | ATTCAGTTGC                             | CGATCAAGGC                             | 2340 |
|            | TCTGGCATTC     | AGAGAACCCT                    | TGCAACTCGA    | GAAGCTGTTT  | TTATTTCGTT                             | TTTGTTTTGA                             | 2400 |
| 65         | TCCAGTGCTC     | TCCCATCTAA                    | CAACTAAACA    | GGACCCATTE  | CAAGGGGGG                              | GATATTTTAA                             | 2460 |
|            | ACACCCAAAA     | TCTTCCCCC                     | Chimmus s s   | Colonians a co-   | CA CAS CACA                            | CARDONAL                               |      |
|            | CTACCOCATA     | TOTAL COURT CT                | GALLITCAAA    | CITITAAACT  | CACIACIGAT                             | GATTCTCACG                             | 2520 |
|            | CIAGGCGAAT     | TIGICCAAAC                    | ACATAGTGTG    | TGTGTTTTGT  | ATACACTGTA                             | TGACCCCACC                             | 2580 |
|            | CCAAATCTTT     | GTATTGTCCA                    | CATTCTCCAA    | CAATAAAGCA  | CAGAGTGGAT                             | TTAATTAAGC                             | 2640 |
| 70         | ACACAAATGC     | TAAGGCAGAA                    | TTTTGAGGGT    | GGGAGAGAAG  | AAAAGGGAAA                             | GAAGCTGAAA                             | 2700 |
| 70         | ATGTAAAACC     | ACACCACCCA                    | GGAAAAATTO    | CATTCACAAC  | CAGCAAAGAG                             | TGAATTTCTC                             |      |
|            |                |                               |               |   |  |  | 2760 |
|            | AGGIGITT       | MULCIGUCA                     | CAAGAATGCA    | ATTTUGTTAA  | IGGAGATGAC                             | TTAAGTTGGC                             | 2820 |
|            | AGCAGTAATC     | TTCTTTTAGG                    | AGCTTGTACC    | ACAGTCTTGC  | ACATAAGTGC                             | AGATTTGGCT                             | 2880 |
|            | CAAGTAAAGA     | GAATTTCCTC                    | AACACTAACT    | TCACTGGGAT  | AATCAGCAGC                             | GTAACTACCC                             | 2940 |
|            | TAAAAGCATA     | TCACTAGCCA                    | AAGAGGGAAA    | de de la  | TOTTO CTOTO                            | CCTATATTAA                             | 3000 |
| 75         | CACTACTACA     | V VACCAL COCCU                |               |   |  | COLUMNIA                               |      |
|            | CUCTUGIACH     | WIGIRGIA.                     | GICTICCAAC    | TTTCATTGAA  | AATGCCATAT                             | CTATACCATA                             | 3060 |
|            | TTTTATTCGA     | GTCACTGATG                    | ATGTAATGAT    | ATATTTTTTC  | ATTATTATAG                             | TAGAATATTT                             | 3120 |
|            | TTATGGCAAG     | ATATTTGTGG                    | TCTTGATCAT    | ACCTATTAAA  | ATAATGCCAA                             | ACACCAAATA                             | 3180 |
|            | TGAATTTTAT     | GATGTACACT                    | TTGTGCTTY     | CATTALANCA  | AAAAAAAA                               | CATCCTGGAA                             |      |
|            | GTCTCTAACT     | difficultal and an arrange of |               |   | ADADAMA                                | CAICCIGGAA                             | 3240 |
| 80         | TOTAL          | .GIIIITIGT                    | ANCIGIAGGT    | CITCAAAGTT  | AAGAGTGTAA                             | GTGAAAAATC                             | 3300 |
| OO.        | TGGAGGAGAG     | GATAATTTCC                    | ACTGTGTGGA    | ATGTGAATAG  | TTAAATGAAA                             | AGTTATGGTT                             | 3360 |
|            | atttaatgta     | ATTATTACTT                    | CAAATCCTTT    | GGTCACTGTG  | ATTTCAAGCA                             | TGTTTTCTTT                             | 3420 |
|            | TTCTCCTTTA     | TATGACTTTC                    | TCTGAGTTGG    | GCAAAGAAGA  | AGCTGACACA                             | CCGTATGTTG                             | 3480 |
|            | TTAGACTCTT     | THATCHCOM                     | ACCCCANACA    | y y y demands o   | CONCOUNTER                             | ATGTCTTCCT                             |      |
|            | CACTCACCACA    | -10101010                     | AUTOGONAACA   | AAATUTTUAC  | CUNGCIGAAC                             | AIGICITCCT                             | 3540 |
|            | GHG1 CAG1GC    | CIGAATCITT                    | ATTITITAAA    | TIGAATGTTC  | CTTAAAGGTT                             | AACATTTCTA                             | 3600 |
|            |                |                               |               |   |  |  |      |

| 5   | ACGAATAGCA<br>AATGAAAAGT<br>AGTTCTATTG<br>AAATCATTTA<br>ATGAAAGGGG<br>ACTAGAATTT | AAGAAAGACT<br>GATAAATGATG<br>GGATAAACAG<br>ACATTCCTCA<br>AAAACGGCAA<br>AGTTGATAGT<br>AATTTTCACC<br>CTATTCTTTC | ACTAGTTCAC AACATTTATA AGATATTTAA AGAATTATAT CTCATAAAAC CCAATAATGT | ACATAAAGTC<br>AGTGATCAGT<br>TATCAACTGC<br>AGACTATGAG<br>TAATTTGGCT | CTTTTAAGGA<br>TAATGCCTAA<br>ATTATGTATT<br>GTACCTTGCT<br>TCAAGTTTCA | GAAAATCTAA<br>GAGTGAAAGT<br>ATGTCTGCTT<br>GTGTAGGAGG<br>TGAATCTGTA | 3660<br>3720<br>3780<br>3840<br>3900<br>3960<br>4020<br>4049 |
|-----|--|---|---|--|--|--|--|
| 10  | Nucleic Aci  | C45 DNA Sec<br>id Accession<br>lence: 200   | #: Eos sec  | neuce  |  |  |  |
| 15  | 1  | 11  | 21  | 31   | 41   | 51   |  |
| 13  | ATACTTTCTT   | GATCAGTGAG<br>TCCAAACAGC<br>TCTGGTGTGA  | ATAAGAAGTG  | ATTGAGCCAC   | AAGTATACTG   | AAGGAAGGC  | 60<br>120<br>180   |
| 20  |  | CCAGGGAAAA  |   |  |  |  | 240  |
| 20  |  | CACGGTGGCT  |   |  |  |  | 300<br>360   |
|     |  | GATTCCAAGG  |   |  |  |  | 420  |
|     | TCCATTATTA   | TGGTCACATG  | GGCTAATTAG  | <b>AATTATCAGA</b>  | GCAAAGGCTA   | CCACAGACTG   | 480  |
| 25  |  | AATGGAGTCC  |   |  |  |  | 540  |
| 23  |  | GATCCCCAGA<br>AACAACCTCA  |   |  |  |  | 600<br>660   |
|     |  | ATTAATGAAA  |   |  |  |  | 720  |
|     |  | GCAAATGGAA  |   |  |  |  | 780  |
| 30  |  | GTTCAGGTCA<br>AGCAGTGCAT  |   |  |  |  | 840<br>900   |
| 50  |  | CTTCACAAGC  |   |  |  |  | 960  |
|     | AGCCCAGTGT   | AATGACATTG  | TCTTTGGATT  | TGGGTCCAAG   | GATGATGAAT   | ATACCCTGCC   | 1020   |
|     |  | GGCTACAGGG  |   |  |  |  | 1080   |
| 35  |  | ACTTGTGTGC<br>GCCACTGAGG  |   |  |  |  | 1140<br>1200   |
|     |  | CCATCAACCA  |   |  |  |  | 1260   |
|     |  | CTGTCACTGG  |   |  |  |  | 1320   |
|     |  | GCTGACAATA<br>AAGTATGCCA  |   |  |  |  | 1380<br>1440   |
| 40  | GGTGCCTCCG   | ACAGCTCTTC  | CTCTGAATTT  | TTCTCGGAAA   | TTCATTGACT   | GGAAAGGGAT   | 1500   |
|     |  | AAAAGCCAAC  |   |  |  |  | 1560   |
|     |  | ATTCCCATCA<br>ACTATTATCA  |   |  |  |  | 1620<br>1680   |
| 4.5 |  | AATGCTCAGG  |   |  |  |  | 1740   |
| 45  |  | GTTTTCCTAT  |   |  |  |  | 1800   |
|     |  | GATTTCAGTC<br>ATCGTGACGT  |   |  |  |  | 1860<br>1920   |
|     |  | CCCTCTACAA  |   |  |  |  | 1980   |
| 50  |  | GGAAGTCTCA  |   |  |  |  | 2040   |
| 50  |  | CAAACCTCTC<br>GATGTCTGGT  |   |  |  |  | 2100<br>2160   |
|     | TGGAGTCTGC   | ACAGCTGCTG  | TGTTCTTTAC  | ACACTTCTTC   | TACCTCTCTT   | TGTTCTTCTG   | 2220   |
|     |  | CTTGGCATCC  |   |  |  |  | 2280   |
| 55  |  | ATGATGGCTG<br>ATTGCTGTCA  |   |  |  |  | 2340<br>2400   |
| •   | GCTTAACTGG   | TCCAATGGAA  | GCAAACCACT  | CCTGGCTTTT   | GTTGTCCCTG   | CACTGGCTAT   | 2460   |
|     |  | AACTTCGTTG<br>CTGAGTCGGG  |   |  |  |  | 2520   |
| -a  |  | CIGAGICGGG  |   |  |  |  | 2580<br>2640   |
| 60  | CCAGAATCTG   | GCTTGGCATG  | TTATTTTTGC  | TTTACTCAAT   | GCATTCCAGG   | GATTTTTTAT   | 2700   |
|     |  |   |   |  |  | ACAAGTTGTC   | 2760   |
|     |  |   |   |  |  | TTTCTCATAC   | 2820<br>2880   |
| 65  |  |   |   |  |  | AAGGCAAGGA   |  |
| 65  |  |   |   |  |  | ATGTCAATGA<br>ATAAAACAAG   | 3000<br>3060   |
|     | AATGTCTCAG   |   | GAICGGGIII  | ICIGATITAG   | GGGICIGGGA   | AIAAAACAAG   | 3078   |
| 70  | Seq ID NO:<br>Nucleic Ac   | C46 DNA Se<br>id Accessio<br>quence: 75   | n #: NM_000   | 584.1  |  |  |  |
|     | 1  | 11  | 21  | 31   | 41   | 51'  |  |
| 75  | AGCAGAGCAC   | <br>: ACAAGCTTCT  | <br>  AGGACAAGAG  | <br>  CCAGGAAGAA   | <br>  ACCACCGGAA   | <br>  GGAACCATCT   | 60   |
|     | CACTGTGTGT   | AAACATGACT  | TCCAAGCTGG  | CCGTGGCTCT   | CTTGGCAGCC   | TTCCTGATTT   | 120  |
|     |  |   |   |  |  | AGATGTCAGT   | 180  |
|     |  |   |   |  |  | AGAGTGATTG<br>GGAAGAGAGC   | 240<br>300   |
| 80  | TCTGTCTGG  | CCCCAAGGAA  | AACTGGGTGC  | AGAGGGTTGT   | GGAGAAGTTT   | TTGAAGAGGG   | 360  |
|     | CTGAGAATTC   | TAAAAAATA   | TCATTCTCTC  | TGGTATCCAR   | GAATCAGTGA   | AGATGCCAGT   | 420  |
|     |  |   |   |  |  | TGTAGGGTTG<br>AATAGTTTTT   | 480<br>540   |
|     |  |   |   |  |  | TTTGAATCTA   | 600  |
|     |  |   |   |  |  |  |  |

|     | CAAAAAACAA | CAAATAATTT                | TTAAATATAA | GGATTTTCCT        | AGATATTGCA               | CGGGAGAATA               | 660          |
|-----|------------|---------------------------|------------|-------------------|--------------------------|--------------------------|--------------|
|     | TACAAATAGC | AAAATTGAGC                | CAAGGGCCAA | GAGAATATCC        | GAACTTTAAT               | TTCAGGAATT               | 720          |
|     |            |                           |            |                   | AAAATGATGG               |                          | 780          |
| 5   |            |                           |            |                   | TTTCTGTTAA               |                          | 840          |
| 5   |            |                           |            |                   | GTGCCTTGGT               |                          | 900          |
|     | TECANCENCE | GAAAAAGTAT                | TAGCCACCAT | CTTACCTCAC        | AGTGATGTTG               | TGAGGACATG               | 960          |
|     | CTATTTATTA | TTTATCTTATT               | TATTTANCO  | TCAAATTATT        | TTCAAGTGTA<br>GTGCAAGAAT | ACTTATTAAC               | 1020         |
|     | AGAAGATGAA | TCATTGATTG                | AATAGTTATA | AAGATGTTAT        | AGTAAATTTA               | TTTTATETA                | 1080<br>1140 |
| 10  | GATATTAAAT | GATGTTTTAT                | TAGATAAATT | TCAATCAGGG        | TTTTTAGATT               | AAACAAAGAA               | 1200         |
|     | ACAATTGGGT | ACCCAGTTAA                | ATTTTCATTT | CAGATAAACA        | ACAAATAATT               | TTTTAGTATA               | 1260         |
|     | AGTACATTAT | TGTTTATCTG                | AAAGTTTTAA | TTGAACTAAC        | AATCCTAGTT               | TGATACTCCC               | 1320         |
|     |            |                           |            |                   | ATTACGGAAT               |                          | 1380         |
| 15  |            |                           |            |                   | ATTTCTTGCT               |                          | 1440         |
| 15  |            |                           |            |                   | ATGACTGCAT<br>CTCCAAATTT |                          | 1500         |
|     |            |                           |            |                   | TAAAATATAA               |                          | 1560<br>1620 |
|     | AAGTAAAAA  | AAAAAAAA                  |            |                   | I/UUUIIAI/UI             | IIIGIIGICA               | 1639         |
| 20  |            |                           |            |                   |                          |                          |              |
| 20  |            |                           |            |                   |                          |                          |              |
|     |            | C47 DNA Sec               |            |                   |                          |                          |              |
|     |            | id Accession<br>mence: 13 |            |                   |                          |                          |              |
| 0.5 |            |                           | .50        |                   |                          |                          |              |
| 25  | 1          | 11                        | 21         | 31                | 41                       | 51                       |              |
|     | ]          | 1                         | 1          | 1                 | 1                        |                          |              |
|     |            |                           |            |                   | ATTCTCAGCC               |                          | 60           |
|     |            |                           |            |                   | ATGACCAGGG<br>ACCGGGAGCC |                          | 120<br>180   |
| 30  | GAATGTACAT | GGCAAGTCAA                | AGCAAACGAT | CGCAAGTACC        | ACGAACAACC               | TCACTTTATC               | 240          |
|     | AACACAAAAT | TCTTGTGTAT                | TAAGGAGAGT | AAATATGCGA        | ATAATGCAAT               | TAAAACATAC               | 300          |
|     | AAGTACAACG | CATTTACCTT                | TATACCAATG | AATCTGTTTG        | AGCAGTTTAA               | GAGAGCAGCC               | 360          |
|     |            |                           |            |                   | CTCAAATCTC               |                          | 420          |
| 35  |            |                           |            |                   | TCACTGCAAT               |                          | 480          |
| 55  | ATTANGATG  | GCAGCTTCAA                | TAAAATGGAT | AAGGAAATCA        | ACAATAGGAC<br>TTCAAGTTGG | GTGTGAAGTC               | 540          |
|     | CGTCTGAAAA | AAAATGATTT                | TGTTCCAGCT | GACATTCTCC        | TGCTGTCTAG               | CTCTCACCCT               | 600<br>660   |
|     | AACAGCCTCT | GCTATGTGGA                | AACAGCAGAA | CTGGACGGAG        | AAACCAATTT               | AAAATTTAAG               | 720          |
| 40  | ATGTCACTTG | AAATCACAGA                | CCAGTACCTC | CAAAGAGAAG        | ATACATTGGC               | TACATTTGAT               | 780          |
| 40  | GGTTTTATTG | AATGTGAAGA                | ACCCAATAAC | CGACTAGATA        | AGTTTACAGG               | AACACTATTT               | 840          |
|     |            |                           |            |                   | TGTTACGTGG               |                          | 900          |
|     | AGGAACACCG | GGRARACCAG                | ATTTANANCA | ATTITTGCAG        | GTGCTGACAC<br>ATTACTTGAT | TAAAATAATG               | 960          |
|     | GTTTACACGA | TCTTTGTTGT                | TCTTATTCTG | CTTTCTGCTG        | GTCTTGCCAT               | CCCCCATCCT               | 1020<br>1080 |
| 45  |            |                           |            |                   | ATGATGGAGA               |                          | 1140         |
|     | CCCTCCTACC | GTGGATTCCT                | CATTTTCTGG | <b>GGCTATATCA</b> | TIGITCICAA               | CACCATGGTA               | 1200         |
|     | CCCATCTCTC | TCTATGTCAG                | CGTGGAAGTG | ATTCGTCTTG        | GACAGAGTCA               | CTTCATCAAC               | 1260         |
|     | CTCAATCAAC | AAATGTACTA                | TGCTGAGAAG | GACACACCCG        | CAAAAGCTAG               | AACCACCACA               | 1320         |
| 50  | CAAAATATCA | TGACCETTEA                | AAAGTGCTGT | ATCANCEGE         | ATAAGACGGG               | GACACTCACA<br>GGACCATCGG | 1380<br>1440 |
|     | GATGCCTCTC | AACACAACCA                | CAACAAAATA | GAGCAAGTTG        | ATTITAGCTG               | GAATACATAT               | 1500         |
|     | GCTGATGGGA | AGCTTGCATT                | TTATGACCAC | TATCTTATTG        | AGCAAATCCA               | GTCAGGGAAA               | 1560         |
|     | GAGCCAGAAG | TACGACAGTT                | CTTCTTCTTG | CTCGCAGTTT        | GCCACACAGT               | CATGGTGGAT               | 1620         |
| 55  | AGGACTGATG | GTCAGCTCAA                | CTACCAGGCA | GCCTCTCCCG        | ATGAAGGTGC               | CCTGGTAAAC               | 1680         |
| 55  |            |                           |            |                   | AGAACACCAT               | CACCATCAGT               | 1740<br>1800 |
|     | AAGCGAATGT | CTATCATTGT                | AAGAACCCCA | GAAGGCAATA        | TCAAGCTTTA               | CTGTAAACCGG              | 1860         |
|     | GCTGACACTG | TTATTTATGA                | ACGGTTACAT | CGAATGAATC        | CTACTAAGCA               | AGAAACACAG               | 1920         |
| 60  | GATGCCCTGG | ATATCTTTGC                | AAATGAAACT | CTTAGAACCC        | TATGCCTTTG               | CTACAAGGAA               | 1980         |
| 00  |            |                           |            |                   | TGGCTGCCAG               |                          | 2040         |
|     |            |                           |            |                   | TTGAAAAAGA<br>TTCCAGAAAC |                          | 2100         |
|     | CTTGCAAAAG | CTGACATTAA                | GATCTGGGTG | CAGGATGGAG        | TTCCAGAAAC<br>ACAAAAACGA | AACTGCTGAA               | 2160<br>2220 |
|     | AATATAGGAT | TTGCTTGTGA                | ACTTCTGACT | GAAGACACCA        | CCATCTGCTA               | TGGGGAGGAT               | 2280         |
| 65  | ATTAATTCTC | TTCTTCATGC                | AAGGATGGAA | AACCAGAGGA        | ATAGAGGTGG               | CGTCTACGCA               | 2340         |
|     | AAGTTTGCAC | CTCCTGTGCA                | GGAATCTTTT | TTTCCACCCG        | GTGGAAACCG               | TGCCTTAATC               | 2400         |
|     | ATCACTGGTT | CTTGGTTGAA                | TGAAATTCTT | CTCGAGAAAA        | AGACCAAGAG               | AAATAAGATT               | 2460         |
|     | ACCCTACAAC | AGTTCCCAAG                | AACAGAAGAA | GAAAGACGGA        | TGCGGACCCA               | AAGTAAAAGG               | 2520         |
| 70  | AGCGCAGTCA | TCTCCTCCC                 | CGTCACCCCC | AAAAACTTTG        | CCATGGTCGC               | CTGCGAGTGC<br>GGACCTGGTG | 2580         |
|     | AAGAGGTACA | AGAAAGCCAT                | CACGCTGGCC | ATCGGAGATG        | GGGCCAATGA               | CGTGAACATG               | 2640<br>2700 |
|     | ATCAAAACTG | CCCACATTGG                | CGTTGGAATA | AGTGGACAAG        | AAGGAATGCA               | AGCTGTCATG               | 2760         |
|     | TCGAGTGACT | ATTCCTTTGC                | TCAGTTCCGA | TATCTGCAGA        | GGCTACTGCT               | GGTGCATGGC               | 2820         |
| 75  | CGATGGTCTT | ACATAAGGAT                | GTGCAAGTTC | CTACGATACT        | TCTTTTACAA               | AAACTTTGCC               | 2880         |
| 13  | CACCATTTCC | TTCATTTCTG                | GTACTCCTTC | TTCAATGGCT        | ACTCTGCGCA               | GACTGCATAC               | 2940         |
|     | GGGCTCCTCC | ACCACCATO                 | CTACAACGTG | CTGTACACCA        | GCCTGCCCGT               | GCTCCTCATG<br>GTTATACATA | 3000         |
|     | GTGGGACAAA | GAGACTTACT                | ATTCAACAAA | AAGAGATTOT        | THETALLETIN              | GTTATACATA<br>GTTGCATGGG | 3060<br>3120 |
| 0.0 | GTCCTAACAT | CGATGATCCT                | CTTCTTCATA | CCTCTTGGAG        | CTTATCTGCA               | AACCGTAGGG               | 3120         |
| 80  | CAGGATGGAG | AGGCACCTTC                | CGACTACCAG | TCTTTTGCCG        | TCACCATTGC               | CTCTGCTCTT               | 3240         |
|     | GTAATAACAG | TCAATTTCCA                | GATTGGCTTG | GATACTTCTT        | ATTGGACTTT               | TGTGAATGCT               | 3300         |
|     | TTTTCAATTT | TTGGAAGCAT                | TGCACTTTAT | TTTGGCATCA        | TGTTTGACTT               | TCATAGTGCT               | 3360         |
|     | AGACAGCCAT | ACATTTCC                  | AACTATCATT | CAATTTACAG        | GCACAGCTTC               | AAACGCTCTG<br>ACTACCCGTC | 3420         |
|     |            |                           |            | -raverarra        | CIGIGIOCIT               | WINCOUNT.                | 3480         |

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GTTGCCATTC GATTCCTGTC AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG
                                                                                        3540
       CATCGCAAGC GGTTGAAGGC GGAGGAGCAG TGGCAGCGAC GGCAGCAGGT GTTCCGCCGG
                                                                                        3600
       GGCGTGTCAA CGCGGCGCTC GGCCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC
                                                                                        3660
        ATCTCCTCCG GGCGCAGCAT CCGCAAGAAG CGCTCGCCGC TTGATGCCAT CGTGGCGGAT
                                                                                        3720
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        GGCACCGCGG AGTACAGGCG CACCGGGGAC AGCTGA
                                                                                        3756
        Seq ID NO: C48 DNA Sequence
       Nucleic Acid Accession #: XM_044533
        Coding sequence: 238..2751
10
       GCTCTGCCCA AGCCGAGGCT GCGGGGGCCGG CGCCGGCGG AGGACTGCGG TGCCCCGCGG
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        AGGGGCTGAG TTTGCCAGGG CCCACTTGAC CCTGTTTCCC ACCTCCGGCC CCCCAGGTCC
                                                                                        120
15
        GGAGGCGGGG GCCCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCCGCCCGTG
                                                                                        180
       AGTCCGGCCG AGCCACCTGA GCCCGAGCCG CGGGACACCG TCGCTCCTGC TCTCCGAATG
CTGCGCACCG CGATGGGCCT GAGGAGCTGG CTCGCCGCCC CATGGGGCGC GCTGCCGCCT
                                                                                        240
                                                                                        300
        CGGCCACCGC TGCTGCTGCT CCTGCTGCTG CTGCTCCTGC TGCAGCCGCC GCCTCCGACC
                                                                                        360
        TGGGCGCTCA GCCCCGGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCCTCAGA
                                                                                        420
20
        TTCGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC
CTGTACGTGG GTGCTCGAGA GGCCCTCTTT GCACTCAGTA GCAACCTCAG CTTCCTGCCA
                                                                                        480
                                                                                        540
        GGCGGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCAG AGAAGAAACA GCAGTGCAGC
                                                                                        600
       TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAAACTACA TCAAGATCCT CCTGCCCCTC AGCGGCAGTC ACCTGTTCAC CTGTGGCACA GCAGCCTTCA GCCCCATGTG TACCTACATC
                                                                                        660
                                                                                        720
25
        AACATGGAGA ACTTCACCCT GGCAAGGGAC GAGAAGGGGA ATGTCCTCCT GGAAGATGGC
                                                                                        780
        AAGGGCCGTT GTCCCTTCGA CCCGAATTTC AAGTCCACTG CCCTGGTGGT TGATGGCGAG
                                                                                        840
        CTCTACACTG GAACAGTCAG CAGCTTCCAA GGGAATGACC CGGCCATCTC GCGGAGCCAA
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        AGCCTTCGCC CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG
                                                                                        960
        GCCTCAGCCT ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC
                                                                                        1020
30
        TTTTTCTTCA GCGAGACTGG CCAGGAATTT GAGTTCTTTG AGAACACCAT TGTGTCCCGC
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        ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC
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        TCCTTCCTCA AGGCCCAGCT GCTGTGCTCA CGGCCCGACG ATGGCTTCCC CTTCAACGTG
                                                                                        1200
        CTGCAGGATG TCTTCACGCT GAGCCCCAGC CCCCAGGACT GGCGTGACAC CCTTTTCTAT
                                                                                        1260
        GGGGTCTTCA CTTCCCAGTG GCACAGGGGA ACTACAGAAG GCTCTGCCGT CTGTGTCTTC
                                                                                        1320
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        ACAATGAAGG ATGTGCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA
CAGCAGTGGT ACACCGTGAC CCACCCCGGTG CCCACACCCC GGCCTGGAGC GTGCATCACC
                                                                                        1380
                                                                                        1440
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                                                                                        1500
        TTCCTCAAGG ACCACTTCCT GATGGACGGG CAGGTCCGAA GCCGCATGCT GCTGCTGCAG
                                                                                        1560
        CCCCAGGCTC GCTACCAGCG CGTGGCTGTA CACOGGTCC CTGGCCTGCA CCACACCTAC GATGTCCTCT TCCTGGGCAC TGGTGACGGC CGGCTCCACA AGGCAGTGAG CGTGGGCCCC
                                                                                        1620
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        CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGGACCCC
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                                                                                        1920
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        TCGGTTGTGT CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC
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        CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC
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        TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCTCCT GCCACGTGCT ACCCACTGGG
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        GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGCTGGTC ACTAGAGGAG
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                                                                                        2280
                                                                                        2340
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                                                                                        2400
        TGCACGCTCT TTGTGCTGGC CGTGCTGCTC CCAGTTTTAT TCTTGCTCTA CCGGCACCGG
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CCTGTGGTGC TGCCCCCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCCC TAGCACCCCG
                                                                                        2520
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                                                                                        2580
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                                                                                        2700
                                                                                        2760
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                                                                                        2880
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ACAGCCGTGG CCCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCCTAGGTT GGTGGAACAG
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                                                                                        3000
        TGCTCCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAACTAGAAT
                                                                                        3060
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GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAAC
                                                                                        3120
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                                                                                        3180
        TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT
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        CAGGACCAGC TTGGGCTGCG TGCGTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTTGTTG
                                                                                        3300
        CTGCCGTCGT CCCACCACCT CAGGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA
        GGTCCTGGGC TCGGACCCAA CTCCTGGACC TTTCCAGCCT GTATCAGGCT GTGGCCACAC
                                                                                        3420
70
        GAGAGGACAG CGCGAGCTCA GGAGAGATTT CGTGACAATG TACGCCTTTC CCTCAGAATT
                                                                                        3480
        CAGGGAAGAG ACTGTCGCCT GCCTTCCTCC GTTGTTGCGT GAGAACCCGT GTGCCCCTTC
                                                                                        3540
        CCACCATATC CACCCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACTAA CTGCACCCTG
                                                                                        3600
        GTCCTCTCCC CAGCCCCAG TTCACCCTCC ATCCCTCACC TTCACCAT CTAAGGGATA
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG
                                                                                        3660
                                                                                        3720
75
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                                                                                        3766
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        Nucleic Acid Accession #: NM_007019.1
80
        Coding sequence: 41..580
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        GGCACGAGCG AGTTCCTGTC TCTCTGCCAA CGCCGCCCGG ATGGCTTCCC AAAACCGCGA
```

|             | CCGGGGTCCG<br>TAAAGGGATT               | ACTAGCGTCG<br>GTGGGCAAAA<br>TCTGCCTTCC               | GGCTACAGCA<br>CTGAATCAGA               | GGAGCTGATG<br>CAACCTTTTC               | ACCCTCATGA<br>AAATGGGTAG               | TGTCTGGCGA<br>GGACCATCCA               | 120<br>180<br>240        |
|-------------|--|--|--|--|--|--|--------------------------|
| 5           | TGGCTACCCT<br>GGACACCCAG<br>TGTCAGGACC | GGAACAGTAT<br>TACAATGCGC<br>GGTAACATAT<br>ATTCTGCTCT | CCACAGTGAA<br>GCCTGGACAT<br>CCATCCAGAG | GTTCCTCACG<br>CCTGAAGGAA<br>CCTTCTAGGA | CCCTGCTATC<br>AAGTGGTCTG<br>GAACCCAACA | ACCCCAACGT<br>CCCTGTATGA<br>TTGATAGTCC | 300<br>360<br>420<br>480 |
| 10          | AGAAACCTAC<br>CTTGTGTCGT               | CATGCTGCCG<br>TCAAAGCAGG<br>CTTTTTAATT<br>CTTGAGCTGT | TCACCAGCCA<br>TTTCCTTAGA               | GGAGCCCTGA<br>TGGTCTGTCC               | CCCAGGCTGC<br>TTTTTGTGAT               | CCAGCCTGTC<br>TTCTGTATAG               | 540<br>600<br>660<br>720 |
|             |  | TGTATATTAA   |  |  |  |  | 780<br>783               |
| 15          | Nucleic Aci                            | C50 DNA Sec<br>d Accession<br>lence: 227             | #: NM_0145                             | 584.1                                  |  |  |                          |
| 20          | 1                                      | 11   | 21                                     | 31                                     | 41                                     | 51                                     |                          |
| 20          | TGGCGATCGC                             | CGGGCTGCCG<br>TGAGAGGCAG<br>GCCGGCCCGC               | GAGGGCCGAG                             | GCGGGCCTGG                             | GAGGCGGCCC                             | GGAGGTGGGG                             | 60<br>120<br>180         |
| 25          |  | CTCCCAAGCG   |  |  |  |  | 240                      |
| 25          |  | TTTGGCCTCC   |  |  |  |  | 300                      |
|             |  | GAGACAGCGG<br>GATGTTGAAA                             |  |  |  |  | 360<br>420               |
|             | ACAAAAACTT                             | CTTGAAAGTG   | ACTACTTTAG                             | GTATTACAAG                             | GTAAACCTGA                             | AGAGGCCGTG                             | 480                      |
| 30          |  | AATGACATCA   |  |  |  |  | 540                      |
| 30          | ATCTGATGAA                             | GTTCCTGATG<br>GAAGAATGTG                             | GAATTAAATC                             | TGCGAGCTAC                             | AAGTATTCTG                             | AAGAAGCCAA                             | 600                      |
|             | TGAGGAAACA                             | CAGAAGGCTG   | TTCTTCAGTG                             | GACCAAGCAT                             | GATGATTCTT                             | CAGATAACTT                             | 660<br>720               |
|             | CTGTGAAGCT                             | GATGACATTC   | AGTCCCCTGA                             | <b>AGCTGAATAT</b>                      | GTAGATTTGC                             | TTCTTAATCC                             | 780                      |
| 35          | AGAAAACTCT                             | TTTAAGCCAC   | AGGGACCAGA                             | TGCTTGGAAA                             | ATATGGAATG                             | TCATCTACGA                             | 840<br>900               |
|             |  | GAAGAGAACA   |  |  |  |  | 960                      |
|             |  | AGACTTATAT   |  |  |  |  | 1020                     |
|             | ACAGCGATTT                             | CAAGAGACCT<br>GATGGAATTT                             | GGTTAGAAAA<br>TGACTGAAGG               | GAAATGGGGA                             | CACAACATTA                             | CAGAATTTCA                             | 1080                     |
| 40          |  | TTAATAGAAC   |  |  |  |  | 1140<br>1200             |
|             |  | CTCTTTACTG   |  |  |  |  | 1260                     |
|             |  | CATGAAATCA<br>AAAGAAGCAC                             |  |  |  |  | 1320                     |
| 4.5         |  | ATGGATTGTG   |  |  |  |  | 1380<br>1440             |
| <b>45</b> , | TCAGGGTTTG                             | GGCACTGCTC   | TGAAGATCTT                             | ATTTTCTGAG                             | AAATTGATAG                             | CAAATATGCC                             | 1500                     |
|             |  | CCTAGTTATG   |  |  |  |  | 1560                     |
|             |  | AGAATTTCTA<br>TAAAGAAAAC                             |  |  |  |  | 1620<br>1680             |
| 50          | AGTGGAATTT                             | CATTCAAAGG   | CATAATAGCA                             | ATGACAGTCT                             | TAAGCCAAAC                             | ATTTTATATA                             | 1740                     |
| 50          | AAGTTGCTTT                             | TGTAAAGGAG   | AATTATATTG                             | TTTTAAGTAA                             | ACACATTTTT                             | AAAAATTGTG                             | 1800                     |
|             | TTTAAAGTTT                             | GTATAATACT<br>AATATTGAAT                             | AAAAGGAGGA                             | TTATCAAATT                             | CATATATGAT                             | AAAAGTGAAT                             | 1860<br>1920             |
|             | GTTCTAAGTC                             | TCTCAAACTA   | GCGTTTTATG                             | TAATAATATG                             | TAATATAAAT                             | AAAACTATGG                             | 1980                     |
| 55          |  | AAGCATTTAA   |  |  |  | ACCCATAATT<br>AAAATAAAGA               | 2040                     |
|             | TTGCCCAGTT                             | AGATTTGAAT   | TTCAGATAAA                             | CAATTAGTTT                             | TTTAATATTT                             | TACATGGAAT                             | 2100<br>2160             |
|             | ATTTGGAAAA                             | TACTTATACT   | AAAAAATTAT                             | TTGTTTGAAA                             | TTCACATTTA                             | ACTGGGAGTC                             | 2220                     |
|             |  | TCTGGCAATC   |  |  |  | TTTAGAAGTA                             | 2280                     |
| 60          |  | TCTAAACATT   |  |  |  |  | 2340<br>2400             |
|             | TTTCACTAAT                             | ACTAAATAAA   | ATTTGGGGAA                             | CACTTTTTAT                             | TTTTATATAA                             | TTTCCAATTT                             | 2460                     |
|             |  | TTCAAAAATA<br>TCTTTCATGC                             |  |  |  |  | 2520                     |
| <i></i>     |  | AGTCAGTTAT   |  |  |  |  | 2580<br>2640             |
| 65          | ATACTGAATA                             | ATTACTAAAA   | ATGATTTTCT                             | CAGAAAAAAA                             | AACTCCCACA                             | ATTCTGGAAC                             | 2700                     |
|             |  |  |  |  |  | AGTTCTTTTT<br>ATTTATTTTA               | 2760                     |
|             |  |  |  |  |  | TTGAACGACT                             | 2820<br>2880             |
| 70          | GGGCTGAAGT                             | GATCTTCCCA   | CCTCAGCCTC                             | CCAAGTAGCT                             | GGGAATACAG                             | GTGTCTGCCA                             | 2940                     |
| 70          | CCATACCCAG                             | TTTCATTTT  | GTTTTTTATA                             | CCCGAAGTTC                             | ATTTCCTTTG                             | TCTCCCTAAA<br>AAAGCTATTT               | 3000                     |
|             |  |  |  |  |  | TATATACCTC                             | 3060<br>3120             |
|             | AAAATCGTGC                             | CCTCTTTACA   | TATGTCTTAT                             | CAGGTATAAC                             | ATGTTGAAAT                             | GTCACATTAG                             | 3180                     |
| 75          |  |  |  |  |  | TGCTGTATAC                             | 3240                     |
| ,,,         |  | GATGAAAAA  |  |  | ACATACTIGG                             | TATCCAATAA                             | 3300<br>3334             |
| 80          | Nucleic Ac                             | C51 DNA Se<br>id Accessio<br>uence: 37               | n #: NM_002                            | 888.1                                  |  |  |                          |
|             | į                                      | 11   | 21                                     | 31                                     | 41                                     | 51                                     |                          |
|             | 1                                      | 1  |  | 1                                      | 1                                      | 1                                      |                          |
|             |  |  |  |  | 11                                     | 229                                    |                          |
|             |  |  |  |  |  | ·                                      |                          |

```
CCACGTCCGG GGTGCCGAGC CAACTTTCCT GCGTCCATGC AGCCCCGCCG GCAACGGCTG
       CCCGCTCCCT GGTCCGGGCC CAGGGGCCCG CGCCCACCG CCCCGCTGCT CGCGCTGCTG
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       CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGGCGCGCGC GGCGCTTCAC
                                                                                   240
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                                                                                   300
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CGCTACAACC CAGAGTCTTT ACTTCAGGAA GGTGAGGGAC GTTTGGGGAA ATGTTCTGCT
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                                                                                   420
       CGAGTGTTTT TCAAGAATCA GAAACCCAGA CCAACCATCA ATGTAACTTG TACACGGCTC
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                                                                                   720
       TGAAAATTAA CTTGTGCCAC AAGAGTTACA ATCAAAGTGG TCTCCTTAGA CTGAATTCAT
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25
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       TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC
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       ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT
                                                                                   300
       AAAGGACAAC GATGCCTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT
                                                                                   360
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                                                                                   480
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                                                                                   540
       GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA
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       CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT
       GGITACCATC GGAGTITACA AAGTGCITTC ACGTTCTTAC TTGTTGTATT ATACATTCAT
                                                                                   720
35
       GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT
                                                                                   780
       GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT
                                                                                   840
       CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG
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                                                                                   900
                                                                                   960
       CCAAATATCA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT
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       TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA
                                                                                   1080
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                                                                                   1140
                                                                                   1200
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                                                                                   1260
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        CTCAGCGCGC TCAACCGCTT CCAGCCCGAG GGCGACCTGG AGCGCCTGGT CGCTCCCAGC
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                                                                                    300
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       TCCCCAACCG GGGACAATAT TTTGCTCCAG GCTGAGGGGA TCCTGCAGAC CCACCGAGCC GTGCTGGAAA TGAAGGTGAA CCACAAGGGC TATAATTATA CTTTTTCCCA TCTGTGTGTG
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                                                                                   420
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        GCCCTCCTGT CCATCAGGAG AAGGAAAGGA TAAACCCTGG GCCATGAGGC TACCCCTGCT
                                                                                    120
75
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                                                                                    180
                                                                                    240
        CGCAGCTTGC AACCAGGATG CCGAATCACA GAAATTCCGA TGGGTGTCCG AATCTCAGAT
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        420
80
                                                                                    480
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        CAATCTGTGC TCCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC
                                                                                    600
        AACCTGTGCA TTCCCGTTCA AGTTTGAAAA CAAGTGGTAC GCAGATTGCA CGAGTGCTGG
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                                                                                    660
                                                                                    720
```

|    | TGGATATTGT  | CCATTGAAAT  | TTGAGGGCAG  | TGAAAGCTTA | TGGAATAAAG               | ACCCCCTGAC               | 780          |
|----|-------------|-------------|-------------|------------|--------------------------|--------------------------|--------------|
|    |             |             |             |            | TGGCACCAAG               |                          | 840          |
|    |             |             |             |            | ATACATGAGC               |                          | 900          |
| -  |             |             |             |            | GGACTTAACA               |                          | 960          |
| 5  |             |             |             |            | TATTTGAACT               |                          | 1020         |
|    | AAGTCCATCA  | GCTGAACCTG  | GAAAAAGCTG  | TGTGTCACTA | AATCCTGGAA               | AAAATGCTAA               | 1080         |
|    | ATGGGAAAAT  |             |             |            |                          |                          | 1140         |
|    |             |             |             |            | ACTCACTGTC               |                          | 1200         |
| 10 |             |             |             |            | Gagaaaaaa                |                          | 1260         |
| 10 |             |             |             |            | AGTATCCACA               |                          | 1320         |
|    |             |             |             |            | GACGAATTGT               |                          | 1380         |
|    |             |             |             |            | GGGACCCCTG               |                          | 1440         |
|    |             |             |             |            | CAGGAGGATT               |                          | 1500         |
| 15 |             |             |             |            | GTCGAAAAAG               |                          | 1560         |
|    |             |             |             |            | CATACGCTTT               |                          | 1620         |
|    |             |             |             |            | ACAACTATTG               |                          | 1680<br>1740 |
|    |             |             |             |            | GAAAAATATT               |                          | 1800         |
|    |             |             |             |            | ATCGAGGAAG               |                          | 1860         |
| 20 |             |             |             |            | TGTGTTGCCA               |                          | 1920         |
|    |             |             |             |            | AAGGCAAAAT               |                          | 1980         |
|    |             |             |             |            | ACGACTCCCG               |                          | 2040         |
|    |             |             |             |            | TTCAAGCTGT               |                          | 2100         |
| 25 | AAAACATGAG  | AAGAAAACGT  | GGTTTGAATC  | TCGAGATTTT | TGTCGAGCTC               | TGGGTGGAGA               | 2160         |
| 25 | CTTAGCTAGC  | ATCAATAACA  | AAGAGGAACA  | GCAAACAATA | TGGCGATTAA               | TAACAGCTAG               | 2220         |
|    | TGGAAGCTAC  | CACAAACTGT  | TTTGGTTGGG  | ATTGACATAT | GGAAGCCCTT               | CAGAAGGTTT               | 2280         |
|    | TACTTGGAGT  | GATGGTTCTC  | CTGTTTCATA  | TGAAAACTGG | GCTTATGGAG               | AACCTAATAA               | 2340         |
|    |             |             |             |            | CCTACTATGT               |                          | 2400         |
| 30 |             |             |             |            | CAAAAAGGAC               |                          | 2460         |
| 50 |             |             |             |            | ACTGAAGATG               |                          | 2520         |
|    |             |             |             |            | ACCATGGACA               |                          | 2580         |
|    |             |             |             |            | AGTGAAAGTG<br>TATTTTATTG |                          | 2640         |
|    |             |             |             |            | GTGGATTACG               |                          | 2700<br>2760 |
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|    |             |             |             |            | TOGGTCCCAT               |                          | 2940         |
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|    | AGGAGTCCAT  | TACACAAACT  | GGGGGAAAGG  | TTACCCTGGT | GGAAGAAGAA               | GCAGTCTTTC               | 3240         |
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| 30                               | GGACCTTGAA   | AAAGCTATTA   | AGGGTGTGGT   | TGTGATGGAT   | TCTGCATTGG   | AGGCACTCTC   | 1620   |
|                                  |  | CTTGTTGGAA   |  |  |  |  | 1680   |
|                                  |  | GGAAAACCTT   |  |  |  | TACAGGACTG   | 1740<br>1800   |
|                                  |  |  |  |  |  | ATTTGCTAGG   | 1860   |
| 35                               |  |  |  |  |  | ATGGTGTTTA   | 1920   |
|                                  |  |  |  |  |  | TGCTTGCTGA   | 1980   |
|                                  |  |  |  |  |  | CAACTCAAAA<br>GTGAACGTAA   | 2040<br>2100   |
| 4.0                              |  |  |  |  |  | TGTTAAAAAC   | 2160   |
| 40                               |  | ACTCGGCACT<br>CAAATTTATA   |  |  | TTGCTTTGTC   | AGTTGGATGA   | 2220<br>2256   |
|                                  | Com ID NO.   |  |  |  |  |  |  |
| 45                               | Nucleic Ac   | C60 DNA Second Accession uence: 14   | quence<br>n #: J02761  |  |  |  |  |
| 45                               | Nucleic Ac   | C60 DNA Sed  | quence<br>n #: J02761  |  | 41<br>!  | 51<br>I  |  |
|                                  | Nucleic Ac<br>Coding seq   | C60 DNA Second Accession Lence: 14   | quence<br>n #: J02761<br>1159<br>21  | .1<br>31<br>   | 1  |  | 60   |
| <b>45 50</b>                     | Nucleic Ac<br>Coding seq<br>1<br> <br>GAATTCCGGT<br>GCTCTGTGGC   | C60 DNA Second Accession uence: 14   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC   | .1 31   GCTGCAGTGG CACCTCATCC  | CTGCTGCTGC TTGGCCTGTG  | TGCTGCCCAC<br>CCCAGGGCCC   | 120  |
|                                  | Nucleic Ac Coding seq  | C60 DNA Serid Accession uence: 14  11   GCCATGGCTG CCAGGCACTG TGCCAAAGCC   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC  | .1 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGG   | CTGCTGCTGC TTGGCCTGTG  | TGCTGCCCAC<br>CCCAGGGCCC<br>GGCATTGCCT   | 120<br>180   |
|                                  | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGGGC TGAGTTCTGG   | C60 DNA Serid Accession uence: 14  11    GCCATGGCTG CCAGGCACTG TGCCAAAGCC TGGGACATG  | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCCAAGC TGGGAGCCGA  | .1<br>31<br> <br>GCTGCAGTGG<br>CACCTCATCC<br>ATTGCAGTGC<br>TGACCTATGC  | CTGCTGCTGC<br>TTGGCCTGTG<br>AGAGCCCTAG<br>CAAGAGTGTG   | TGCTGCCCAC<br>CCCAGGGCCC<br>GGCATTGCCT<br>AGGACATCGT   | 120<br>180<br>240  |
| 50                               | Nucleic Ac Coding seq  1   GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAGG  | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAGC TGGAGCAGC TGCAGGAGCCGA  | .1 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC CATTTTCAGG GCTGCTCATG  | CTGCTGCTGC<br>TTGGCCTGTG<br>AGAGCCCTAG<br>CAAGAGTGTG<br>GACACGATGA<br>CCCCAGTGCA   | TGCTGCCCAC<br>CCCAGGGCCC<br>GGCATTGCCT<br>AGGACATCGT<br>GGAAGTTCCT<br>ACCAAGTGCT   | 120<br>180   |
|                                  | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAG TGACGACTACCT  | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TGGGAGCCGA CCAAGGAGGC TCCCCTGGAC TCCCCTTGAC TCATCGACTA   | 31<br>  GCTGCAGTGG<br>CACCTCATCC<br>ATTGCAGTGC<br>TGACCTATGC<br>CATTTCCAG<br>GCTGCTCATG<br>CTTCCAGAAC  | CTGCTGCTGC<br>TTGGCCTGTG<br>AGAGCCCTAG<br>CAAGAGTGTG<br>GACACGATGA<br>CCCCAGTGCA<br>CAGACTGACT   | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT GGAAGTTCCT ACCAAGTGCT CAAACGGCAT   | 120<br>180<br>240<br>300<br>360<br>420   |
| 50                               | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAG TGACGACTAC CTGTATGCAC   | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TGGAGCAAGC TCGCGTTGAA CCAAGGAGGC TCCCCTTGAA TCATCGACTA GCAAATCCCG  | .1  31   GCTGCAGTGG CACCTCATCC TTGACTGC TTGACCTATGC CATTTTCAG GCTGCTCATAG GCTTCCAGAAG GCAGCCAGAG   | CTGCTGCTGC<br>TTGGCCTGTG<br>AGAGCCCTAG<br>CAAGAGTGTG<br>GACACGATGA<br>CCCCAGTGCA<br>CAGACTGACT<br>CCAGAGCAGG   | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCCT GGAAGTTCCT ACCAAGTGCT CAAACGGCAT AGCCAGGGAT  | 120<br>180<br>240<br>300<br>360<br>420<br>480  |
| 50                               | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGTGGC TGAGTTCTGG CCACATCCTT GGAGCAGAGT TGACGACTAC CTGTATGCAC GTCAGACCCCC  | 11   GCCATGGCTG ACAAGACTG ACAAGATGG TGCAAAGATGG TGCAAGATGG TGCAAGATGG TGCAAGATGG TGCAAGATGG TGCAAGATGG TGCAAGATGG TGCAAGATGG TGCAAGATGG CTGGGCCTGT CTGCCCAAAG  | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAGCGA CCAAGGAGGGC TCCCCTTGAA TCATCGACT GGAACTCA GCAAATCCAG  | .1  31    GCTGCAGTGG CACCTCATCC ATTGCAGTGC CATTTTCCAG GCTGCTCATG CTTCCAGAAC GCAGCCAGAG CCCTCTGCCA  | CTGCTGCTGC TTGGCCTGTG TTGGCCTTGTG CAAGAGTGTG GACACGATGA CCCCAGTGCA CAGACTGAC CCAGAGCAGG GACCCTCTGC   | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT GGAAGTTCCT ACCAAGTGCT CAAACGGCAT   | 120<br>180<br>240<br>300<br>360<br>420   |
| 50<br>55                         | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGACTCCTG GGAGCAGGAG TGACAGCACTAC CTGTATGCAC GTCAGACCCCC CCTCCCCCCCCCC   | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTTGAC TGGGAGCAAGC TCGCGTGAG CCAAGGAGC TCCCCTTGA TCATCGACTA GCAAATCCCG CTCTGCGGGA GGGCCTCCA  | 31<br>  GCTGCAGTGG<br>CACCTCATCC<br>ATTGCAGTGC<br>TGACCTATGC<br>CATTTTCCAG<br>GCTGCTCATG<br>CTTCCAGAAC<br>GCAGCCAGAG<br>CCCTCTGCCA<br>GGCGAGGCCT<br>CTATTGCTGG   | CTCTGCTGCTGCTGCTGCTGCAGAGCCCTAGACACGATGACCCAGTGCACGAGCAGGCAG   | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT GGAAGTTCCT ACCAAGTGCT CAAACGGCAT AGCCAGGGAT TGGACAAGTCT CACAGGATCT CACAGGATCT CCCAGGATCT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660   |
| 50                               | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGTGGC TGAGTTCTGG CCACATCCTT GGAGCAGGAG TGACGACTAC GTCAGACCCC GTCAGACCCC GTCCTCCCCC CTCCGAGCAG GCGGATCCAA  | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAGG TCCCCTTGAA TCATCGACTA GCAAATCCCG CTCTGCGGGA TCCTCCCCTCC   | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC CATTTTCAG GCTGCTCATGC CTTCCAGAAC GCAGCCAGAG CCCTCTGCCA GGCGAGGCCT CTATTGCTGCA GGCTAGCCT GGCAGCCT GCCAGGGCCT GCTATGCTGC   | CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTGAGAGCCCTAGGACAGGAGAGAGA  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGGACATTCCT ACCAAGTGCT CAAACGGCAT AGCCAGGAT TGGACAAGT CTCTGATCAA   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720  |
| 50<br>55                         | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGCAGTAGT CGAGCAGGAGTC GTCAGACCCC GTCAGACCCC GTCCTCCCAGCAG GCGGATCCAA  | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TCGCAGGAGC TCCCCTTGAA TCATCGACTA GCAAATCCCG GCTCTGCGGA GGGCCTCCA TTCCTCTCCC CCAAGGGTGC   | 31<br>  GCTGCAGTGG<br>CACTCATCC<br>ATTGCAGTGC<br>TGACCTATGC<br>CATTTCCAG<br>GCTGCTGATGC<br>CTTCCAGAAC<br>GCAGCCAGAG<br>CCCTTGCCA<br>GGCAGGCCT<br>CTATTGCTGG<br>GCTAGCTGTG<br>CCAGTGCCTG  | CTGCTGCTGC TTGGCCTGTG AGAGCCCTAG CAAGAGTGTG GACACGATGA CCCCAGTGCA CAGACCAGG GACCCTCTGC GGGCCTCACA CTCTGCAGGG GCAGTGGCAC GCTGAGCGGC GCTGAGCGC GCTGAGCGCC GCTGAGCGCC GCTGAGCGCC  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGCAAGTGCT ACCAAGTGCT CACAGGCAT AGCCAGGCAT AGCCAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT AGCTGGATCAA AGGTGTGCCG ACTCCGTCAT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660   |
| 50<br>55                         | Nucleic Ac Coding seq  I GARTTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAG TGAGACCCC GTCTCCCT CTCCGAGCAG GCGGATCCAA CGTGGTACCAC GTGGTACCAC GTGGTACCAC GTGGTACCAC GTGGTACCAC GTGGTACCAC GTGGTACCAA  | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAGGCACTG TGGGGACATG ACAAGATGG TGCAAGGTCC TTCCCCTGG CTGCCCAAGC GTGCTGCCAAAC GTGCTGCCCAAGC CAATTCCCCA GCCATGATTC CTGGTGGCGG ACGCTGCTGGGCGG ACGCTGCGGGCGG ACGCTGCGGGGGGAGATGCGGGAGATACGGGGAGATACGGGGAGATACGGGAGATACAGGGGAGAACAGGGGAGATACAGGGGAGATACAGGGGAGAACAGGGGAGATACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGGAGAACAGGGAGAACAGGAGAGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA  | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TCCCCTTGAA CCAAGGAGGC TCCCCTTGAA GCAAATCCCG CTCTGCGGA GGGCCCTCCA TTCCTCTCCC CCAAGGGTGC CCAAGGGTGC GCCGCATCTG   | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC GCTGCTCATG GCTGCTCATG GCAGCCAGAG GCCAGAGC CCTCTGCCA GGGAGGCCT CTATTGCTGG GCTAGCTGG GCAGGCGGGGGGCCT GCCCGGCTG GCCCGGCTG GCCCGGCTG  | TIGGCTGCTGC TTGGCCTGTG AGAGCCTTAG AGAGCCTTAG CAAGAGTGTG GACACGATGAC CCCAGAGCAGG GACCTCTGC GGGCCTCACA CTCTGCAGGGC GCTGAGCGCT GTCTGCAGGC GCTGAGCGCT GGTCTGCAGGC GGAGAATGGCC GGGAGAATGGCC GGGAGAATGGCC  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGGACATCGT CAAACGCAT AGCCAGGGAT TGGACAAGTCT CACAGGGAT TGGACAAGTC CTCTGATCAA AGGTGTGCCG ACTCCGTCCT TGCCCGCAGA   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>720<br>780<br>840<br>900  |
| 50<br>55<br>60                   | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGTGGC TGAGTTCTGG TGAGTCTGT GGAGCAGGAG TGAGGAGTAC CTGTATGCAC GTCAGACCCC CTCCGACCAC CTCCGACCAC CTGCTCCAC GTGGTACCA GTGGTCCAC GTGGTCCAC CTTGGTGGACCC CTTGGTGGACCC CTTGGAGTGCC  | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TCCCCTTGAA TCATCGACTA GCAAATCCCG GCTCTGCGGA GCTCTGCGGA GGGCCCTCCA TTCCTCCCC CCAAGGGTGC GCGCATGCT CTGGCCAAG   | 31   GCTGCAGTGG CACTCATCC ATTGCAGTGC TGACCTATGC CATTTTCCAG CCTCTGCAG GCTGCTGCAG GCGGGGGCCT CCTATTGCTGG GCTGCTGCAG GCTGCTGCAG GCTAGCTGCAG GCTAGCTGCAG GCTAGCTGCAG CCAGTGCCTG GCCCAGCTG GTCGCCGACAG CACCCAGGCC   | CTGCTGCTGC TTGGCCTGTG AGAGCCTAG AGAGCTGTG AGAGCAGTGCA CCCAGTGCA CCAGAGCAGG AGACCTCTGC GGGCCTCACA CTCTGCAGGG GCAGTGGCC GCTGAGCGGT GCTGCGGGC GCTGAGCGGC GCTGAGCGCT GCTGGCGCC GGAGAATGGC GGAGAATGGC GGAGAATGGC  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGCAAGTGCT ACCAAGTGCT AGCCAGGAT TGGACAAGCT CACAGGATCT CACAGGATCT CACAGGATCT CTCTGATCAA AGCTGCCCC ACTCCGTCAT TCGTCCTCCG TGCTCCCG  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900   |
| 50<br>55                         | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGCATCCTT GGAGCAGGAG TGACGACACC CTCTGTATGCAC CTCTGAGCAG GCGGATCCCT CTCGAGCAG GCGGATCCAC CTGCTCGAC CTGCTCCAC CTCTCCTCCCC CTCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCCTCCAC CCTCTCCAC CCTCTCCAC CCTCTCCAC CCTCTCCAC CCTCTCCAC CCTCTCCAC CCTCTCACC CCATACCACAC CCATACCACAC  | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TGGAGCAAGC TCCCTTGAA TCATCGACTA GCAAATCCCG CTAGGAGCCTCCA TTCCTCCCG CCAAGGAGCC CCAAGGAGC GGGCCATCCA TTCCTCCCC GCGGCATCTG GCGCCATGCT CTGGCCCAAG TGCCCCAAG   | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC CATTTCCAGAAC GCTCTCAGAAC GCAGCCAGAG CCTCTGCCA GGCAAGGCCT CTATTGCTGG GCTAGCTGTGG GCAGTGCCTG GCCCAGCTG GCCCAGCTG GCCCAGCTG GCCCAGCTG GTCGCCGACA CACCCAGGCC TGGCTCTGGGC  | CTGCTGCTGC TTGGCCTGTG AGAGCCCTAG CAAGAGTGTG GACACGATGA CCCCAGTGCA CAGACTGACT CCAGAGCAGG GACCCTCTGC GGGCCTCACA CTCTGCAGGG GCTGAGGGG GTGAGGGC GGGAAATGGC GGGAAATGGC CTGGCAGC CTGGCAGC GGGAAATGGC CTGGACAGG   | TGCTGCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGCAAGTGCT ACCAAGTGCT CAAACGGCAT AGCCAGGATCT CTGAACAGCT CACAGGATCT CTCTGATCAA AGGTGTGCCG ACTCCGTCAT TCGTCCTCCG TCGCCAGGAC AGAGGACAGGC AAAAGTGCAA  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020  |
| 50<br>55<br>60                   | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAG TGAGACCCC GTCTCCCT CTCGAGCAG GCGGATCCAA GCGGTCCCCAT CCTGTCGAGCAG GCGATCCAA GTGGTACCA CCTGTCGACCAG GCGATCCAAG GTGCTCCAAG GTGCTCCAAG GTGCTCCAAG GTGCTCCAAG GTGCTCCAAG GTGCTCCAAG GCAATTTGTG   | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAAAGCC TGGGGACATG ACAAGATGG TGCCCCAAAG CTGGGCCTGG CTGCCCAAAG CTGCTGCCCAAAG CGCATTCCCCA GCCATGTGCGGC CAATTCCCCA GCCATGTGCGGC CAATTCCCCA GCCATGATGC CTGGTGCGG CAATTCCCCA GCCATGATGC CTGGTGCGG CAATCCCCA GCCATGATGC GAGCATGCTGC GAGCATGCTCGC GAGCAGCTCCG GAGCAGCACAGCGC CAATGCTCCG GAGCAGCACACAGCGC CACGGCACACAGCGC CACGGGACACACAGCGC CACGGCACACAGCCC CACGGCACACACA  | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGGGAGCAGC TCCCCTTGA CCAAGGAGC TCCCTTGAC GCAAATCCCG CTCTCCCGGGA TTCCTCTCCC CCAAGGGTGC CCAAGGGTGC CCCAGGAGC CCTGCCGGAGC TTCCTCCCC CCAAGGGTGC CCGCCAGGTGC CCGCCAGGTGC CCGCCCAGGTGC CCGCCCAGGTGC  | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC GCTGCTATG GCTGCTAGG GCTGCTAGG GCTGCTAGG GCAGGCCT CTATTGCTGG GCAGGCCT GCAGTGCCT GCCAGTGCCT GCCCAGCTG GCCCAGCTG GCCCAGCCG GCCCAGCCG GCCCAGCCG GCCCAGCCG GCCCAGCCG GCCCAGCCG GCCCAGCCG GCCCAGCCG GCCCAGCCG GCCCAGCCCG GCCCAGCCCG GCCCAGCCCG GCCCACCCGGCCG GCCCACCCGGCCG GCCCACCCGGCCC  | CTGCTGCTGC TTGGCCTGTG AGAGCCTAG AGAGCTGTG AGAGCTGAC CCAGAGCAGC AGACTGAC CCAGAGCAGC GAGCTCACA CTCTGCAGGG GCAGTGACC GCTGAGCGC GTTGCAGGG GCAGTAGCC GCTGAGCGGC GGAGAACAGC CTGGCAGC GTGCCCC GGAGAACAGC CTGGCAGC GTGCCCC   | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGCAAGTGCT ACCAAGTGCT AGCCAGGAT TGGACAAGCT CACAGGATCT CACAGGATCT CACAGGATCT CTCTGATCAA AGCTGCCCC ACTCCGTCAT TCGTCCTCCG TGCTCCCG  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900   |
| 50<br>55<br>60                   | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGCAGGAGTAC CGACATCCTT GGAGCAGGAG TGACGACTAC CTCTATECAC CGTCTCCACCAC CGTCCTCCAC CGTCCTCCAC CGTGGTACCAC CCTCTGAGTACCAC CCACACCACCCCCCACACCCCCCCCACACCCCCC   | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAGC TGGAGCAGC TCCCCTTGAA TCATCGACTA CCAAGGAGCC GCAAATCCCG GCAAATCCCG CTTCCCTGGAC GCGCCTCCA TTCCTCTCCC GCGGATGCT GCGGCCTGGAC AGGCTTGTGCCAGGGT CCGCCCAGCT CTGCCCAGGT CTGCCGGGTTGC CGAGAACTCAG   | 31   | CTGCTGCTGC TTGGCCTGTG AGAGCCCTAG CAAGAGTGTG GACACGATGA CCCCAAGTGCA CAGACTAGCT GACACTAGCA GACCTCTGC GGGCCTCACA CTCTGCAGGG GCAGTGGCCC GCTGAGCAGGG GTGCCCG GTGACAGGC CTGGCAGGC GTGCCCGC GGGAAAGGCAGC CTGGACAGGC CTGGCCCG GGGAACAGCC CTGGCCCGC GGGAACAGCA CTGGCCCGC TCCAGCCCTG GCCAAAGGAAA   | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGCAAGTGCT ACCAAGTGCT CACAGGCAT AGCCAGGATCT CTCTGATCAA CGCTGTCAT CTCTCCTCAT AAAGTGCAA CTCCATGTAT AGCCAAGTGA   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140   |
| 50<br>55<br>60<br>65             | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAG TGACACCAC GTCGGAGCAG GCGGATCCAA GCGGATCCAA GCGGATCCAA GCGGATCCAA GCGACACCAC CCACACCACC CACACCCCC CACACGCCC CACAGGCCC GACGGGCTCT   | C60 DNA Seid Accession uence: 14  11   | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAGC TGGAGCAGC TCCCTTGGAC TCCCTTGGAC TCCCTTGGAC TCCCTTGGAC TCAGGAGCCA CCAAGGAGCC CTCTCCGGGA TCCTCCCGGGA TTCCTCCCC CCAAGGTGC GCGCATCTC GCCCCAAGC TGCCCAAGC TGCCCAAGC TGCCCAGCT CGGCCCTGCT TCGGGGTGTG CGGCACCCAGCT TCGGCCTAGCT TCGGGGTGTG TGGCCCAGCT TCGGGGTGTG TGGCCCAGCT TGGCCCAGCT TCGGGGTGTG TGACCAGGCT TGACCAGGCT TGACCAGGCT TGACCAGGCT  | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC CATTTTCAGA GCTGCTCATG CTTCAGAAC GCAGCCAGAG CCCTCTGCCA GCAGCCAGAG GCTAGCTGT CTATTGCTGG GCTAGCTGT GCCCCAGCTG GCCCAGCTG TGGCTCCTGG TGGCTCCTGG TGGCTCCTGG TGGGACCATG CTTCCCCTGC   | CTGCTGCTGC TTGGCCTGTG AGAGCCTTAG AGAGCTGTG AGAGCTGTG CAGACTGACT CCAGAGCAGG GACCCTCTGC GGGCCTCACA CTCTGCAGGG GCAGTGACT GTTGCAGGG GCAGTGACC GTTGCAGGG GTTCTGCAGGG GTTCTGCAGGG TTCTGCAGGG TTCTGCAGGG TTCTGCAGGG TTCTGCAGGC TTCGAGCCCT TCGAAGCAGC TCCAGCCTTG CGCAAAGGAAF TCCCTGGCCCC   | TGCTGCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGCAAGTCCT ACCAAGTGCT CAAACGGCAT AGCCAGGATT TGGACAAGCT CACAGGATCT CACAGGATCT CTCAGCACAC ACTCGTCAT TCGTCCTCCG TCGCCAGCAGC AAAAGTGCAA GCCAGGATCA AGCTGGACAG CCCAGGATCA AGCCAAGAGCAA TCCCAGTGTAT AGCCCAAGTGA TCGCCAGCTG  | 120<br>180<br>240<br>300<br>360<br>420<br>600<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1140<br>1260   |
| 50<br>55<br>60                   | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGG TGAGTTCTGG ACAGCAGGAG TGAGACCCC CTGTATGCAC GTCAGACCCC CTGCTCCCT CTCGAGCAG GCGATCCAA CGTGGTACCAA CGTGGTACCAA CGTGCTCCAAGCCCC CACAGCCCC CCACAGCCCC CCACAGCCCC CCACAGCCCC CCACAGCCTC CCAGGCTGAA  | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAGGCACTG TGGGGACATG ACAAGATGG TGCAGAGTCC TTGCCCAGG CAATTCCCCAG GCAATTCCCCAG GCATTCCCCAG CAATTCCCCAG CAATTCCCCAG GAGCAGCACATGCCG GAGCACATGCCG GAGCAGCCCG GAGCATGATGC TGCCAGGCCCG GAGCACACATGCCCG GAGCACACATGCCAG CAATGCTCCAG GAGCACACACATGCCAGCCCCGAATGCTCCAGAGCCCCGAACCATGCAATGCTCCAGAGCACAATGCCAGAGCACAATGCCAGGCCCCGAACCATTGATAGAAGAAGCCCCCAAGACCATGCCAGACAATGCCAGGCCCCAAAGAAGAAGCCCTCAGAAAGAA   | quence n #: J02761 1159 21   | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC GTGCTCATGC CATTTTCCAG GCTGCTCATG GCAGCCAGAG GCAGCCAGAG GCCCAGCTG GCCCAGCTG GCCCAGCTG GCCCAGCTG GCTGCCCAGCTG GCTGCCCAGCTG CACCCAGCCG TGGCTCCTG TGGGACCATG CTTCCCCTGC CCCCCCTGCCAGCC CCCCCCCCCC   | CTGCTGCTGC TTGGCCTGTG AGAGCCCTAG CAAGAGTGTG CAAGAGTGTG CAAGAGCAGG GACCCCAGTCCA CCCAGTGCA CCCAGTGCA CCCAGTGCA CCCAGTGCA CCCAGTGCA CCCAGTGCA CCCAGTGCA CCTCTGCAGCG CCTGTGCAGCG CGCAGTGGCC CGCAGACGCG CGCAGACGCG CGCAGACGCG CTCAGCCC CCCAGCCCT CCCAGCCCT CCCAGCCCT CCCAGCCCT CCCCCTGCCC CACCTCCCCT  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGGACATCGT CAAACGGCAT AGCCAGGATCT CACAAGGATC CCCAGGATCT CCCAGGATCT CTCTGATCAA AGGTGTCCT TCGTCCTCCT TGCCGCGAGA GCGAGCAGGC AAAGGTGCA AGCTGGTCAT TCGTCATCAA AGCTGGTCAT TCGTCATCAA CCCAGGATGC TCCAGTGTAT AGCCAAGGATGC TCCAGTGTAT AGCCAAGTGA AGCCAAGTGA TCGCCAGCTG CCTCGGCAGT   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1140<br>1200<br>1320   |
| 50<br>55<br>60<br>65             | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAG TGACACCC GTCTGCTC CTGTGAGCAG GCGGATCCAA GCGGATCCAA GTGGTACCAC GTGCTCCAC GTGCTCCAC GTGCTCCAC GTGCTCCAC GTGCTCCAC GTGCTCCAC GTGCTCCAC GTGCTCCAC GCAATTCTG CCACACCAC CCACAGCCC CCACAGCCC CCACAGCCC CACAGCCC CACACAGCC CACAGCCC CACAGCCC CACAGCC C | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAGGCACTG TGCCAAAGCC TTGCCCAAAGCC TTGCCCAAGC CAATTCCCCA GCCATGATTCCCCA GCCATGATTCCCCA GCCATGCTGC GAATTCCCCA GCATGCTGCGCAAC GCAATTCCCCA GCAATTCCCCA GCAATTCCCCA GCAATTCCCCA GCAATTCCCCA GCAATTCCCCA GCAATTCCCCA GCAATTCCCCA GCAATTCCCCA GCAATTCCCC GAGCACACTTGCCAGCCC CGACTTTGAT GGGACCACA GGAACATGCGCCC GACCTTTGAT GGGACCACA GGAACCATGGACCCC GACCTTTGAT GGGACCACA GGAACCATGGACCAC GGACACCAGGACCACA GGACACCAGGACCACA GGACACCAGGACCACA GGACACCAGGACCACA GGACACCAGGACCACA GGACACCAGGACCACA GGACACCAGGACCACA GGACACCAGGACCACA GGACACCAGGACCACAGGACACAGGACCACAGGACCACAGGACCACAGGACCACAGGACCACAGGACCACAGGACCACAGGACCACAGGACCACAGGACCACAGGACACACAGGACCACACAGGACCACACAGGACCACACAGGACCACACAGGACCACACAGGACCACACAGGACCACACAGGACCACACAGGACCACACAGGACCACACAGAGACCACACAGGACCACACAGGACACACACAGGACCACACACACACACACACACACACACACACACACACACA | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAGC TGCAGCAGC TCCCTTGAA TCATCGACTA GCAAATCCGC TTCCTGGAG GCGCATCCA TTCCTCCCC GCGAGCTCCA TTCCTGCGGGT GCCCCAGCT CTCGCGGGT TGCGCGATCCT GCCCCAGCT TCGGGGTGT TGGGCGTGCC AGGCCTCCAC TGGCCCAGCT TCGGGGTGTC TGGGCGTGCC TGGCCCAGCT TGGCCCAGCT TGGCCCAGCT TGGCCCAGCT TGGCCCAGCT TGGCCCAGCT TGGCCCAGCT TGGCCCCAGCT TGGCCCCCAGCT TGGCCCCAGCT TGGCCCCAGCT TGGCCCCAGCT TGGCCCCAGCT TGGCCCCAGCT TGCCCCACCT TCCCCACT TCCCCCCACCT TCCCCCCCACCT TCCCCCCCACCT TCCCCCCCC  | 31   GCTGCAGTGG CACCTCATCG TGACCTATGC CATTTCCAGAAC GCAGCCAGAG GCTGCTCATG CTATTGCTGG GCTAGCCTATGC CTATTGCTGG GCTAGCTGTGC CAGTGCCTGGCC TGGCCAGCTG GCCCAGCTGG GCTGCCCAGCTG GCTGCCCAGCTGGCTCCTGGCCCCGCCTGGCCCCGCCTGGCCCGCCTGGCCCCGCCCCGCCCCCC  | CTGCTGCTGC TTGGCCTGTG AGAGCCTAG AGAGCTGTG AGAGCTGTG CACAGATGCA CCCCAGTGCA CACAGCAGG GACCCTCTGC GGGCCTCACA CTCTGCAGGG GGAATGGCC GGGAAACAGCA CTCTGCAGGG GGAACAGCA CTCTGCAGGG GGAACAGCA CTCTGCAGGC CTGGCCCCTG CGGAACAGCA CTGGCCCTCTGCTGCCCCTT GCAAGGAAC CTCTGCAGGC CCACCTCCTTTGCCC CCACCTCCTTTGCCCCTT GCCCTTGCCCTT  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGCAGTGCT CAAACGGCAT AGCCAGGGAT TGGACAAGTCT CACAGGATCT CACAGGATCT CTCAGACAGCT CACAGGATCT CTCAGACAGC AGCTGCCAG AGCTGCCAG AAAGTGCCAG AAAAGTGCAA GCCAGGATGA TCGCAGGATGA TCGCAGGATGA TCGCAGGTGA AGCCAAGTGA TCGCCAGGTGA TCGCCAGGTGA TCGCCAGTGTA TCGCCAGCTG CTCCAGCTGA TCCCAGCTGA TCCCAGCTGA TCCCAGCTGA TCCCAGCTGA TCCCAGCTGA TCCCAGCTGA TCCCAGCTGA TCCCAGCTCAG TCCAGCTCAG TCCAGCTCAA TCCCAGCTCAA TCCCAGCTCAA TCCCAGCTCAA  | 120<br>180<br>240<br>300<br>360<br>420<br>600<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1140<br>1260   |
| 50<br>55<br>60<br>65             | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGG TGAGTTCTGG ACAGCAGGAGT CCACATCCTT GGAGCAGGAG GTCAGACCCC GTCTCCCT CTCGAGCAG GCGGATCCAAC CTGCTCACAC CACACCCC CACAGCCC CACAGCCC CACAGCCC CACAGCCC CACAGCCC CACAGCCC CACAGCCC CACAGCCC CACAGCCC CCACAGCCC CCACACCC CCACAGCCC CCACACCC CCACAGCCC CCACACC CCACACCC CCACACC CCACAGCCC CCACACC CCACAGCCC CCACACC CCACAC CCACACC CCACACC CCACAC CCA | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAAAGCC TGGGGACATG ACAAGATGG TGACCAAAGCC GTGCCCAAAGC GTGCTGCCAAAGC GTGCTGCCGAATG ACACTGTGGGACATG GACATGATGC CTGTGCCAAAGC TGCAGACTCCCAAAGC TGCAGACTCTGCAGCC CAATTCCCCA GACATGATGC GAGCAGCACA TGCAGGCCC GACCTTTGAATC GGGACCATGGACAGCC GACCTTTGAATC GGGACCATGGACAGCC GACCTTTGAATC GGGACCATGGACAGCC GACCTTGAATC GGGACCACAGAGC GACACCAGAGC GACCTTTGCATGATC GACACCAGAGC GACCCTTGCACACCACAC   | quence n #: J02761 1159  21  | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC GCTGCTATG GCTGCTATG GCTGCTATG GCAGCCAGAG GCTGCTATG GCAGCCAGAG GCCAGTGCT GCCCAGCTG GCCCAGCTG GCTGCCAG GCTGCCTG GCTGCCAG TGGCTCCTG TGGGACCATG CTGCTGCTG TGGGACCATG CTGCTGCTG TGGCTCTGC CCTGCTCCTG CCTGCTCCAGCT CTTCCCCTGC CCCTGTTCCAG TCCTCTCTGC CCCTGTCTCAGC TCCTCTCTGC CCCTGTCCAGC TCCTCTCTGC CCTCTCTCAGC   | CTGCTGCTGC CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAGAGCAGGA GACACCATGCAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGC   | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATTGCT AGCAAGTGCT CAAACGGCAT TGGACAACGCAT TGGACAACGCAT CCCAGGATCT CCCAGGATCT CTCTGATCAA AGCTGCTCAT TCGTCCTCCG TGCCGCGAGA GCGAGCAGGC AAAAGTGCAA GCTGGGATGC TCCAGTGTAT AGCCAAGTGT CCTCAGTGTAT AGCCAAGTGCA TCCAGCTGT CCTCGGCAGT CCTCAGCTGT TCTCAGCTCA TCCAGCTGT TCTCAGCTCA TCCAGCTGT TCTCAGCTCA TGCGCAGGCAG TCCCAGCTGT TCTCAGCTCA TGGGCAGGCA  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1380<br>1450   |
| 50<br>55<br>60<br>65<br>70       | Nucleic Ac Coding seq  I   GAATTCCGGT GCACTCTGGGC TGAGTTCTGG CCACATCCTT GGAGCAGAGAG TGACGACCCC CGTCTCCCAC CGTCCTCCCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CGTCCCAC CGTCCTCCAC CCACACCCC CACACCCCC CACACCCCCC   | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAAAGCC TGGCAAAGCC TGGGACATG TTCCCCCTGG CAATTCCCCAAAC GTGCTGCCAAAC GTGCTGCAAAC GTGCTGCAAAC GCCATGATGCGG CAATTCCCCAAAC GCAATGCTGC GAGCAGCAC GAGCAGCAC GACCTTTGAT GGGACCACAG GAGCACCAC GACCACAG GGACCACAG GAGCACCACG GACCACAGGC CACCTGCAAC TGCAAGCCCC GACCTTTGAT GGGACCACAG GAGACCACAG GAGCACCACAG GAGCACCACAG GAGCTCTGCC CACTGCTTTA   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TGGAGCAAGC TCCCCTTGAA TCATCGACTA TCATCGACTA CCAAGCAGGC GCTCTGCGGA GGGCCCTCCA TTCCTCTCC CCAAGGAGGC GCGCCAAGC TGCCCAAGC TGCCCCACT TCGGGGTGC CGAGCACCACG CCCACTTCCACAC GGGCCCCACG CCCACTTCCACAC CGCCCCACT CCACACCACA  | 31   GCTGCAGTGG CACTCATCC ATTGCAGTGC TGACCTATGC CATTTTCCAG GCTGCTATGC CTATTGCTGG CCTCTGGCA GGCAGCAGAG GCTGCTGGCA GCCCAGGTG CCAGTGCCTG GCCCAGCTG GTCCCAGCTG GTCCCAGCT GTCCCAGCT CTGCCCAGCT CTGCCCAGCT GCCCCACTG CCTGCCCAGCT CCTGCCCAGCT CCTGCCCAGCT CCTGCCCAGCT CCTGCCCAGCT CCTGCCCAGCT CCTGCCCAGCT CCTGCCCAGCT CCTGCCAGCT CCTGCCCAGCT CCTGCCAGCT CCTGCCAGCT CCTGCCAGCT CCTGCCAGCT CCTGCCAGCT CCTGCCAGCAC GGTTGAAGCT CTTACACGAC   | CTGCTGCTGC TTGGCCTGTG AGAGCCTAG AGAGCTGTG AGAGCAGTGCA CCCAAGTGCA CCAGAGCAGG AGACCTCTGC GGGCCTCACA CTCTGCAGGG GCAGTGGCC GGAGAATGGC GGAGAATGGC GGAGAATGGC GGAGAATGGC GGAGAATGGC GGAGAATGGC GGAGAATGGC CTGGCAGGG TCCAGGCCT GCAAGGAAG TCCAGGCC TCCAGGGC TCCAGGGC CTCCAGGGC TTGTGGGCCCG GCAAGGAAG TTGAGGCAG TTGAGGCAG TCCAGGGC TCCCCTGCCC TCCAGGGC TCCCAGGGC TCCCAGGGC TCCCAGGGC TCCCAGGGC TCCCAGGGC TCCCAGGGC TCCCAGGGC TCCCAGGGC TGCCCGCCC TGGCCCCCCCC  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGGACATCGT AGCAAGTGCT AGCAAGGCAT AGCCAGGAT TGGACAAGGCT CACAGGATCT CACAGGATCT CACAGGATCT CTCTGATCAA AGCTGCGCAC ACTCCGTCAT TCGTCCTCCG ACTCCGGAGA GCGAGCAGGC AAAAGTGCAA GCTGGGATGC TCCAGGTTAT AGCCAAGTGA TCGCCAGCTG TCCCAGGTTAT AGCCAAGTGA TCGCCAGCTG TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCAC TGCCAACCCAC   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>1020<br>1080<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560  |
| 50<br>55<br>60<br>65             | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGC TGAGTTCTGG ACAGGAAGTCCCC CACATCCTT GGAGCAGGAG TGACGACCCC GTCCTCCCACCCCC CTCCGAGCCAG CCGTCTCCAC CTCTGAGTCCAC CCTCTGAGTCCAC CCACACCCCC CACAGCCCC GACGGGTTCAC CCACAGCCCC GACGGCTCAC CCACAGCCCC CCACAGCCCC GACGGCTCAC ACCACCCCC CCACAGCCCAC CCCCAGGCTGAAC CCCCATGCACCAC CCCCATGCACCAC CCCCATGCACCAC CCCCATGCACCAC   | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG TGCCAAAGCC TGGGGACATG TGCCCAAGCCTT CTGCCCAGG CAATTCCCCAG CAATTCCCCA GCCATGATTC TGGGACACG CACCTCTGAG CACCTCTGAG CACCTTTGAT TGGGACACACG GACATTCCCA GAGAGACACACG GACATTCCCA GAGAGACACACG GACATTCCCA GAGAGACCACA AAGAAGCCT GGTGGACACC GACCTTGAT TGGGACACACG CACCTCTGAT TGGGACACACG GACACCACGAGAGAGACACA AAGAAGCCT CGGTGGACCACG CACCTTTGAT TGGACACCACGAGAGAGACCACA CACCACCAGAGAGAGACCACACACA   | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TGGAGCAAGC TCCCTTGAA TCATCGACTA GCAAATCCCG CCAAGGAGC CCAAGGAGC GGGCCATCCA TCCTCCACAG TGCCCAGGT CCCCAGGT CCCCAGGT CCCCAGGT CCCCAGCT CCCAGGCCCAGC TGCCCAGC CAGGCCCAGCT CGGGCCCAGCT CGGGCCCAGCT CGGGCCCAGCT CGGGCCCAGCT CGGGCCCAGCT CGGGCCCAGCT CGGGCCCCAGCT CGGGCCCAGCT CGGGCCCCAGCT CGGGCCCCAGCT CGGGCCCCAGCT CGGGCCCCAGCT CGGGCCCCAGCT CGGGCCCCAGCT CCCACTTCCACAC CCCACTTCCACAC CCCACTTCCACAC CCACGACCACGC GGATTTTACAG  | 31   GCTGCAGTGG CACTCATCC ATTGCAGTGC TGACCTATGC CATTTCCAG GCTGCTCAGA GCTGCTCAGA GCAGCCAGAG CCTATGCTGG GCTAGCGTGG CCAGTGCTGG GCCAGCTG GCCCAGCTG GCCCAGCTG GCTGCCCAGC TGGCTCCTGG CCTGCCCAGC TGGCTCCTGG CTGCTCCTGG CTGCTCCTGG CTGCTCCTGG CTGCTCCTGG CTGCTCCTGG CTGCTCCTGG CTGCTCCTGG CTTCCCTGG CTTCCTCTGG CTTCTCTCGG CTTCTTCCCAG CTTCTTCCAG CTTCTTCCCAG CTTCTCTCTCTCTCCAG CTTCTTCCCAG CTTCTTCCCAG CTTCTTCCCAG CTTCTTCCCAG CTTCTCTCTCTCTCTCTCCAG CTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT   | CTGCTGCTGC CTGCTGCTGCTGCTGCTGCTGCAGAGAGTGTGC CAGAGAGTGTGCAGAGAGTGCACAGACAGGGCAGGCAGGC  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATTGCT AGCAAGTGCT CAAACGGCAT TGGACAACGCAT TGGACAACGCAT CCCAGGATCT CCCAGGATCT CTCTGATCAA AGCTGCTCAT TCGTCCTCCG TGCCGCGAGA GCGAGCAGGC AAAAGTGCAA GCTGGGATGC TCCAGTGTAT AGCCAAGTGT CCTCAGTGTAT AGCCAAGTGCA TCCAGCTGT CCTCGGCAGT CCTCAGCTGT TCTCAGCTCA TCCAGCTGT TCTCAGCTCA TCCAGCTGT TCTCAGCTCA TGCGCAGGCAG TCCCAGCTGT TCTCAGCTCA TGGGCAGGCA  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1380<br>1450   |
| 50<br>55<br>60<br>65<br>70       | Nucleic Ac Coding seq  I   GAATTCCGGT GCTCTGTGGC TGAGTTCTGGC CCACATCCTT GGAGCAGGAG TGAGCACAC CTGTAGCACC CTGTAGCACC CTGTCTCCAC CTCTCCAGCAC CTGCTCCAT CTCTGAGTACC CTGCTCGAGT CCACACCCC CACAGCCC CACACCC CACACCC CACACCC CACACCC CACACCC CCCATGCAC AAAAAAAATGCGC AAAAAAAATTC  | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAAGCACTG TGCCAAAGCCTG TGGGACATG TGCCCTGG TGCCCAAAC TGCCCAAAC GCCATGCTGCAAAC GCCATGATGCCAAAC GCATGCTGCAAAC GCATGCTGCAAAC GGAGAGCAC GACCTCTGCA GGACCAGAC GGACCAGAC GGACCAGAGC CACCTCTGCA GGACCAGAG GGACCAGAG GACACCAGAG GACACCAGAG GACACCAGAG GACACCAGAG CACCTCTGCA ACCAGAGCTGCAAACAGAACAG  | quence n #: J02761  1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TGGAGCAAGC TCCCCTTGAA TCATCGACTA TCATCGACTA GCAAATCCGG GCTCTGCGGA GGGCCCTCCA TTCCTCTCCC CCAAGGAGG GGGCCTAGAC TGTCCGTAAC TGTCCGTAAC TGTCCGTAAC TGTCCGTAAC TGCCCAAGC TGCCCAAGC TGCCCAAGC TGCCCAAGC TGCCCAAGC TGCCCAAGC TGCCCAAGC TGACCAGCT CGGGCCCAAGC CCACTTCCACA CGGGCCCAAGC CCCACTTCCACAC CGGGCCCAAGC CCCACTTCCACAC CGCTCCACAC CAGGACAGGG GATTTTACAA  | 31   GCTGCAGTGG GCACTCATCC ATTGCAGTGC TGACCTATGC ATTTTCCAG GCTGCTATGC CTTCCAGAAC GCAGCCAGAG GCCGCTGCA GCCAGCTG GCTCCAGCAG GCTGCCAGCAG GCTGCCAGCAG GCTGCCAGCAG CCCCCAGCTG GTGCCCAGCTG TGGCTCCTGCACAC CCCCCCTCCT CCTTCCCCTGG CCTGCCCAGCTG CCTGCCCAGCTG CCTGCCCAGCTG CCTGCCCAGCTG CCTGCCCCTCCTG CCTGCTCCTGCCG CCTCCTCTGCCG CCTCCTCTGCCG CCTCCTCTGCCG CCTCCTCTGCAGCC CCTCCTCTGCAGCC CCTCCTCTGCAGCC CCTCCTCTGCAGCC CCTCCTCTGCAGCC CCTCCTCTGCAGCC CCTCCTCTCCCC CCTCCTCTGCAGCC CCTCCTCTGCAGCC CCTCCTCTCCCC CCTCCTCTCCC CCTCCTCCTCCC CCTCCT  | CTGCTGCTGC TTGGCCCTAG AGAGCTGTA AGAGCCCTAG CACAGATGCA CCCCAGTGCA CCAGAGCAGG GACCCTCTGC GGGCCTCACA CTCTGCAGGG GCAGTGGCC GGAGATGGCC GGAGATGGCC GGAGATGGCC GGAGATGGCC GGAGATGGCC GGAGATGGCC GGAGATGGCC GGAGATGGCC GGAGATGGCC TTCAGAGGG TCCAGGCC CTGCCCTGCC  | TIGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGGACATCGT ACCAAGTGCT ACCAAGTGCT CACAGGATCT CACAGGATCT CTCTGATCAA AGCCAGGATCT CTCTGATCAA AGTCCGTCAT TCGTCCTCGT CTCTGCTCAT AGCCAGGATGC TCCCGGCAGA GCGAGCAGGC AAAAGTGCAA GCTGGGATGC CTCCAGCTGAT TCCAGCTGAT TCCAGCTCAT CCCCAGCTGTAT AGCCAAGTGA TCCCAGCTG CCTCAGCTGAT CCTCAGCTCA CCTCAGCTCA CCTCAGCTCA TCCAGCTCA CCTCAGCTCA TCACACCCAC AGAAGAATAA TTAAGCTTTT CTCGCCAGTTTT   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560<br>1620<br>1680                         |
| 50<br>55<br>60<br>65<br>70       | Nucleic Ac Coding seq  I GAATTCCGGT GCACTCTGGGG TGAGTTCTGG TGAGTTCTGG TGAGACTACCT GGAGCAGGAGT TGAGGACTACC CTCTGAGCCC CTCTCGAGCAC CTGTGTCCAC GTGGTCCAC GTGCTCCAC GTGCTCCAC GTGCTCCAC CAATTCTGAGTGC CACACCAC CACACCAC CACACCAC CACACCAC CACACCAC   | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG TGCCAAAGC TGGGGACATG TGGGACATG TTCCCCTGG CTGGGCTGT CTGGCCAAAC GTGTGCCAAAC GTGTGCCAAAC GTGTGTGCGGCGGCATG ACGCTGTGGGCCTGT CTGGGCCTGG GATGATGCTCG GAGCACCAC GACCTTTGAT GGAGAGCCCC GACCTTTGAT CTGGACCAGGCCCC GACCTTTGAT CTGGACCAGGCCCC GACCTTTGAT CTGGACCACGCCC GACCTTTGAT CTGGTGGACCAC GACACTGCTGC CACCTCTGCA CTGAAAGAACCTG CACCTCTGAAAACACTGC CACTGCTTAAT CTCAAAGATTGA CATACAGAAC CACGGCAAGGACAC ACCAGGAAGAACCTCTCAAAGATTCC CACGGCAAGGACACAACACA  | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAGC TGGAGCAGC TCCCCTTGAA TCATCGACTA TCATCGACTA GCAAATCCCG GCGCATCTCC GCGGGATCTG GCGCCCAGCT TCCCTGGGA TGCCCCAGCT GCGCCCAGCT TGGCCCAGC TGCCCCAGCT CGGGCTCCACA CGGCCCCCAGCT CGGGCCCCAGCT CCCACCACCC CCCACTTCCACAC CCCACTTCCACAC CCCACTTCCACAC CCACGCTCACAC CCACGCTCCACAC CCACTTCCACAC CCACTTCCAC | 31   GCTGCAGTGG CACTCATCC ATTGCAGTGC TGACCTATCC GTGCCAGAGC CTATTCCAG GCTGCTAGC GCTGCGCA GGCAGGCCT GCCAGGCG GCTGGCAGC GCTGGCAGC GCTGGCAGC GCTGGCAGC GCTGGCAGC TGGCTCCTGGC CTATGCTGG GCTGCCAGC GCTGCCCAGC TGGCTCCTGG CTGCCCAGC TGGCTCCTGG CTGCCCTGC CTGCCTCCG CTGCTCCCGCC CTGCTCCCGCC CTCCCTGCT CCCTGTTCC CCTGTGCAG CTACACCAG CGGTTGAAGCT CTACACCAG CGGTTGAAGCT CTACTCCAG AGACATCAGT AAGGGTGGAC GAGATGCTCT CGAGGGGACCAC CTACTTGCAA AGGGTGGAC CTACTTGCAA AGGCTGGAC CGAGATGCTCT CGAGGGACCACC CTACTTGCAA AGGCTGGAC CGAGATGCTCT CGAGAGCTCCT CGAGGGGGAC CGAGATGCTCT CGAGGGGACC CTACTTGCAA AGGGTGGAC CGAGATGCTCT CGAGGGGAC CGAGATGCTCT CGAGGGGAC CGAGATGCTCT CGAGGGGAC CGAGATGCTCT CGATGCAGC CGAGATGCTCT CGAGGGGAC CGAGATGCTCT CGAGGGACC CGAGATGCTCT CGATGCAGC CGAGATGCTCT CGATGCAGC CGAGATGCTCT CGAGACC CGAGATGCTCT CGAGGGGAC CGAGATGCTCT CGATGCAGC CGAGATGCTCT CGAGATGCTCT CGAGGGAC CGAGATGCTCT CGAGGACC CGAGCTCGC CGAGCTCC CGCCCC CGCCCCC CGCCCCCC | CTGCTGCTGC TTGGCCTGCT AGAGCCCTAG CAAGAGTGTG GACACGATGA CAGACAGAC GACACCTAGC GACACCTAGC GACACCTAGC GCAGCAGGC GCTGAGCGC GCTGAGCGC GCTGAGCGCC GCTGAGCGCC GCTGAGCAGC GTGCCCAGGC GTGCACACCCTCTGCAGGCC GCAGAGCAGGC TCCAGGCC GCAGAGCAGC TCCAGGCC TCAAAATTC AATTGTTAAA  | TGCTGCCAC CCCAGGGCCC GGCATTGCT AGGACATCGT AGGACATCGT ACCAAGTGCT CACAGGCAT AGCCAGGCAT AGCCAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT CTCTGATCAA AGGTGGCAG ACTCCGTCAT TCGTCATCAC AGCAGGATGA CTCGGCAGA GCTGGGATGC TCCAGGTGAT AGCCAAGTGA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA AGCCAGGGCA TAGAGCAGGC AAAGTGAA TCTCAGCTCA AGCAAGTCA TGGCATCAC AGAAGAATAA TTAAGCTTTT CTGCCATGTT CTGCATTGTT CTGCATTTTC CTGCATTTC CTGCATTTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTC CTGCATT | 120 180 240 300 360 420 540 660 720 780 840 1020 1080 1140 1200 1380 1440 1500 1620 1680 1740 1800   |
| 50<br>55<br>60<br>65<br>70<br>75 | Nucleic Ac Coding seq  I GARTTCCGGT GCTCTGTGGC GCTCTGTGGC TGAGTTCTGG ACAGGAAGTC CCACATCCTT GGAGCAGGAG GCGGATCCAG GCGGATCCAG GCGGATCCAG GCGGATCCAG GCGGATCCAG GCGGATCCAG GCGATCCAG GCGGATCCAG GCAATTTGTG CCACACCACC CCACAGCCC CACAGCCC CACAGCCC CACAGCCC CACAGCCC CACAGGCTGA ACAACAG GCATTCCAG GCATTCGAG ACACAGGCT ACCACAGGCT CACACAGGCT CACACAGGCT CACACAGGCT ACACAGGCT ACACAGGCT CACACAGGCT CACACAGGCG CACACAGGCACAGGCG CACACAGGCG CACACAGGCC CACACAGGCG CACACAGGCACAGGCG CACACAGGCG CACACAGGCACAGGCG CACACAGGCG CACACAGGCACAGGCG CACACAGGCACAGGCG CACACAGGCACAGGCG CACACAGGCACAGGCACAGAGCACAGGCACAGAGCACAGAGCACAGAGCACAGAGACACAGAGCACAGAGCACAGAGACACAGAGACAGACAGACACAGACAGACACAGACACACAGACACA | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAGGCACTG TGCCAAAGCC TGGGGCCTGT CTGCCCAAGC GTGCTGCCGG GAGTGCTGCG GAGCACTGCAGGCACACAGACACAGACACAGAACACAGAACACAGCAG  | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAGC TGGAGCAGC TCCCTTGAA TCATCGACTA GCAAATCCGG CTTGCCGGGA TCCCCTCGA TTCCTCCCC CCAAGGAGC GGGCATCTG GCGCCATGCT CTGGGGGTGC TGGAGCTGCA TGCCCAGG TGCCCAGGC CTGGCCCAGC CGGAGCTCTG CGGGCCCCAGC CGGGCCCCAGC CGGGCCCCAGC CCCACTTCCA CGGGCCCCAGC CCCACTTCCAC CGGGTAGT CCCACTCCAC CGGGCCCCAGC CCCACTTCCCC CGGGTAGT CCCACTCCCAC CGCGCTAGCT CCCACTTCCCCCCCCCC  | 31   GCTGCAGTGG CACCTCATCC ATTGCAGTGC TGACCTATGC CATTTCCAGAAC GCAGCCAGAG GCTGCCAGAG GCTAGCTATGC CTATTGCTGG GCTAGCTGGC CAGTGGCAGAGGCCT GCCCAGCTGGCCAGCTG GCCCAGCTGGCCAGCTG GCTGCCCAGCTGGCTCCCAGCTGGCTCCCAGCTGGCTCCAGCT TGGGACCATGGCTCCAGCT CCTTCCCCTGGCCTGG   | CTGCTGCTGC CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAGGCTGCAGGCCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCTGCAGGCCTGCAGGCCTGCAGGCCTGCAGGCAG  | TGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGCT AGGACATCGCT AGCAAGTGCT CCAAAGGGCAT AGCCAGGATCT CTGAACAGCT CACAGGATCT CTCTGATCAA AGGTGTGCCG AGGACAGCG AAAAGTGCAA GCCAGGATCAT CTCGTCAT TCCTCAGCAGAC AAAAGTGCAA GCCAGCAGGC AAAAGTGCAA CTCCGCCAGCAG TCCCACGAGATCA CTCCGCCAGCAGC TCCAGCTGTAT AGCCAAGTGA CTCCGCCAGC TCCAGCTGTAT AGCCAAGTGA CTCCAGCCAC AGCAGGGCCA AGCAAGATAA TTAAGCTTTT CTGGCATGTT CTCGGCATGT CTCAGCCAC AGAAGAATAA TTAAGCTTTT CTCGGCATGTT AGCTATTGCT AGCAGATTTT  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>900<br>900<br>1080<br>1140<br>1260<br>1320<br>1320<br>1440<br>1500<br>1660<br>1620<br>1680<br>1740  |
| 50<br>55<br>60<br>65<br>70       | Nucleic Ac Coding seq  I GAATTCCGGT GCTCTGTGGG TGAGTTCTGG TGAGCACTGT GGAGCAGGAG TGAGACCCC CTGTATGCAC GTCAGACCCC CTCTCCTC CTCGAGCAG GCGATCCCAT CTCAGACCCC CACAGCCCC CCCATGCAC ACACAGCCCC CCCATGCAC CCCCATGCAC CCCCATGCAC CCCCATGCAC CCCCATGCAC CCCCATGCAC CCCCATGCAC CCCCATGCAC CCCCATGCAC CCCATGCAC CCCA | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAAGGCACTG TGCCAAAGCCCCTG TGGGACATG TTCCCCCTGG CAATTCCCCAAAGCCGCAAAGCCGCAAAGCCCCCAAACGCACCGGACACAGCACCCCCAAACGCACCGGACACAGCACCCCCC   | quence n #: J02761 1159 21   AGTCACACCT CTGCCTGGAC TGGAGCAAGC TGGAGCAAGC TCCCCTTGAA TCATCGCGA GCAAATCCG CTCTCCCGGA GGGCCCTCCA TTCCTCTCCC CCAAGGAGG GGGCCTCCA TTCCTCTCCC CCAAGGAGG TGCCCCAAGC TGCCCCAAGC TGCCCCAAGC TGCCCCAAGC TGCCCCAAGC TGCCCCAAGC TGCCCCAAGC TGCCCCAAGC TGCCCCAAGC TCACACACACACACACACACACACACACACACC CCACTTCCC CACGCTTCCCACACACACACACACACACACACCC CCCACTTCCC CCACTTCCC CCCACTTCCC CCACTTCCC CCACTTCCC CCCACTTCCC CCCCCCCC  | 31   GCTGCAGTGG GCACTCATCC ATTGCAGTGC TGACCTATGC ATTTCCAG GCTGCTCATG CTTCCAGAAC GCAGCCAGAG CCCTCTGCA GGCGAGGCCT GCCCAGCTG GCTGCCAG GCTGCCAG GCTGCCAG CTACTCCTGG CTACCCAGGC TGGCTCCTG CTCCCTGCA CCCCAGCTG CTGCCACAG CCTGCCCTG CCTGCCAGGC CTGCCCTGC CCTGCCCTGC   | CTGCTGCTGC TTGGCCCTGT AGAGCCCTAG AGAGCTGTA CAAGAGTGTA CCCAGTGCA CAGACAGATCA CCCAGTGCA CAGACAGATCA CTCTGCAGCG GCAGTGCA GCAGTGCA GCAGTGCA GCAGTGCA GCAGTGCA GCAGTGCA GCAGTGCA GCAGTGCA GCAGTGCCC GCAAAGCAAG TTCCAGCCC CACCTCCCTT GCCTTGCC CTCCAGGG TTCAAAGTAT AATTTTAA ACTGCACGC AACTGCACGC TGAAAGCAT AATTTGCAGCCT AACTGCACGC TGAAAGCAT AATTTGCAGCCT AACTGCACGCT TGAAAGCAT AATTTGCACGCT AACTGCACGCT TGAAAGCAT AATTTGCAGCGCT TGAAAGCAT AATTTGCACGCT TGAAAGCAT AATTTGCACGCT TGAAGGCACGCT TGAAAGCAT AATTTGCACGCT TGAAGGCACGCT TGCAAGCGCT TGCAAGGGCACGCT TGCAAGGGACGCT TGCAAGGGACGCT TGCAAGGGACGCT TGCAAGGGACGCT TGCAAGGGACGCT TGCAAGGACGCT TGCAAGGGACGCT TGCAAGGACGCT TGCAAGGACGCT TGCAAGGACGCT TGCAAGGACA TGCAGCGCT TGCAGGGCACGCT TGCAAGGACA TGCAGCGCT TGCAAGGACA TGCAGCGCT TGCAAGGACA TGCAGCGCT TGCAGGGCACGCT TGCAGGCACGCT TGCAGGGCACGCT TGCAGGGCACGCT TGCAGGCACGCT TGCAGGCCCCCC TGCTGCTTGACACC TGCACGCT TGCAGCCCCCC TGCACGCCCCC TGCACGCCCCC TGCACGCCCCCC TGCACCCCCCC TGCACGCCCCC TGCACGCCCCCC TGCACGCCCCCC TGCACGCCCCCC TGCACCCCCCCC TGCACGCCCCCCC TGCACGCCCCCC TGCACGCCCCCC TGCACGCCCCCCC TGCACGCCCCCCCC TGCACGCCCCCCCCCC   | TGCTGCCAC CCCAGGGCCC GGCATTGCT AGGACATCGT AGGACATCGT ACCAAGTGCT CACAGGCAT AGCCAGGCAT AGCCAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT CACAGGATCT CTCTGATCAA AGGTGGCAG ACTCCGTCAT TCGTCATCAC AGCAGGATGA CTCGGCAGA GCTGGGATGC TCCAGGTGAT AGCCAAGTGA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA TCTCAGCTCA AGCCAGGGCA TAGAGCAGGC AAAGTGAA TCTCAGCTCA AGCAAGTCA TGGCATCAC AGAAGAATAA TTAAGCTTTT CTGCCATGTT CTGCATTGTT CTGCATTTTC CTGCATTTC CTGCATTTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTTC CTGCATTC CTGCATT | 120 180 240 300 360 420 540 660 720 780 840 1020 1080 1140 1200 1380 1440 1500 1620 1680 1740 1800   |
| 50<br>55<br>60<br>65<br>70<br>75 | Nucleic Ac Coding seq  I   GAATTCCGGT GCACTCTGGGC TGAGTTCTGGG TGAGTTCTGG TGAGCACGGGGT TGAGCACCCC CGTCCTCCTC CTCCGACGAG CGTGGTACCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CGTCCTCCAC CACACCAC CCACACCAC CCACACCAC CCACACGCCC CACACGGCTC CCACAGGCTC CCCATGCAC AAAAAGGC CCCCATGCAC AAAAAGGGG CTTGTTAAGAAT GGGATGGCG GATTGTAAAAAGGGGGTTTGTTAAGAGGGGGGTTGTCC CGGTTGTCC CGGTTGTCC CGGTTGTCC CGCTTGTCC CGCTTGCC CGCTTGTCC CCCCTTGTCC CGCTTGTCC CGCTTGTCC CCCCTTGTCC CGCTTGTCC CCCCTTGTCC CCCTTGTCC CCCCTTGTCC CCCCTTGTCC CCCCTTGTCC CCCCTTGTCC CCCCTTGTCC CCCTTGTCC CCCTTGTCC CCCTTGTCC CCCTTGTCC CCCTTGTCC CCCTTGTCC CCCTTGCTC CCCTTGTCC CCTTGTCC CCCTTTCTC CCCTTTCTC CCCTTTCTC CCTTTTCC CCCTTTCTC CCTTTTCC CCTTTTCT CCCTTTCT CCCTTTCT CCTTTTCT CCCTTTCT CCTTTTCT CCTTTTCT CCTTTTCT CCTTTT CCTTTT CCTTTT CCTTTT CCTTTT CCTTTCT CCTTTT CCTTT CCTTTT CCTTT  | C60 DNA Seid Accession uence: 14  11    GCCATGGCTG CCAAGGCACTG TGCCAAAGCCCCTG TGGGACATG TTCCCCCTGG CAATTCCCCAAAGCCGCAAAGCCGCAAAGCCCCCAAACGCACCGGACACAGCACCCCCAAACGCACCGGACACAGCACCCCCC   | quence n #: J02761 1159  21   AGTCACACCT CTGCCTGGAC TGGAGCAGC TGGAGCAGC TCCCCTTGAA TCATCGACTA TCATCGACTA GCAAATCCCG GCTCCCCACT TCCTCTCCC CCAAGGGTGC GCGCCAGCT CTGGCCAAG TGGCCAGCT TGGCCAAG TGGCCACCA TGCCCTGAA TGCCCTGAA TGCCCTGAA TGCCCAGCT CTGGCCAAG TGCCCAGCT TCGGGAACTCAG TGCCCAGCT CTGGCCAAG TTCCTTCCC GGCCCCAGCT CTGGCCAAG TGCCCAGCT CTGACAGGTGC CGCCCCAGCT TCGGGAACTCAG TGACCAGCT CCACTTCCCAC CCACTTCCCAC CCACTTCCTGT TTTCTTCCTCC TTTCTTTCTCCC TTTCTTTC   | 31   GCTGCAGTGG GCACTCATCC ATTGCAGTGC TGACCTATGC TGACCTATGC CATTTTCCAG GCTGCTATGC CTATGCTGG GCTGCTATGC GCAGGAGGCCT GCAGGAGGCCT GCAGGAGCCT GGCTGCCAGGC TGGCTCCTGG GCTGCCAGCT GCTGCTCCT GCCCTGCT GCCCTCCT GCCCCCC GCCCTCCT GCCTCTCCC GCTCTCCCT GCTCTCCC GCTCTCCCT GCTCTCCCT GCTCTCCCT GCTCTCCCT GCTCTCCCT GCTCTCCCC GCTCTCCCC GCCCTCCT GCCCTCCC GCCCTCCT GCCCCCC GCCCCCC GCCCCCC GCCCCCC GCCCCCC   | CTGCTGCTGC TTGGCCTGTG AGAGCCCTAG CAAGAGTGTG GACAGCAGG GACCCTCTGC GGGCCTCACA CTCTGCAGGG GCAGTGCA GGAGATGGC GCAGTGCA GGAGAATGGC GCTGAGCGCT GGAGAATGGC GGAGAATGGC GGAGAATGGC GGAGAATGGC GGAGAATGGC GGAGAATGGC CTCTGCAGGG GGAGAATGGC CTGGCCCGG GCAGTGACAGC TTCCAGGGC TTCCAGGCC TTCCAGGCC TTCAGACAGC TTCCAGGCC TTCAAAATTA AATTGTTAAA AATTGTTAAA AATTGTTAAA AATTGTTAAC AAGTGGACC TACTGCAGGC TACTGCTGCT TAGAGTGAGC TACTGCTGAC TAGAGTGAGC TACTGCTGAC TATCTGCTGAC TTCTGCTGAC TTTGCTGACC TTTGCTGACC TTTGCTGACC TTTGCTGAC TTTGCTGACC TTTGCTGACC TTTGCTGACC TTTGCTGACC TTTGCTGACC TTTGCTGAC TTTGCTGACC TTTGCTGAC TTTGCTGACC TTTGCTGACC TTTGCTGACC TTTGCACC TTTTCACC TTTTTCACC TTTTCACC TTTTCACC TTTTCACC TTTTCACC TTTTCACC TTTTCACC TTTTCACC TTTTTCACC TTTTCACC TTTTTCACC TTTTTTCACC TTTTTCACC TTTTTTCACC TTTTTTTCACC TTTTTTCACC TTTTTCACC TTTTTTCACC TTTTTTCACC TTTTTTCACC TT | TIGCTGCCCAC CCCAGGGCCC GGCATTGCCT AGGACATCGT AGGACATCGT ACCAAGTGCT ACCAAGTGCT AGCACAGGAT TIGGACAAGCT CCCAGGATCAT AGCCAGGATCT CCCAGGATCAT AGCCAGGATCAT CCCTGATCAA AGGTGTGCCA ACTCCGTCAT TCCAGCAGC TCCAGGATGC TCCAGCTGT TCCAGCTGA TGCCAGCTG TCCAGCTGAG TCACACCCAC AGAAGAATAA TTAAGCTTTT CCTGCATGAT AGCTTATGCT TCCAGATTTT AGCTCAGATTTT TCCAGATTTT AGCTCAGATTTT TCCAGATTTT TCCAGATTT TCCAGATTTT TCCAGATTTT TCCAGATTTT TCCAGATTTT TCCAGATTTT TCCAGATTTT TCCAGATTTT TCCAGATTTT TCCAGATTTT TCCAGCTCAGCT   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1080<br>1140<br>1260<br>1320<br>1380<br>1450<br>1560<br>1680<br>1740<br>1860<br>1860 |

Nucleic Acid Accession #: NM\_139172.1 Coding sequence: 19..552 31 5 GGGGTCTGGG GAGGTGACAT GTTGGGCTGT GGGATCCCAG CGCTGGGCCT GCTCCTGCTG 60 CTGCAGGGCT CGGCAGACGG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG 120 GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180 TGCCTGCGTC TCCGGTGCTG CTACCGCAAT GGGGTCTGCT ACCACCAGCG TCCAGACGAA 240 10 AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGACGT GCAGCGGCCT CCTCCTCCTG 300 AGCTGCAGCA TCTGCTTGTT CTGGTGGGCC AAGCGCCGGG ACGTGCTGCA TATGCCCGGT 360 TTCCTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCAA GCACCGAGGG 420 ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCAGTCGCCC TGTCCAAAGA GTCCAGGGAT 480 GTGGAGGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA 540 15 GAGGAGGATT AGGGGAGTCC CCGGGGGACT GCTCAATACA GATACGGTGG ACG 593 Seg ID NO: C62 DNA Seguence Nucleic Acid Accession #: NM\_054023.2 Coding sequence: 98..379 20 41 51 21 31 GGGGACACTT TGTATGGCAA GTGGAACCAC TGGCTTGGTG GATTTTGCTA GATTTTCTG 60 ATTTTTAAAC TCCTGAAAAA TATCCCAGAT AACTGTCATG AAGCTGGTAA CTATCTTCCT 25 GCTGGTGACC ATCAGCCTTT GTAGTTACTC TGCTACTGCC TTCCTCATCA ACAAAGTGCC 180 CCTTCCTGTT GACAAGTTGG CACCTTTACC TCTGGACAAC ATTCTTCCCT TTATGGATCC 240 ATTANAGCTT CTTCTGAAAA CTCTGGGCAT TTCTGTTGAG CACCTTGTGG AGGGGCTAAG GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAC TGCTGGAGGC 300 360 GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGGAAGATGA 420 30 480 AAAAAAAAA 550 Seq ID NO: C63 DNA Sequence 35 Nucleic Acid Accession #: FGENESH predicted Coding sequence: 1..2874 21 41 51 31 40 ATGCCCCTGT CCTATGCCTA TAAAAACGCT GAGACCCTAG CAGGCAGACA CACAAGCAGC TGGATGTCGA GAGGAGCATA TCAGCGGAGG AACACACGGG CAGCTGGACG TCCAGAGGAA 120 TGCACTGACA GAAACTGGCA TGCTGGCAGA ACACGTGGAA TTTGGCTGGG GCAGTTGGAG GAGAGATGTT CAGATGTGTT CGGAGTTTCT TTCTTCTGGT GGGTTCGTGG TCTCGCTGGC TCAGGAGCGA AGCTGCAGAC CTTCACGCCA GCCCAGGAAG GGGCTCCCAC AGTGCAGCGG 300 45 CAGGCTGAAG CGCTCCTCAA GTGCCGCCAG AGTGGGCGTC CAGGCAGAGG AGGCGCCGAG 360 AGCGAGCGAG CGAGGGATGC CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC 420 CCAACGTCCT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACCGAAAT TGCTCACAAG AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCCCTCCTTG 540 GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTCAC CATTTCTTGT GACTCATTTG 600 50 TACTITCIGG GGGTTGTCAC CACTGGGATG GAACAACTAG ATTTTGAAAC AGGACCAAAC 660 ATATTTGATT TGCAGATTTA TGTGAAGGAT GAGGTTGGTG TCACAGACCT GCAAGTCCTG 720 ACTGTCCAGG TAACAGATGT GAACGAGCCA CCTCAGTTTC AAGGCAACTT GGCAGAAGAT 780 CATCTCCGTG CAGACCAGCC ACATTTCAAT GCTCATAGTC ACACGTACGT GAGGGTAGTG 840 GCTACTGCAT TGGCCAGGCA CAGGCTTAGA TCTAGCATTG GTTCCCCCTT CCTGGGCACC 900 55 TTCTGTGTTG TGGTGGGCAT GCAGTATTTC CTGATTTCTC CCCCAAAGAG CTTCAGAATG 960 TCTGCTAATG GCACCCTCTT CTCCACAACA GAATTGGACT TTGAAGCAGG ACACAGAAGT TTCCATCTCA TCGTGGAGGT GAGGGACAGT GGAGGCCTCA AAGCCTCCAC AGAGCTCCAG 1020 1080 GTGAACATCG TGAACCTCAA CGACGAAGTC CCTCGCTTTA CCAGCCCGAC ACGAGTGTAC 1140 ACAGTCCTGG AGGAACTGAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1200 60 GATGATGAAG GTTTTCCCAG CCACCTCCTC TACAGCATTA CCACTGTTAG CAAATATTTC
ATGATAAATC AGTTGACTGG TACAATCCAA GTGGCCCAAA GGATAGACCG AGATGCAGGT 1260 1320 GAATTGAGAC AAAATCCCAC CATTTCCCTG GAAGTTCTAG TGAAGGACAG ACCATATGGG 1380 GGTCAGGAGA ATCGCATCCA GATAACCTTC ATTGTGGAAG ACGTCAACGA CAATCCTGCC ACATGCCAAA AGTTCACCTT CAGATCCAGT CTCCACCCTG CTCTGTGCTC CAAGACGCTG 1440 1500 65 ACCTGGATGG ATACCGTATT AGACTGTTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1560 GGGCGATTTA CAAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1620 CTCACAATCA TGGCAGAAGG CAAGGAGGAG CAAGTCACAT CTTACATGGA TGGCAGCAGG 1680 CAAAGAGATA GAGCTTGTGT AGGGAAACTC CTCCTTATAA AGCCATCAGA TCTCATGAGA 1740 CTTAGTCACT ATCACGAGAA CAACTCAGGA AAGACTTGCC CCCATGATTC CATTTCCTCC 1800 70 TACCAGGTCC CTCCCACAAC ATGTAGGAAT TCAAGAATCC AGGCCACCAA CAACGAAGAC 1860 ACAAGCTCTG TCACTGTTAC TGTGAACATC CTTGAAGAAA ATGATGAAAA GCCAATTTGT ACTCCAAACT CTTATTTCCT GGCCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATTCAG 1920 1980 AATTTCAAGC TGACATGTAC CGACCTTGAT TCCAGCCCCA GATCTTTCCG TTATTCCATT 2040 GGCCCAGGTA ACGTCAACAA TCATTTCACC TTCTCTCCCA ATGCTGGTTC CAATGTCACA 2100 75 2160 CECCTGCTGC TTACATCTCG CTTTGACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC AAGCTACTTG TCTACGTAAC TGATGACAAC TTGATGTCTG ACAGGAAGAA AGCGGAGGCT 2220 CTTGTTGAGA CAGGAACAGT GACACTGAGT ATTAAAGTCA TTCCCCACCC AACCACTATC 2280 ATCACCACGA CCCCCAGGCC CAGGGTCACC TATCAGGTCC TGAGGAAAAA CGTTTACTCT CCATCTGCAT GGTACGTGCC GTTTGTCATC ACTTTGGGCT CCATATTGCT TCTGGGTCTC 2340 2400 80 CTCGTGTACC TGGTCGTCCT ATTGGCCAAA GCCATCCACA GACACTGCCC CTGCAAGACT 2460 GGGAAGAACA AGGAACCTCT GACAAAGAAA GGAGAAACGA AGACTGCAGA GAGAGACGTC 2520 GTGGTGGAAA CTATCCAGAT GAACACTATC TTTGATGGAG AAGCCATAGA TCCAGAGCCT GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCCAGCT GCTGCGACCC TAGTCCAGTA 2580

ACCCTAAGAA AGGTCCAGGT GTGTGGGGAG AGTGAAGAGA CCGGTCAGTG TTCCGGCCAC

2700

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|     | TTAAGCTTCC           | AAGGAAGTCA<br>GCCGTCTCAA<br>GTTCTCAATG       | CCCCTCACAG               | GAGCTTACTG               |            |                          | 1140<br>1200<br>1237 |
|-----|----------------------|--|--------------------------|--------------------------|------------|--------------------------|----------------------|
| 5   | Sea ID NO:           | C70 DNA Sec                                  | nience                   |                          |            |                          |                      |
|     | Nucleic Ac           | id Accession<br>Jence: 1381.                 | #: NM_022                | .54.2                    |            |                          |                      |
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|     | CATATGTACG           | TAGTTTTTCC<br>CAAATCCTGG<br>GTTTGAGGGC       | TAAGAAGTGG<br>GGCGTTTGCA | CGTGGTTTGG<br>AACCCGGATC | CGGGGCGTCT | GGCCCCATGC               | 60<br>120<br>180     |
| 15  | CTGGTGGCCT           | TTATCTCTGT                                   | CCCCCTTTGT               | CCTCTTTATC               | TCAGGCTCTC | CAGGAGGCCG               | 240                  |
|     | CGCGAGCTGC           | TCCGCCTATC<br>TGTTCTTTCG                     | AAGGCGCCGG               | AGAACCAGGG               | GCGTCCCGCG | CCACCTCTGA               | 300<br>360           |
|     |                      | CGCCGAGCAC<br>CTGCGCGGCA                     |                          |                          |            |                          | 420                  |
| 20  |                      | GCGCGGTGGC                                   |                          |                          |            |                          | 480<br>540           |
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|     |                      | CGGCGCAGCT                                   |                          |                          |            |                          | 660                  |
|     |                      | AGCCTGGCCA<br>GCTTTTCAAA                     |                          |                          |            |                          | 720<br>780           |
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|     |                      | ATTCAGAAGT<br>TCGGATTGAT                     |                          |                          |            |                          | 900                  |
|     |                      | TTGTGGGGCT                                   |                          |                          |            |                          | 960<br>1020          |
| 20  | ATTCCAGAGG           | CATTTGGATT                                   | TGATCCCAAA               | GTCGACAGTT               | ATGTTGAGAA | GGCAGTTGCT               | 1080                 |
| 30  |                      | GATTTTACCT                                   |                          |                          |            |                          | 1140                 |
|     |                      | CTAAAGCATT                                   |                          |                          |            | TCAAGAAAAA<br>AAATCCTGCT | 1200<br>1260         |
|     | GTCACAGAAG           | CTAATGGACA                                   | TATCCATTTT               | GATAATGTCA               | GTGTGGTATC | TCTACAGGAT               | 1320                 |
| 35  |                      | AGCCAAGTTC                                   |                          |                          |            |                          | 1380                 |
| 55  |                      | GGATGATAAC                                   |                          |                          |            |                          | 1440<br>1500         |
|     |                      | TTCCCCACGA                                   |                          |                          |            |                          | 1560                 |
|     |                      | CCTTGCTATT<br>TGGTGGGCAA                     |                          |                          |            |                          | 1620                 |
| 40  |                      |  |                          |                          |            | GCTGAGAGAA               | 1680<br>1740         |
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|     |                      | CAGCCATTCT AAGATGGTGT                        |                          |                          |            | ATTGGAGTAA               | 1860                 |
|     |                      |  |                          |                          |            | CTGTAGGTCC               | 1920<br>1980         |
| 45  | AGAAAACTAA           | TTATTGGCAT                                   | CAGTCTGTGA               | AATAGTCCAT               | TATTTGTTGT | TAAAAATGCT               | 2040                 |
|     |                      |  |                          |                          |            | GGGAAATACT               | 2100<br>2160         |
|     |                      |  |                          |                          |            | TGCATTCTAT               | 2220                 |
| 50  | CTCTATGGTA           | GGATCAAAGA                                   | TTCAAATGGT               | TTCAGAGAGG               | TTTTATTTCA | ATTAATTTGT               | 2280                 |
| 30  |                      |  |                          |                          |            | GCAACACTAA<br>CAGCTTTTTG | 2340<br>2400         |
|     |                      |  |                          |                          |            | TCTAAAATAA               | 2460                 |
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| 55  |                      |  |                          |                          |            | TTCTGACTTA<br>ACACCTCGGT | 2580<br>2640         |
| 55  |                      |  |                          |                          |            | GAGAAAGAAA               | 2700                 |
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|     |                      |  |                          |                          |            | TAACTGGAAA<br>GTGTTCAGCC | 2820<br>2880         |
| 60  |                      |  |                          |                          |            | TTTTTCTACC               | 2940                 |
|     |                      |  |                          |                          |            | GTCTAAAATT               | 3000                 |
|     |                      |  |                          |                          |            | GGAAAATGAT               | 3060<br>3120         |
| 65  |                      |  |                          |                          |            | TATTTCACTT               | 3180                 |
| 65  | TATGACTGAC<br>AAAAAA | AAAAAATTAA :                                 | TATTGTTTGG               | CCAAATAGTA               | AACACCCTTI | TGAAACCATG               | 3240<br>3246         |
| 70  | Nucleic Ac           | : C71 DNA Se<br>cid Accessio<br>quence: 188. | n #: NM_004              | 184.2                    |            |                          |                      |
|     | 1                    | 11   | 21                       | 31                       | 41         | 51                       |                      |
| 75  | CGVVVVVC             | <br>   | ן<br>ארדאאארארי          | , yanan cakaca           |            | CTCTCACCAC               | 60                   |
| , 5 |                      |  |                          |                          |            | CTCTCAGCAG<br>CTGGTCTTGA | 60<br>120            |
|     | CTCGTCTGC:           | C GAACAAATCO                                 | TCTGACCTC                | GCCCGCTGT                | GAACGTAGT  | CCTGAGAGAT               | 180                  |
|     |                      |  |                          |                          |            | GCATCGCCAC<br>AAATTGATTC | 240                  |
| 80  |                      |  |                          |                          |            | GGGAGGATTA               | 300<br>360           |
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                                                                                                         1260
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                                                                                                         1380
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        CTCTGTGACC CCAATTTGAG TTTTGATGCT GTCACTACCG TGGGAAATAA GATCTTTTTC
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                                                                                            960
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| 5        | TGGAGGTATG<br>AACTTCCAAG<br>TATTTCTTCC   | TTTTTAACCC<br>ATGAAAGGAG<br>GAATCGGGCC<br>AAGGATCTAA<br>GCAATAGCTG | ACAGATGATG<br>TAAAATTGAT<br>CCAATTTGAA   | GACCCTGGTT<br>GCAGTCTTCT<br>TATGACTTCC                            | ATCCCAAACT<br>ACTCTAAAAA   | GATTACCAAG<br>CAAATACTAC  | 1200<br>1260<br>1320<br>1380<br>1413  |
|----------|--|--|--|---|--|---|---------------------------------------|
| 10       | Nucleic Act  | C82 DNA Seq<br>id Accession<br>uence: 117                          | #: им_0069   | 952.1   |  |   |                                       |
| 10       | 1  | 11   | 21   | 31  | 41   | 51  |                                       |
| 15       | AATCCCGACA<br>TGGAAATGTG<br>ATCTGACCAA<br>GGCTGCCTGG<br>TGTAGGCATC<br>AGTATATGCC | ATGGCGAAAG ATTATTGGTT CACAGCCTCT ATCGGCATAT ATGAAGTCCA TTTGAAGTGG  | ACAACTCAAC<br>GTTGCGGCAT<br>ACCCACTGCT<br>TTGTGGGCAT<br>GCAGGAAAAT<br>CATCTTGTAT | TGTTCGTTGC TGCCCTGACT TGAAGCCACC CTGCCTCTTC TCTTCTGGCG CACAGCAGCA | TTCCAGGGCC<br>GCGGAGTGCA<br>GACAACGATG<br>TGCCTGTCTG<br>TATTTCATTC<br>ACACAACGAG | TGCTGATTTT TCTTCTTTGT ACATCTATGG TTCTAGGCAT TGATGTTTAT ACTTTTTCAC | 60<br>120<br>180<br>240<br>300<br>360 |
| 20       | TGATGACCAG<br>CAATTGCTGT<br>TGAGAATAAT<br>AGAACCTCTC                             | TTCCTGAAGC<br>TGGAAAAACA<br>GGCGTAAATG<br>GATGCTGACT<br>AACCTGGAGG | ATGGAGTCAC<br>GTCCATCAGA<br>ATCCCTGGCC<br>CTTGTAAACT                             | CAAAACCTGG<br>CTGGCAAAAA<br>TCGTCAATGC<br>AGGCGTGCCT              | GACAGGCTCA<br>TACACATCTG<br>TGTGTTATGA<br>GGTTTTTATC                             | TGCTCCAGGA<br>CCTTCCGGAC<br>ACAATCTTAA<br>ACAATCAGGG              | 420<br>480<br>540<br>600<br>660       |
| 25       | ATTTGCCATT<br>AATTGAATAT   |  | CTTTTTGGGT   |   |  |   | 720<br>780<br>796                     |
| 30       | Nucleic Ac   | C83 DNA Sec<br>id Accession<br>uence: 71                           | #: NM_001  | 793.2   |  |   |                                       |
|          | 1  | 11   | 21   | 31  | 41   | 51<br>1   |                                       |
| 25       |  | GAGCTGAGCG   |  |   |  |   | 60                                    |
| 35       |  | ATGGGGCTCC   |  |   |  |   | 120                                   |
|          |  | TGCGCGGCCT   |  |   |  |   | 180<br>240                            |
|          |  | CAAGAGCCAG   |  |   |  |   | 300                                   |
| 40       |  | GTCCAGGAAA   |  |   |  |   | 360                                   |
| 40       |  | ATCTTACGAA   |  |   |  |   | 420                                   |
|          |  | AAGGGTCCCT<br>ATTTTCTACA   |  |   |  |   | 480<br>540                            |
|          |  | GAGAAGGAGA   |  |   |  |   | 600                                   |
| AF       |  | TATGAGCTCT   |  |   |  |   | 660                                   |
| 45       |  | ATCTCCATCA   |  |   |  |   | 720                                   |
|          |  | CGAGGGAGTG<br>GATGAGGATG   |  |   |  |   | 780<br>840                            |
|          |  | GAACCAAAGG   |  |   |  |   | 900                                   |
| 50       |  | GTCATCTCCA   |  |   |  |   | 960                                   |
| 50       |  | ACAGACATGG<br>GCCAATGACA   |  |   |  |   | 1020<br>1080                          |
|          |  | GCAGTGGGCC   |  |   |  |   | 1140                                  |
|          |  | GCGTGCCGTG   |  |   |  |   | 1200                                  |
| 55       |  | ACCCACCCTG AAAAACCAGC  |  |   |  |   | 1260                                  |
| 55       |  | CCAACCTCCA   |  |   |  |   | 1320<br>1380                          |
|          |  | GTCCCACCCT   |  |   |  |   | 1440                                  |
|          |  | GICTACACTG   |  |   |  |   | 1500                                  |
| 60       |  | GACCCAGCAG<br>CTCGACCGTG   |  |   |  |   | 1560<br>1620                          |
|          | GGTCTTGGCC   | ATGGACAATG   | GAAGCCCTCC   | CACCACTGGC  | ACGGGAACCC   | TTCTGCTAAC  | 1680                                  |
|          |  |  |  |   |  | CCATCTGCAA  | 1740                                  |
|          |  |  |  |   |  | CCCACACCTC  | 1800<br>1860                          |
| 65       |  |  |  |   |  | CATATGACGT  | 1920                                  |
|          |  |  |  |   |  | GGGCCACTGT  | 1980                                  |
| •        |  |  |  |   |  | GTTTCATCCT<br>TTTTGTTGGT  | 2040<br>2100                          |
| 70       |  |  |  |   |  | CCCGTGAÇAA  | 2160                                  |
| 70       |  |  |  |   |  | ACATCACCCA  | 2220                                  |
|          |  |  |  |   |  | TCGCACCAAC  | 2280<br>2340                          |
|          |  |  |  |   |  | ACGACACCCT  |                                       |
| 75       |  |  |  |   |  | CCCTCACCTC  | 2460                                  |
| 75       |  |  |  |   |  | GCCGCTTCAA<br>TGCAGGGCTG  | 2520<br>2580                          |
|          |  |  |  |   |  |   | 2640                                  |
|          | GACTTCGGAC   | CTTGTCAGGA   | AGTGGCCGTA   | GCAACTTGGC  | GGAGACAGGC   | TATGAGTCTG  | 2700                                  |
| 80       |  |  |  |   |  | GTTTGACTTC  | 2760                                  |
| <b>J</b> |  |  |  |   |  | TCCAGAAGCC<br>GTGACTGACC  | 2820<br>2880                          |
|          | TACAGTGGA  | TTTCTCTCTC   | GAATGGAAC  | TTCTTAGGCC  | TCCTGGTGCA   | ACTTAATTTT  | 2940                                  |
|          |  |  |  |   |  |   | 3000                                  |
|          | GCTGGGCCC  | · creecerce  | : IGCATTICIT   | GTTTCCAGAC  | . CCCAATGCCI   | CCCATTCGGA  | 3060                                  |

|     | GTTGCGTTGC                             | CGTTTTTATA<br>TATAGATGAA<br>TTTCCCAGAA                           | GGGTGAGGAC                             | CTAGGTTGCC<br>AATCGTGTAT               | CCTTATTTTT<br>ATGTACTAGA               | TATTTTCCCT<br>ACTTTTTAT                | 3120<br>3180<br>3205            |
|-----|--|--|--|--|--|--|---------------------------------|
| 5   | Nucleic Aci                            | C84 DNA Sec<br>id Accession<br>mence: 639                        | #: NM_0056                             | 529.1                                  |  |  |                                 |
| 10  | 1                                      | 11   | 21                                     | 31                                     | 41                                     | 51                                     |                                 |
|     | CCGCCGCCAC                             | GAGGTGGCGA<br>GAAGGAGAGG<br>CACCGCCACC                           | GCGAGGCGCG<br>GGAGTCGCGG               | CCCGAGCCGC                             | CGCCGCCGCC                             | GCCACCGCCG<br>GGGCCCCGGC               | 60<br>120<br>180                |
| 15  | CCGATGTCGC<br>GCCGCCGCCC<br>GCCGGGCCCC | GGCGCGGCC<br>CCGCGCCCCG<br>GAGCCGCGG<br>GACGCCGCCC<br>AGTGCTTCGT | TTAGGATGAG<br>CAGGAGCCTC<br>GCGCGCCCCC | TCTCGGGTCG<br>GGGAGCCGCC<br>GGGCCCCCGA | GGCGAGGAGC<br>GCCGCCGCCG<br>CACACATGAG | CGCCGCAGCC<br>CCGCCGCCCG<br>ATTCTTCAGG | 240<br>300<br>360<br>420<br>480 |
| 20  | CGTCCGCCCG                             | CCGCCCCGTC   | CCCCGGCCCG                             | GCCGCCCCC                              | GGCCCCCGGC                             | CGGCCCGCGC                             | 540                             |
| 20  |  | CTCCCCGGTG   |  |  |  |  | 600<br>660                      |
|     | ACGGCATCTA                             | TAGCGTGTCC   | GGCGACGAGA                             | AGAAGGGCCC                             | CCTCATCGCG                             | CCCGGGCCCG                             | 720                             |
|     | ACGGGGCCCC                             | GGCCAAGGGC   | GACGGCCCCG                             | TGGGCCTGGG                             | GACACCCGGC                             | GGCCGCCTGG                             | 780                             |
| 25  |  | GCGCGAGACC<br>CTTGGGCAAC   |  |  |  |  | 840<br>900                      |
|     | GTGTGTTCCT                             | TATTCCCTAC   | GTCCTGATCG                             | CCCTGGTTGG                             | AGGAATCCCC                             | ATTTTCTTCT                             | 960                             |
|     |  | GCTGGGCCAG   |  |  |  |  | 1020                            |
|     |  | AGGCCTGGGC<br>GCTGGCCTGG   |  |  |  |  | 1080                            |
| 30  |  | ATGTGGCCAC   |  |  |  |  | 1140<br>1200                    |
|     | AAGACTGTGC                             | CAATGCCAGC   | CTGGCCAACC                             | TCACCTGTGA                             | CCAGCTTGCT                             | GACCGCCGGT                             | 1260                            |
|     |  | CGAGTTCTGG<br>CAACTGGGAG   |  |  |  |  | 1320                            |
|     |  | GAAGGGGGTC   |  |  |  |  | 1380<br>1440                    |
| 35  | CCTACGTGGT                             | CCTGGTCGTG   | CTGCTGGTGC                             | GTGGAGTGCT                             | GCTGCCTGGC                             | GCCCTGGATG                             | 1500                            |
|     | GCATCATTTA                             | CTATCTCAAG   | CCTGACTGGT                             | CAAAGCTGGG                             | GTCCCCTCAG                             | GTGTGGATAG                             | 1560                            |
|     |  | CCAGATTTTC<br>CCGCTTCAAC   |  |  |  |  | 1620<br>1680                    |
| 40  | ACAGTGGGAC                             | CAGCTTCTTT   | GCTGGCTTCG                             | TGGTCTTCTC                             | CATCCTGGGC                             | TTCATGGCTG                             | 1740                            |
| 40  | CAGAGCAGGG                             | CGTGCACATC   | TCCAAGGTGG                             | CAGAGTCAGG                             | GCCGGGCCTG                             | GCCTTCATCG                             | 1800                            |
|     | TCATGCTGTT                             | GGCTGTCACG<br>GCTGCTTGGT   | CTCGACAGCC                             | AGTTTGTAGG                             | TGTGGAGGG                              | TTCATCACCE                             | 1860<br>1920                    |
|     | GCCTCCTCGA                             | CCTCCTCCCG   | GCCTCCTACT                             | ACTTCCGTTT                             | CCAAAGGGAG                             | ATCTCTGTGG                             | 1980                            |
| 45  |  | TGCCCTCTGC   |  |  |  |  | 2040                            |
| 73  |  | GCTGTTTGAC<br>CGTGGTGGTG   |  |  |  |  | 2100<br>2160                    |
|     |  | CGGGTACCGA   |  |  |  |  | 2220                            |
|     |  | CATGGGCATC   |  |  |  |  | 2280                            |
| 50  |  | CGTGTACCCG<br>CGTGCCGCTG   |  |  |  |  | 2340<br>2400                    |
|     | CTGAGCGCTG                             | GCAGCACCTG   | ACCCAGCCCA                             | TCTGGGGCCT                             | CCACCACTTG                             | GAGTACCGAG                             | 2460                            |
|     |  | AGATGTCAGG   |  |  |  |  | 2520                            |
| _ = |  | GGAGAGTGTC<br>CCCCTGCTTC   |  |  |  |  | 2580<br>2640                    |
| 55  | CACTTTTGGG                             | GTCTGCCTGG   | GGGAGGAGGG                             | GAGAAAGCAC                             | CATGAGTGCT                             | CACTAAAACA                             | 2700                            |
|     | ACTTTTTCCA                             | TTTTTAATAA   | AACGCCAAAA                             | ATATCACAAC                             | CCACCAAAAA                             | TAGATGCCTC                             | 2760                            |
|     | CAGTGCTGCA                             | GCCCTAGCCG<br>CTCCTCCTGC   | CCCTGCCACG                             | AGGCCCCGCC                             | GCCCACCTCT                             | CCCCCACCCA                             | 2820<br>2880                    |
| 60  | CTCTGCAGCA                             | CACCCGTGGG   | TGACCCCTCA                             | CCCCAGAAGC                             | AGCAGTGGCA                             | GCTTGGGAAA                             | 2940                            |
| 00  | TGTGAGGAAG                             | GGAAGGAGGG   | AGAGACGGGA                             | GGGAGGAGAG                             | AGAGGAGAAG                             | GGAGGCAGGG                             | 3000                            |
|     | TTATAGAAGC                             | AGAACCAAGG<br>TTAGAGAGCC   | AGCCAGCAAT                             | GGAACCTTCT                             | GGTTCCTGCG                             | CCCATCCCTG                             | 3060<br>3120                    |
|     | CCAGTATCAA                             | TTGTGTGAGC   | TTGGGTGCGA                             | GTGCACGCGT                             | GCGTGAGTAC                             | GGAGAGTATA                             | 3180                            |
| 65  | TATAGATCTC                             | TATCTCTTAG   | CAAAGGTGAA                             | TGCCAGATGT                             | AAATGGCGCC                             | TCTGGGCAAA                             | 3240                            |
| 05  | TTTCTAAAAA                             | GAGGAAGGAG   | CCCAAACCAT                             | ACTIGAGAGA                             | ATGAGATTTC                             | TGCTTGTATA<br>CCCTGTGAGC               | 3300<br>3360                    |
|     | CCTACCTTAC                             | CCCTCTGCCC   | CTAGCCAAGG                             | AGTGTGAATT                             | TATAGATCTA                             | ACTITCATAG                             | 3420                            |
|     |  |  |  |  |  | TGCGTGTGTG                             | 3480                            |
| 70  |  |  |  |  |  | CTGTCCCCAC                             | 3540                            |
|     |  |  |  |  |  | CCCAGGAAGG                             | 3600<br>3660                    |
|     | GACCCTGGAC                             | ACGGCTCCCA   | CGTCCAGGCT                             | TAAGGTGGAT                             | GCACTTCCCG                             | CACCTCCAGT                             | 3720                            |
|     | TGACCCCAAG                             | GCAGCTTTAA   | CCCACGTTTG                             | TCTGTCACGT                             | CCAGTCCCGA                             | GACGGCTGAG<br>GGCTGGGTGA               | 3780                            |
| 75  | GGGTGGCGGG                             | CCTGCGGGGA   | CATTCTACTG                             | TGCTAAAAAG                             | CCACTGCAGA                             | CATAGCAATA                             | 3840<br>3900                    |
|     | AAAACATGTC                             |  | <b>-</b>                               |  |  |  | 3917                            |
|     | Sea ID NO-                             | COE DAYS C-  |  |  |  |  |                                 |
| 00  |  | C85 DNA Sed<br>id Accession                                      |  | 516.1                                  |  |  |                                 |
| 80  | Coding seq                             | uence: 180.  |  |  |  |  |                                 |
|     | 1                                      | 11 .   | 21                                     | 31                                     | 41                                     | E1                                     |                                 |
|     | Ī                                      | ī  | ĩ                                      | 1                                      | Ī                                      | 51<br>                                 |                                 |
|     | TAGTCGCGGG                             | TCCCCGAGTG   | AGCACGCCAG                             |  | ACCAAACGAC                             | GGGGGTCGGA                             | 60                              |

|  | GTCAGAGTCG   |   |  |   |   |   | 120   |
|--|--|---|--|---|---|---|---|
|  | CGCACGCCCG   | TCGCCACCCG  | CGTACCCGGC   | GCAGCCAGAG  | CCACCAGCGC  | AGCGCTGCCA  | 180   |
|  | TGGAGCCCAG   |   |  |   |   |   | 240   |
|  | TTGGCTCCCT   |   |  |   |   |   | 300   |
| 5  |  |   |  |   |   |   |   |
| 5  | AGGAGTTCTA   |   |  |   |   |   | 360   |
|  | TCACCACGCT   | CTGGTCCCTC  | TCAGTGGCCA   | TCTTTTCTGT  | TGGGGGCATG  | ATTGGCTCCT  | 420   |
|  | TCTCTGTGGG   | THEFTHEFT   | AACCGCTTTG   | AADDOODO  | TTCAATGCTG  | ATGATGAACC  | 480   |
|  |  |   | GTGCTCATGG   |   |   |   |   |
|  |  |   |  |   |   |   | 540   |
|  | TGCTGATCCT   | GGGCCGCTTC  | ATCATCGGTG   | TGTACTGCGG  | CCTGACCACA  | GGCTTCGTGC  | 600   |
| 10   | CCATCTATCT   | GCGTGAAGTG  | TCACCCACAG   | CCTTTCGTGG  | GGCCCTGGGC  | ACCCTGCACC  | 660   |
|  |  |   | ATCCTCATCG   |   |   |   | 720   |
|  |  |   |  |   |   |   |   |
|  | GCAACAAGGA   | CCTGTGGCCC  | CTGCTGCTGA   | GCATCATCTT  | CATCCCGGCC  | CTGCTGCAGT  | 780   |
|  | GCATCGTGCT   | GCCCTTCTGC  | CCCGAGAGTC   | CCCGCTTCCT  | GCTCATCAAC  | CGCAACGAGG  | 840   |
| •  |  |   | CTAAAGAAGC   |   |   |   | 900   |
| 15   |  |   |  |   |   |   |   |
| 13   |  |   | AGTCGGCAGA   |   |   |   | 960   |
|  | AGCTGTTCCG   | CTCCCCCGCC  | TACCGCCAGC   | CCATCCTCAT  | CGCTGTGGTG  | CTGCAGCTGT  | 1020  |
|  | CCCAGCAGCT   | GTCTGGCATC  | AACGCTGTCT   | TCTATTACTC  | CACGAGCATC  | TTCGAGAAGG  | 1080  |
|  |  |   | TATGCCACCA   |   |   |   |   |
|  |  |   |  |   |   |   | 1140  |
| ~~   | CTGTCGTGTC   | GCTGTTTGTG  | GTGGAGCGAG   | CAGGCCGGCG  | GACCCTGCAC  | CTCATAGGCC  | 1200  |
| 20   | TCGCTGGCAT   | GGCGGGTTGT  | GCCATACTCA   | TGACCATCGC  | GCTAGCACTG  | CTGGAGCAGC  | 1260  |
|  |  |   |  |   |   |   | 1320  |
|  |  |   | AGCATCGTGG   |   |   |   |   |
|  | TGGGTCCTGG   | CCCCATCCCA  | TGGTTCATCG   | TGGCTGAACT  | CTTCAGCCAG  | GGTCCACGTC  | 1380  |
|  | CAGCTGCCAT   | TGCCGTTGCA  | GGCTTCTCCA   | ACTGGACCTC  | AAATTTCATT  | GTGGGCATGT  | 1440  |
|  |  |   | CTGTGTGGTC   |   |   |   | 1500  |
| 25   |  |   |  |   |   |   |   |
| 23   |  |   | ACCTACTTCA   |   |   |   | 1560  |
|  | ATGAGATCGC   | TTCCGGCTTC  | CGGCAGGGGG   | GAGCCAGCCA  | AAGTGATAAG  | ACACCCGAGG  | 1620  |
|  | ACCITCITTCCA   | TCCCCTGGGG  | GCTGATTCCC   | AAGTGTGAGT  | CGCCCCAGAT  | CACCAGCCCG  | 1680  |
|  |  |   | AGGATCTCTC   |   |   |   | 1740  |
|  |  |   |  |   |   |   |   |
| 20   | AACCTGACAG   | ATGTCAGCCG  | AGCCGGGCCT   | GGGGCTCCTT  | TCTCCAGCCA  | GCAATGATGT  | 1800  |
| 30   | CCAGAAGAAT   | ATTCAGGACT  | TAACGGCTCC   | AGGATTTTAA  | CAAAAGCAAG  | ACTGTTGCTC  | 1860  |
|  |  |   | CAGGTTTTAT   |   |   |   | 1920  |
|  |  |   |  |   |   |   |   |
|  |  |   | TGCCCACATC   |   |   |   | 1980  |
|  | GAGGGTGGAG   | ACTAAGCCCT  | GTCGAGACAC   | TTGCCTTCTT  | CACCCAGCTA  | ATCTGTAGGG  | 2040  |
|  |  |   | CACACTAATC   |   |   |   | 2100  |
| 35   |  |   |  |   |   |   |   |
| 33   |  |   | TTCTGCTGGC   |   |   |   | 2160  |
|  | CATTAGGATT   | TGCCCCTTCC  | CATCTCTTCC   | TACCCAACCA  | CTCAAATTAA  | TCTTTCTTTA  | 2220  |
|  | CCTGAGACCA   | GTTGGGAGCA  | CTGGAGTGCA   | GGGAGGAGAG  | GGGAAGGGCC  | AGTCTGGGCT  | 2280  |
|  |  |   |  |   |   |   | 2340  |
|  |  |   | GCACTGAGGG   |   |   |   |   |
| 40   | GGGAGCCTGC   | AAACTCACTG  | CTCAAGAAGA   | CATGGAGACT  | CCTGCCCTGT  | TGTGTATAGA  | 2400  |
| 40   | TGCAAGATAT   | TTATATATAT  | TTTTGGTTGT   | CAATATTAAA  | TACAGACACT  | AAGTTATAGT  | 2460  |
|  |  |   | GTAAATACAC   |   |   |   | 2520  |
|  |  |   |  |   |   |   |   |
|  |  |   | AAACATGGTT   |   |   |   | 2580  |
|  | TTTGGATGGG   | AGTGAGACAG  | AAGTAAGTGG   | GGTTGCAACC  | ACTGCAACGG  | CTTAGACTTC  | 2640  |
|  |  |   | ACACGTACCT   |   |   |   | 2700  |
| 45   |  |   |  |   |   |   |   |
| 43   |  |   | GAATATATAC   |   |   |   | 2760  |
|  | ATCACATATT   | TGATAGTTGG  | TGTTCAAAAA   | AACACTAGTT  | TTGTGCCAGC  | CGTGATGCTC  | 2820  |
|  |  |   | TTGAATGTGA   |   |   |   | 2856  |
|  |  |   |  |   |   |   |   |
|  |  |   |  |   |   | •   |   |
|  |  |   |  |   |   |   |   |
| 50   | Seq ID NO:   | C86 DNA Se  | quence   |   |   |   |   |
| 50   |  |   |  | 292.2   |   |   |   |
| 50   | Nucleic Ac   | id Accessio   | n #: XM_035  | 292.2   |   |   |   |
| 50   | Nucleic Ac   |   | n #: XM_035  | 292.2   |   |   |   |
| 50   | Nucleic Ac   | id Accessio   | n #: XM_035  | 292.2   |   |   |   |
| 50   | Nucleic Ac   | id Accessio   | n #: XM_035  | 292.2<br>31   | 41  | 51  |   |
|  | Nucleic Ac<br>Coding sequ  | id Accession  | n #: XM_035  |   | <b>41</b>   | 51<br>I   |   |
|  | Nucleic Act<br>Coding sequent  | id Accession<br>mence: 53   | n #: XM_035<br>1576<br>21  | 31<br>  | }   |   |   |
| 50<br>55   | Nucleic According sequents   | id Accession uence: 53  11   cccccccccccccccccccccccccccccc   | n #: XM_035<br>1576<br>21<br> <br>  CGGGTGTCCC   | 31<br> <br>  AGGCCCGGCC   | <br>  GGTGCGCAGA  | <br>GCATGGCGGG  | 60  |
|  | Nucleic According sequents   | id Accession uence: 53  11   cccccccccccccccccccccccccccccc   | n #: XM_035<br>1576<br>21<br> <br>  CGGGTGTCCC   | 31<br> <br>  AGGCCCGGCC   | <br>  GGTGCGCAGA  |   | 60<br>120   |
|  | Nucleic According sequents of the sequents of  | id Accession uence: 53  11  | m #: XM_035<br>1576<br>21<br> <br>  CGGGTGTCCC<br>  CGCTAGCGGC   | 31<br> <br>AGGCCCGGCC<br>GCCGCGGCC  | <br>  GGTGCGCAGA<br>  GAGGAGAAGG  | <br>GCATGGCGGG<br>AAGAGGCGCG  | 120   |
|  | Nucleic According sequences of the contract of | id Accession uence: 53  11  | n #: XM_035<br>1576<br>21<br>  | 31<br> <br>AGGCCCGGCC<br>GCCGGCGCC<br>CGGCTCGGCG  | GGTGCGCAGA<br>GAGGAGAAGG<br>CCGGCAGGCG  | GCATGGCGGG<br>AAGAGGCGCG<br>AGGGCGAGGG  | 120<br>180  |
|  | Nucleic According sequences of the control of the c | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31<br> <br>AGGCCCGGCC<br>GCCGCGCGCC<br>CGGCTCGGCG<br>CAACGGCGTG   | GGTGCGCAGA<br>GAGGAGAAGG<br>CCGGCAGGCG<br>GCCATCATCG  | GCATGGCGGG<br>AAGAGGCGCG<br>AGGGCGAGGG<br>TGGGGACCAT  | 120<br>180<br>240   |
| 55   | Nucleic According sequence of the control of the co | id Accession uence: 53  11  | #: XM_035:<br>1576<br>21<br>   | 31<br> <br>AGGCCCGGCC<br>GCCCGGCCC<br>CGGCTCGGCG<br>CAACGCGTG<br>GGGCGTGCTC   | GGTGCGCAGA GAGGAGAAGG CCGGCAGGCG GCCATCATCG AAGGAGGCAG  | GCATGGCGGG<br>AAGAGGCGCG<br>AGGGCGAGGG<br>TGGGGACCAT<br>GCTCGCCGGG  | 120<br>180<br>240<br>300  |
|  | Nucleic Actions sequently and sequently actions and sequently actions are sequently as a sequently action and sequently action a | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31<br> <br>AGGCCCGGCC<br>GCCGCGGCC<br>CAACGCCGT<br>CATCTTCTCC   | GGTGCGCAGA GAGGAGAAGG CCGGCAGGCG GCCATCATCG AAGGAGGCAG  | GCATGGCGGG<br>AAGAGGCGCG<br>AGGGCGAGGG<br>TGGGGACCAT<br>GCTCGCCGGG<br>CGCTCTGCTA  | 120<br>180<br>240   |
| 55   | Nucleic Actions sequently and sequently actions and sequently actions are sequently as a sequently action and sequently action a | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31<br> <br>AGGCCCGGCC<br>GCCGCGGCC<br>CAACGCCGT<br>CATCTTCTCC   | GGTGCGCAGA GAGGAGAAGG CCGGCAGGCG GCCATCATCG AAGGAGGCAG  | GCATGGCGGG<br>AAGAGGCGCG<br>AGGGCGAGGG<br>TGGGGACCAT<br>GCTCGCCGGG<br>CGCTCTGCTA  | 120<br>180<br>240<br>300<br>360   |
| 55   | Nucleic Actions sequently and the sequently and the sequently are sequently as a  | id Accession uence: 53  11   CCGCGGCTCC AAGCGGCGCA CAGCGGAACA CAGCGAACA GGCATCTTCG GTGTGTGGG  | #: XM_035:<br>1576  21   | 31<br>AGGCCCGGCC<br>GCCGCGGCC<br>CGGCTCGCG<br>CAACGCGTG<br>GGGCGTGCTC<br>CGTCTTCTCC<br>GGGCGGCGAC   | GGTGCGCAGA GAGGAGAAGG CCGGCAGGCG GCCATCATCG AAGGAGGCAG ATCGTGGGCG TACGCCTACA  | GCATGGCGGG<br>AAGAGGCGCG<br>AGGGCGAGGG<br>TGGGGACCAT<br>GCTCGCCGGG<br>CGCTCTGCTA<br>TGCTGGAGGT  | 120<br>180<br>240<br>300<br>360<br>420  |
| 55   | Nucleic Ac: Coding sequence  GCTCGCTGGG TGCGGGCCCG GGAGAAGATG CGTGACCTG TATCGCTCG GCTGGCGCTCG CCTGCGCGCTCC CTACGGCTCG  | id Accession uence: 53  11  | #: XM_035:<br>1576<br>21<br>   | 31<br>}<br>AGGCCCGGCC<br>GCCGGCGGCC<br>CGGCTGGCG<br>CAACGGCGTG<br>GGGCGTGCTC<br>CGTCTTCTCC<br>CGGCGGCGAC<br>CTGGATCGAG  | GGTGCGCAGA GAGGAGAAGG GCGATCATCG AAGGAGGCAG ATCGTGGGCG TACGCCTACA CTGCTCATCA  | GCATGGCGGG<br>AAGAGGCGCG<br>AGGGCGAGGG<br>TGGGGACCAT<br>GCTCGCCGGG<br>CGCTCTGCTA<br>TGCTGGAGGT<br>TCCGGCCTTC  | 120<br>180<br>240<br>300<br>360<br>420<br>480   |
| 55   | Nucleic Ac: Coding sequence  GCTCGCTGGG TGCGGGCCCG GGAGAAGATG CTGACCCTG TATCGGCTCG GCTGGCGCTCG CCTGCGGACCTC CTACGGCTCG ATCGCAGTAC  | id Accession uence: 53  11  | #: XM_035:<br>1576<br>21<br>   | 31   AGGCCCGGCC GCCGCGGCC CGCTCGGCG CAACGCCTTC CGTCTTCTCC GGGCGCGCAC CTGGATCGAG CACCTACCTG  | GGTGCGCAGA GAGGAGAGG CCGCAGGCG GCCATCATCG AAGGAGGCAG ATCGTGGGCG TACGCCTACA CTGCTCATCA   | GCATGGCGGG AAGAGGCGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG CGCTCTGCTA TGCTGGAGGT TCCTGGCCTTC TCCTGCCAC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
| 55   | Nucleic Ac: Coding sequence  GCTCGCTGGG TGCGGGCCCG GGAGAAGATG CTGACCCTG TATCGGCTCG GCTGGCGCTCG CCTGCGGACCTC CTACGGCTCG ATCGCAGTAC  | id Accession uence: 53  11  | #: XM_035:<br>1576<br>21<br>   | 31   AGGCCCGGCC GCCGCGGCC CGCTCGGCG CAACGCCTTC CGTCTTCTCC GGGCGCGCAC CTGGATCGAG CACCTACCTG  | GGTGCGCAGA GAGGAGAGG CCGCAGGCG GCCATCATCG AAGGAGGCAG ATCGTGGGCG TACGCCTACA CTGCTCATCA   | GCATGGCGGG AAGAGGCGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG CGCTCTGCTA TGCTGGAGGT TCCTGGCCTTC TCCTGCCAC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
| 55   | Nucleic Actional Sequence Coding Sequence Code Code Code Code Code Code Code Cod   | id Accession uence: 53  11   CCGCGGCTCC AAGCGGCGCA CAGCGGACA GGCATCTTCG GTGTGTGGG GGCACCACA CTGCCCGCCT ATCGTGGCCC CCCGAGGAGG  | #: XM_035:<br>1576  21   CGGCTGTCCC<br>CGCTAGCGGC<br>AGAGCCCGGA<br>TCACGCCCA<br>CCGCGTGCGG<br>TCTCCAAACC<br>TCCTCAAGCT<br>TCGTCTTCGC   | 31<br>AGGCCCGGCC<br>GCCGCCGGCC<br>CGCTCGGCG<br>CAACGCCTG<br>CGTCTTCTCC<br>GGGCGGCGAC<br>CTGGATCGAG<br>CACCTACCTG<br>CGTGGCTGC   | GGTGCGCAGA GAGGAGAAGG CCGCATCATCG AAGGAGGCAG ATCGTGGGCG TACGCCTACA CTGCATCATCA CTCAAGCCGC   | GCATGGCGGG AAGAGGCGCG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCTTA TGCTGGAGGT TCCGGCCTTC TCTTCCCCAC TGCTGCTCAC  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
| 55   | Nucleic Ac: Coding sequence  GCTCGCTGGG TGCGGGCCCG GGAGAAGATG CTTACCGCTCG GCTGGCCTCG CCTGCGCTCG CTACGCTCG CTACGCTCG CTACGCTCG ATCGCAGTAC CTGCCCGGTG GGCCGTCGAAC  | id Accession uence: 53  11  | #: XM_035:<br>1576<br>21<br>   | 31<br>}<br>AGGCCCGGCC<br>GCCGCCGGCC<br>CGGCTCGGCG<br>CAACGGCGTG<br>GGGCGTGCTC<br>GGGCGGGAC<br>CTGGATCGAC<br>CACCTACCTG<br>CGTGGCCTGC<br>CACCCGGGTC  | GGTGCGCAGA GAGGAGAAGG CCGGCAGCGCG GCCATCATCG AAGGAGGCAG ATCGTGGGCG TACGCCTACA CTGAAGCCGC CTCTGCGTGC   | GCATGGCGGG AAGAGGCGAGGG TGGGGACCAT GCTCGCCGGG CGCTCTGCTA TCCTGGAGGT TCCGGCCTTC TCTTCCCCAC TTGCCGCCCCC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660  |
| 55   | Nucleic Ac: Coding sequilibrium | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31<br>AGGCCCGGCC<br>GCCGGCGGCC<br>CGGCTCGGCG<br>CAACGCGTG<br>GGGCGGCGAC<br>CTGGATCGAG<br>CACCTACCTG<br>CACCCGGGTC<br>CACCCGGGTC<br>GCTGGCCTTC   | GGTGGGCAGA GGAGGAGAGG CCGGCAGGCG GCCATCATCG AAGGAGGCAG ATCGTGGGCG TAGGCCTACA CTGCAGCCG CTCAGAGCCGC CTCAGAGCCGC CTCAGAGCCGC  | GCATGGCGGG AAGAGGGGGAGGG TGGGGACCAT GCTCGCCGGG CGCTCTGCTA TCCTGGAGGT TCCGGCCTTC TTTCCCCAC TGCTGCTCAC TTGCTGCCCCG  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720   |
| 55   | Nucleic Ac: Coding sequilibrium | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31<br>AGGCCCGGCC<br>GCCGGCGGCC<br>CGGCTCGGCG<br>CAACGCGTG<br>GGGCGGCGAC<br>CTGGATCGAG<br>CACCTACCTG<br>CACCCGGGTC<br>CACCCGGGTC<br>GCTGGCCTTC   | GGTGGGCAGA GGAGGAGAGG CCGGCAGGCG GCCATCATCG AAGGAGGCAG ATCGTGGGCG TAGGCCTACA CTGCAGCCG CTCAGAGCCGC CTCAGAGCCGC CTCAGAGCCGC  | GCATGGCGGG AAGAGGCGAGGG TGGGGACCAT GCTCGCCGGG CGCTCTGCTA TCCTGGAGGT TCCGGCCTTC TCTTCCCCAC TTGCCGCCCCC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660  |
| 55   | Nucleic Activities Act | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GCCGCGCGCC CGCTCGGCG CAACGCGTG GGGCGGCGAC CTGGATCGAG CACCTACCTG CGTGGCCTGC CACCCGGGTTC TGAAGGCACC  | GETGCGCAGA GAGGAGAGGCAG GCCATCATCG AAGGAGGCAG ATCGTCGGCG TACGCCTACA CTCGCTCATCA CTCATCAGCCG CTCTGCGTGC CAGGATGCCT GTCCAGATCGCT AAACTGGATGCAGATGCGAGATGCGATGC  | GCATGGCGGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCCTA TGCTGGCGGT TCCTGCCCAC TGCTGCTAC TTCCCCCAC TGCTGCCCAC TGCTGCCCAC TTGCGGCGTA TGCGGCGTAC TTGCGGCGCAACACAT  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>720<br>780   |
| 55   | Nucleic Activities Act | id Accession uence: 53  11   CCGCGGCTCC AAGCGGCGCA CTGGCCGCA CAGCGGACA GGCATCTTCG GTGTTGTGGG GGCACCACCA CTGCCGGCT ATCGTGGCC CCCGAGGAGG TGCTACAGCG GCCTTGGCC CTAGATCCCA TTATACAGCG | #: XM_035: 1576  21   CGGCTGTCCC CGCTAGCGGC AGAGCCCGGA TCACGCTGCT TGACGCCCAC CCGCGTGCGG TCTCCAAATC TCCTCAAGCT TGGCTCTCGC CAGCCAGCCAGCT TGAAGCCCGC TGAAGCT TGAAGCCCGC TGAATCATCT ACTTCTCATT GCCTCTTTGCC     | 31  AGGCCGGGCC GGCTCGGCGC CGGCTCGGCG CAACGGCGTG CGGCTGGTCTCC GGGCGGGAC CTGGATCGAG CACCTACCTG CACCCGGGTC GCTGGCCTGC CTGAGGCGCGCTGC CTGAGGCGCC CTGAGGCGCCC CTGAGGCACC CTGAGGCACC CTGAGGCACC   | GGTGGGCAGA GGTGGGCAGA GCATCATCG AAGGAGGCAG TACGCCTACA CTGCTCATCA CTCAGCCGC CTCAGGCGC CAGGATGCCT CAGGATGCCT CAGGATGCCT CAGGATGCCT CTCAGATCG TGGAATTACT   | GCATGGCGGG AAGAGGCGAGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCTA TGCTGAGGT TCCGGCCTTC TTCTCCCAC TTGCTGCTCAC TTGCGGCCCC GAAAGGGTAC TTGCGGACACAT  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840   |
| <ul><li>55</li><li>60</li><li>65</li></ul>                       | Nucleic Ac: Coding sequitoring | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCGGCC GCCGCGGCC GCGCTGGCG CAACGGCTG GGGCTGCTC GGGCGGGAC CTGGATCACTG CACCTACCTG CACCTGGCTGC CACCCGGGTC CTGAGGCAC CTGGAGGA CTGGGCTCC CTATGGAGGA CCTGCCCTG   | GGTGGCAGA GGTGGCAGA GAGGAAGG GCCATCATCG AAGGAGCAG ATCGTGGGCG TACGCCTACA CTCAAGCCGC CTCTGGTGG CAGGATGCCT AAACTGGATGC AAACTGGATGC TGGAATTACT GCCATCATCA CGCATCATCA  | GCATGGCGGG AAGAGGCGAGGG TGGGGACCAT GCTCGCCGGG CGCTCTGCTA TCCCGAGGT TCCCCCAC TTGCCGCCCC GAAAGGGTGA TGGGGACAT TGGGGACAT TGGGGACAT TGGGACAT TGGGACAT TGGGACAT TGGGGACAT TGGGACAT TGAATTCOT TGAATTCCCCCCCC  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>720<br>780<br>840<br>900   |
| 55   | Nucleic Ac: Coding sequitoring | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCGGCC GCCGCGGCC GCGCTGGCG CAACGGCTG GGGCTGCTC GGGCGGGAC CTGGATCACTG CACCTACCTG CACCTGGCTGC CACCCGGGTC CTGAGGCAC CTGGAGGA CTGGGCTCC CTATGGAGGA CCTGCCCTG   | GGTGGCAGA GGTGGCAGA GAGGAAGG GCCATCATCG AAGGAGCAG ATCGTGGGCG TACGCCTACA CTCAAGCCGC CTCTGGTGG CAGGATGCCT AAACTGGATGC AAACTGGATGC TGGAATTACT GCCATCATCA CGCATCATCA  | GCATGGCGGG AAGAGGCGAGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCTA TGCTGAGGT TCCGGCCTTC TTCTCCCCAC TTGCTGCTCAC TTGCGGCCCC GAAAGGGTAC TTGGGAACAT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840   |
| <ul><li>55</li><li>60</li><li>65</li></ul>                       | Nucleic Ac: Coding sequitary GCTCGCTGGG TGCGGGCCCG GGAGAAGATG CGTGACCCTG GCTGGCGCTG GCTGGCGCTG CTGCGCAGTAC CTGCCCGTAC CTGCCCGTAC CTGCCCGTAC CTGCCCGTAC CAAGTCCTG TGTGCCAAT CACAGAGGAA CACAGAGGAA CATCGTGACG  | id Accession uence: 53  11  | #: XM_035: 1576  21     CGGGTGTCCC CGCTAGCGGC AGAGCCCGCA TCACGCTGCT TGACGCCCAC TCCTCAAATC TCCTCAAGCT TGGTCTTCGC CAGCCAAGCT TGAAGCCCCAC TGATCATCCT ACTTCTCATT GCCTCTTGGAC CCTACAGAAG TGCTACAGAA TTGCTGACCAA | 31  AGGCCCGGCC CGCTCGGCG CAACGCGTG CGGCGTGCTC CGTCTTCTCC GGGCGGGGAC CTGATCGAG CACCTACTG CGTGGCCTGC CATGGCCTGC CTTGATGAGAG ACCTGGCCTGC CTTGCCCTGCCC  | GEGTGGCAGA GAGAGAAGG GCGATCATCG AACGCCTACA CTCAAGCCAC CTCTCACAC CTCAAGCCC CTCTGCGTGC CTCAGATGCCT AAACTGGATG AAACTGGATG TGGAATTACT GCCAATCATCA TTCACCACCC  | GCATGGCGGG AAGAGCGCGG AGGGCAGGG TGGGGACCAT GCTCGCCGGG CGCTCTGCTA TGCTGGCGTT TCTCCCCAC TGCTGCTAC TGCTGCTAC TGCGGGTAC TGCGGCAC TTGCGCCCC TGAAGGGTGA TGGGGAACAT TGAATTTCGT TCTCCCCGC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960  |
| <ul><li>55</li><li>60</li><li>65</li></ul>                       | Nucleic According sequence of the control of the co | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GCCGCCGCCCCCCCCCCCCCCCCCCC   | GCCATCATCA AACTATCACCACCA AACTATCCA AAACTACCA AAACTACCA AAACTACCA AAACTACCA AAACTACCACCA AAACTACCACCA AAACTACCACCACA AAACTACCACCACA AAACTACCACCACA AAACTACCACCACA   | GCATGGCGGG AAGAGGCGAGG TGGGGACCAT GCTCGCCGGG TGCTGCTTA TGCTGGAGGT TCCGGCCTTC TGTTCCCAC TGCTGCTAC TGCTGCCAC TGCTGCTAC TGCGGCCTC TGCAGGTTA TGCAGCCAC TGCAGCTCAC TTGCCGCCAC TTGCCGCCAC TTGCCGCCAC TTGCCGCCAC TTGCCGCCAC TTGCCGCAC TGCACCTCAC TGCACCTAC   | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020  |
| <ul><li>55</li><li>60</li><li>65</li></ul>                       | Nucleic Ac: Coding sequitories  GCTCGCTGGG TGCGGCCCG GGAGAAGATG CGTGACCCTG TATCGGCTCG GCTGGCGTCG CTACGGCTCG ATCGCAGTAC CTACGCTCG ATCGCCAGTAC CAGCTCCTG TGTGTCCAAT TGTGTCCAAT TGTGTCGAAC CACAGAGGAA CATCGTGACG GCAGATGCTG   | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GCCGCCGCCC GCCGCCTGCCCC GCGCTCGCCCCCCCC  | GGTGGGCAGA GGTGGGCAGA GAGGAGAGGCAG AAGAGCAAG CTGCTCATCA CTGCTCATCA CTGCTCATCA CTCTCAGATCG CTCTCAGATCG AAACTGGATG TGGAATACAC TGCAATACAC CACATCATCAC CACATCATCAC CACATCATCAC CACATCATCAC CACATCACC GCCCCGTCAC GGCTCCGTCC GGCTCCGTCC   | GCATGGCGGG AAGAGGCGAGG TGGGGACCAT GCTCGCCGGG TCGCCGGGT TCCGGCCTTC TCTCCCCAC TTGCCGCCCC TTGCCGCCGC GAAAGGGTGA TCGAGACAT TCACTCAC TTGCCGCCCC TGTCACCCC TGTCACCCA TTGCCGCCCC TGTCCCCCC TGTCCACCCA TTGCCGCCCC TGTCCACCGA TTGCCGCC   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>660<br>720<br>840<br>900<br>960<br>1020   |
| <ul><li>55</li><li>60</li><li>65</li></ul>                       | Nucleic Ac: Coding sequitories  GCTCGCTGGG GCTCGCCCGG GGAGAAGATG CTGGCCCCG GCTGGCCCTG GCTGGCCTCG CTGCGCGTCG ATCGCAGTAC CTGCCCGTAC CTGCCCGTAC CTGCCCGTAC CAAGCTCCTG TGTGCTCCAAT TGTGCTGCAC CACAGAGGAA CATCGTGACG GCAGATGCTG GTCACATCCTG   | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GGCTCGGCG CAACGCGTC CGTCTTCTCC GGGCGCGCAC CTGGATCGAG CACCTACCTG CGTCGCCTC TGAAGGCACC CTTGATGAG CACCTGGCTTC TGAAGGCACC CTATGGAGCACC CTTGCCCTTG CCTGCCCTTG CCTGCCCTTG CCTGCCTTC GGTCCTCCTGCTTCGGGACTTCGGG  | GGGCACACCACCACCACCACCACCACCACCACCACCACCA  | GCATGGCGGG AAGAGGCCGG AAGAGGCCAGG TGGGGACCAT GCTGGCGGG CGCTCTGCTA TGCTGGCGTCAC TGCTGCCAC TGCTGCCAC TGCGGCGTCAC TTGCCGCCCT TTGCCCCCC TTGCCGCCCTC TTGCGCGCTCAC TTGGGGAACAT TGAATTTCGT TCTCCCTGCC TGTCCACCGA TGGGGGTCAT ATGGGTCCT  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140                                  |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Nucleic Ac: Coding sequitories  GCTCGCTGGG GCTCGCCCGG GGAGAAGATG CTGGCCCCG GCTGGCCCTG GCTGGCCTCG CTGCGCGTCG ATCGCAGTAC CTGCCCGTAC CTGCCCGTAC CTGCCCGTAC CAAGCTCCTG TGTGCTCCAAT TGTGCTGCAC CACAGAGGAA CATCGTGACG GCAGATGCTG GTCACATCC   | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GGCTCGGCG CAACGCGTC CGTCTTCTCC GGGCGCGCAC CTGGATCGAG CACCTACCTG CGTCGCCTC TGAAGGCACC CTTGATGAG CACCTGGCTTC TGAAGGCACC CTATGGAGCACC CTTGCCCTTG CCTGCCCTTG CCTGCCCTTG CCTGCCTTC GGTCCTCCTGCTTCGGGACTTCGGG  | GGGCACACCACCACCACCACCACCACCACCACCACCACCA  | GCATGGCGGG AAGAGGCGAGG TGGGGACCAT GCTCGCCGGG TCGCCGGGT TCCGGCCTTC TCTCCCCAC TTGCCGCCCC TTGCCGCCGC GAAAGGGTGA TCGAGACAT TCACTCAC TTGCCGCCCC TGTCACCCC TGTCACCCA TTGCCGCCCC TGTCCCCCC TGTCCACCCA TTGCCGCCCC TGTCCACCGA TTGCCGCC   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>660<br>720<br>840<br>900<br>960<br>1020<br>1080   |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Nucleic According sequence of the control of the co | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GCCGCGCGCC CGCTCGCCGC CAACGCGTG GGGCGGCAC CTGCATCACTG CGTCTCTCC GCTGGCTTC CACCCGGGTT TGAAGGCACC CTATGGAGCA CCTGCCCTG CCTGCCCTG CCTGCCCTAC GGACTTCGGG GTCCTGCTAC GGTCCTGCCCTAC GGTCCTGCCCTAC GGTCCTGCCCTAC GTCCTGCCCTAC   | GGCCCCTGC   | GCATGGCGGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TCGTGCTA TCCTGCCCAC TTCCCCCAC TGCTGCCAC TTCCCGCCT TTCCCGCCCC TTCCCCCCC TTCCCCCCC TTCCCCTCC TTCCCTCCCT TCTCCCTCC TCTCCCTCC TCTCCCTCC TCTCCCTCC TCTCCCTCCC TCTCCCTCCC TCTCCCTCCC  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080                                  |
| <ul><li>55</li><li>60</li><li>65</li></ul>                       | Nucleic Ac: Coding sequitories  GCTCGCTGGG TGCGGCCCG GGAGAAGATG CGTGACCCTG TATCGGCTCG GCTGGCCTG CTTGCCCGTG ATCGCAGTAC CTGCCCGTG ATCGCAGTAC CAAGCTCCTG TGTGTCCAAT TGTGTCAAT CAAGAGGAA CATCGTGACC GCAGATGCTG GTCAATAC GTCAATAC   | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GCCCGCCGCCC CGCTCGCCCC CGCTCGCCCC CGCTCTCTCC GGCCGCGAC CTGCATCGAC CACCCCGGTC CACCCGGGTC CACCCGGGTC CTGACCCCC CTATGAGGA CCTGCCCTG CCTGCCCTG CCTGCCTTG GGACTTCCCCCCCCCC  | GCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | GCATGGCGGG AAGAGGCGAGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCTA TGCTGACGT TCCCCAC TTGCTCAC TTGCTCAC TTGCTCAC TTGCTGCAC TTGCTCAC TTGCTCAC TTGCACCT CCTCCATCCT CCTCCATCCT TCACTTCTT   | 120<br>180<br>240<br>300<br>360<br>420<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1140<br>1200<br>1260                        |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Nucleic Ac: Coding sequitorial coding sequitorial coding sequitorial coding sequitorial coding sequitorial coding sequitorial coding co | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GGCTCGGCG CAACGCGTC CGCTTCTCC GGGCGGCGC CTCTTCTCC GGGCGCGCAC CTGATCGAG CACCTACCTG CATCGCCTC CATCGCCCTC CATCGCCCCCCC CTATCGAGC CCTATCGAGC CCTGCCCTC CCTGCCCTC GCTCCCCTG CCTGCCTAC CGTCCCCCTG CCTCCCCCTC CCTCCCCTCC  | GGTGGGCAGA GGGGGGGGGGGGGGGGGGGGGGGGGGGGG  | GCATGGCGGG AAGAGGCCGG AAGAGGCCAGG TGGGGACCAT TGCTGGCGGG TCTGCTA TCCTGCAC TGCTGCTCAC TGCTGCTCAC TGCTGCTCAC TGCGGCACAT TGAATTTCGT TCTCCCGCC TGTCCACGC TGTCCACGC TGTCCACGC TGTCCACGC TGTCCACGC TGTCCACGA TGGGGAACAT TCAATTTCGT TCTCCTGCC TGTCCACGA TGGGCGTCAT ATGGGTCAT TGAGTTCTT ACAGAAAGCC   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1140<br>1200<br>1200<br>1320                        |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Nucleic Ac: Coding sequitorial coding sequitorial coding sequitorial coding sequitorial coding sequitorial coding sequitorial coding co | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GGCTCGGCG CAACGCGTC CGCTTCTCC GGGCGGCGC CTCTTCTCC GGGCGCGCAC CTGATCGAG CACCTACCTG CATCGCCTC CATCGCCCTC CATCGCCCCCCC CTATCGAGC CCTATCGAGC CCTGCCCTC CCTGCCCTC GCTCCCCTG CCTGCCTAC CGTCCCCCTG CCTCCCCCTC CCTCCCCTCC  | GGTGGGCAGA GGGGGGGGGGGGGGGGGGGGGGGGGGGGG  | GCATGGCGGG AAGAGGCGAGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCTA TGCTGACGT TCCCCAC TTGCTCAC TTGCTCAC TTGCTCAC TTGCTGCAC TTGCTCAC TTGCTCAC TTGCACCT CCTCCATCCT CCTCCATCCT TCACTTCTT   | 120<br>180<br>240<br>300<br>360<br>420<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1140<br>1200<br>1260                        |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Nucleic According sequence of the control of the co | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GCGCGCGCCC CGGCTCGCCC CGCTTCTCCC GGGCGCGCAC CTGCATCACT CGTCGCTCC CGCTGGCTTC CGCCCTGCCCCTC CCTGCCCTAC CGTCCCCCTC CCTCCCCCCCCCC  | GCCTCGTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | GCATGGCGGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TCGTGCTA TGCTGGCGGG TGTGCCAC TGCTGCCAC TGCTGCCAC TGCTGCCAC TGCTGCCAC TGCACGAACGGTA TGAATTCOT TCTCCCCGC TGTCACCGA TGGGGAACAT TGAATTCOT TCTCCCTGC CTCACCGA TGGGCGTCAT ATGGTCCCT CCTCCATCCT CCTCATCCT CCTCAGAAAGCC | 120<br>180<br>240<br>300<br>360<br>480<br>540<br>660<br>720<br>780<br>840<br>1020<br>1080<br>1140<br>1200<br>1200<br>1320                       |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Nucleic According sequences of the control of the c | id Accession uence: 53  11  | #: XM_035: 1576  21  | AGGCCCGGCC GCCGGCCGGCC GCGCTCGCGCGCGCGCCGCCGCCGCCGCCCGC   | GCATCATCA AACTATCA CGCATCATCA AACTATCAC CGCATCATCA CGCATCATCA AACTATCAC CCCATCATCA CCCATCATCA CCCATCATCA CCCATCATCA CCCATCATCA CCCATCATCA CCCATCATCA CCCATCATCA CCCCTCATCATCA CCCCTCATCATCA CCCCTCATCATCA CCCCTCATCATCATCA CCCCTCATCATCATCATCATCATCATCATCATCATCATCCACCCC CCCTCTTTCTT  | GCATGGCGGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCTTA TGCTGGCGGT TCCGGCCTTC TGTTCCCAC TGCTGCTAC TGCTGCCAC TGCTGCTAC TGCAGGTT TGCGGCCCAC TGCAGCTCAC TGCACCTCAC TGCACCTCAC TGCACCTCAC TGCTCACCT ATGGGTCAC ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT TCACCTTCCTCCT CCTTCTTT ACAGAAAGCC TCCTGGCCTG  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1020<br>1080<br>1140<br>1200<br>1260<br>1380<br>1380        |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | Nucleic According sequence of the control of the co | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GGCTCGGCG CGCTCGGCG CAACGCCTG GGGCGGCAC CGTCTTCTCC GGGCGGCAC CTGGATCAGAG CACCTACCTG CATCGAGCAC CTGGCCTTC CTGAACGCATC CTTGCCCCTG CCTGCCCTG CTGCCCTG CTGCCTAC GGACTTCGGG GTCCTGCTCT CTCCGCCTC CTTCCCGTC CTTCCGGCAAC CGACTCGGCAC CGCCTGCCTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT                               | GGTGGCAGA GAGGAGAAGG CCGGCAGGCG GCCATCATCG ATCGTGGGCG ATCGTGGTGC CTCCAGGCGCAGCC CTCTGGTGC CAGGATGCCT AAACTGAATCG AAACTGAATCACC AAACTGAATCACC GGCTCGTCA GGCACCGTC GGCTCGTCT CGGTTCCT CGGTTCTC TTCGCTTCCT TTCACCACC CTCTTTTCT TTCACCACC CTCTTTTCT CGGCTCGTCT CGGTTCTCT TTCACCACC TTCGTTTTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTCTCT TTCGTTTCTCT TTCGTTCTCT TTCGTTCT TTCGTTCTCT TTCGTTCTCT TTCGTTCT TTCT TTCGTTCT TTCT TTCGTTCT TTCT TTCGTTCT TTCT TTCGTTCT TTCT | GCATGGCGGG AAGAGGCCAA AAGAGGCCAGG AGGGCAGGG TGGGGACCAT TGCTGGCAGT TCCTGCCAC TGCTGCTCAC TGCTGCTCAC TGCTGCCCCC GAAAGGGTGA TGCGGAACAT TGAATTTCGT TCTCCCGCC TGTCCACCAC TGCGCTCAC TGCACCGA TGGGGAACAT TCAATTCGT TCTCCCTGCC TGTCCACCCA TGGGCTTCAT ATGGGTCAT ATGGGTCAT CCTCCATCCT CCTCCATCCT CCTCCATCCT TCACGCTTCTT ACAGAAAGCC TCCTGGCCT TCACGCTTCAC ACAGGCCAA   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>960<br>1020<br>1140<br>1200<br>1326<br>1326<br>1440<br>1500        |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | Nucleic According sequence of the control of the co | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC GGCTCGGCG CGCTCGGCG CAACGCCTG GGGCGGCAC CGTCTTCTCC GGGCGGCAC CTGGATCAGAG CACCTACCTG CATCGAGCAC CTGGCCTTC CTGAACGCATC CTTGCCCCTG CCTGCCCTG CTGCCCTG CTGCCTAC GGACTTCGGG GTCCTGCTCT CTCCGCCTC CTTCCCGTC CTTCCGGCAAC CGACTCGGCAC CGCCTGCCTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT                               | GGTGGCAGA GAGGAGAAGG CCGGCAGGCG GCCATCATCG ATCGTGGGCG ATCGTGGTGC CTCCAGGCGCAGCC CTCTGGTGC CAGGATGCCT AAACTGAATCG AAACTGAATCACC AAACTGAATCACC GGCTCGTCA GGCACCGTC GGCTCGTCT CGGTTCCT CGGTTCTC TTCGCTTCCT TTCACCACC CTCTTTTCT TTCACCACC CTCTTTTCT CGGCTCGTCT CGGTTCTCT TTCACCACC TTCGTTTTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTTCTCT TTCGTTCTCT TTCGTTTCTCT TTCGTTCTCT TTCGTTCT TTCGTTCTCT TTCGTTCTCT TTCGTTCT TTCT TTCGTTCT TTCT TTCGTTCT TTCT TTCGTTCT TTCT TTCGTTCT TTCT | GCATGGCGGG AGGGCGAGGG TGGGGACCAT GCTCGCCGGG TGCTGCTTA TGCTGGCGGT TCCGGCCTTC TGTTCCCAC TGCTGCTAC TGCTGCCAC TGCTGCTAC TGCAGGTT TGCGGCCCAC TGCAGCTCAC TGCACCTCAC TGCACCTCAC TGCACCTCAC TGCTCACCT ATGGGTCAC ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT ATGGGTCAT TCACCTTCCTCCT CCTTCTTT ACAGAAAGCC TCCTGGCCTG  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1020<br>1080<br>1140<br>11260<br>1380<br>1380               |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | Nucleic Activities Act | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC CGGCTCGGCG CAACGCGTC CGGCTTCTCC CGGCGCGCGCA CTCGATCGAG CACCCGGGTC CACCCGGGTC CACCCGGGTC CTGACCAG CTGCCCTG CCTGCCCTG CCTGCCCTG CCTCGCCTAC CGTCCCCTGC CTTCTCCGGA CGTCCCTTCCCGTC CTTCTCCGTC CGCCTTCCCGCTC CGCCTTCCCGCTC CGCCTTCCCGTC CCTCCCCTGCCCTC CCTCCCCTGCCCTCCCCTCCCCTCCCCCTCCCCCTCCCCCTCCCCCTCCCC | GGTGGGCAGA GAGGAGGAGGCAG ATCGGCAGGCG CCATCATCG TACGCCTACA CTGCATCATCA CTCAAGCCC CTCTGGGTGC CAGGATGCCT AAACTGGATG TTCACCACCC AACTATCACC GGCCACCTGC CTCGGTTCC TCCAAGCCC TTCACACCC TCCAAGTGCCT TCACACCC TCCAACTTCACC TCCAACTTCACC TCCAACTTCACC TCCGTGTTCC TTGGTTCCC TTGGTTGGCC TTGGTTGG  | GCATGGCGGG AAGAGGCCAA AAGAGGCCAGG AGGGCAGGG TGGGGACCAT TGCTGGCAGT TCCTGCCAC TGCTGCTCAC TGCTGCTCAC TGCTGCCCCC GAAAGGGTGA TGCGGAACAT TGAATTTCGT TCTCCCGCC TGTCCACCAC TGCGCTCAC TGCACCGA TGGGGAACAT TCAATTCGT TCTCCCTGCC TGTCCACCCA TGGGCTTCAT ATGGGTCAT ATGGGTCAT CCTCCATCCT CCTCCATCCT CCTCCATCCT TCACGCTTCTT ACAGAAAGCC TCCTGGCCT TCACGCTTCAC ACAGGCCAA   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>900<br>900<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500        |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | Nucleic Activities Act | id Accession uence: 53  11  | #: XM_035: 1576  21  | 31  AGGCCCGGCC CGGCTCGGCG CAACGCGTC CGGCTTCTCC CGGCGCGCGCA CTCGATCGAG CACCCGGGTC CACCCGGGTC CACCCGGGTC CTGACCAG CTGCCCTG CCTGCCCTG CCTGCCCTG CCTCGCCTAC CGTCCCCTGC CTTCTCCGGA CGTCCCTTCCCGTC CTTCTCCGTC CGCCTTCCCGCTC CGCCTTCCCGCTC CGCCTTCCCGTC CCTCCCCTGCCCTC CCTCCCCTGCCCTCCCCTCCCCTCCCCCTCCCCCTCCCCCTCCCCCTCCCC | GGTGGGCAGA GAGGAGGAGGCAG ATCGGCAGGCG CCATCATCG TACGCCTACA CTGCATCATCA CTCAAGCCC CTCTGGGTGC CAGGATGCCT AAACTGGATG TTCACCACCC AACTATCACC GGCCACCTGC CTCGGTTCC TCCAAGCCC TTCACACCC TCCAAGTGCCT TCACACCC TCCAACTTCACC TCCAACTTCACC TCCAACTTCACC TCCGTGTTCC TTGGTTCCC TTGGTTGGCC TTGGTTGG  | GCATGGCGGG AAGAGGCCAA AAGAGGCCAGG AGGGCAGGG TGGGGACCAT TGCTGGCAGT TCCTGCCAC TGCTGCTCAC TGCTGCTCAC TGCTGCCCCC GAAAGGGTGA TGCGGAACAT TGAATTTCGT TCTCCCGCC TGTCCACCAC TGCGCTCAC TGCACCGA TGGGGAACAT TCAACTTCGT TCTCCTGCC TGTCCACCCA TGGGGTCAT ATGGGTCAT ATGGGTCAT CCTCCATCCT CCTTGTTGTGAT TCAAGATTTCTT TAAGATTTCTT TCAGCTTCTT ACAGAAAGCC TCCTGGCCTCAC ACAAGCCCAA   | 120<br>180<br>240<br>300<br>360<br>480<br>540<br>660<br>720<br>780<br>940<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560 |

Seq ID NO: C87 DNA Sequence Nucleic Acid Accession #: NM\_005268.1

Coding sequence: 168..989 5 TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCGAAAAC CTTCCCCGCT TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 120 180 TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240 TGTCTCTGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 10 GTGATGACCA CAAGGACTIC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360 TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420 CATGCCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTCAG GAGAAGAGGC 480 ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540 GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT 600 15 TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC 660 ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720 TTTTCACCCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA 840 TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCCTG CAAACAAGAC GACCTCCTTT 900 20 CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCCTCC TCTCTTACCA GACCGCCCCC 960 GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG 1020 CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1080 1140 TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200 25 GCTCGGTTTC CTTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC 1243 Seq ID NO: C88 DNA Sequence Nucleic Acid Accession #: NM\_005130 Coding sequence: 98..802 30 CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCACTGGATC CGTGTGCTCA GAACAAGGTG AACGCCCAGC TGCAGCCATG AAGATCTGTA GCCTCACCCT 120 35 GCTCTCCTTC CTCCTACTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA GAATGGACTT CACAGCAAAG TGGTCTCAGA ACAAAAGGAC ACTCTGGGCA ACACCCAGAT TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAAGACC AAGCCAACTG 240 300 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360 GGACCATGAA TITTCCTGTG TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 40 TGAGAGAGTC TATTGGAAAC AAGTTGCCYYS GAATCTGCGC TCACAGAAAG ACATCTYSTAG 480 ATATTCCAAG ACAGCTGTGA AAACCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540 TAAGCTAGTC AGCTCCACTC TATTTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600 GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCC TCTAGCCTAG CAGTGACCCA GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT 720 45 780 AGTGCAGGAC ACGTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840 TGTCGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACTTT 900 TGTGCTTAGT GAGTGCAACG AAATATTTAA ACAAGTTTTG TATTTTTTGC TTTTGTGTTT 960 TGGAATTTGC CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCCTG CAGCATGTAT 1020 50 TTCCATGGCC CACACAGCTA TGTGTTTGAG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080 GAGTGATAAT TTCAGTGCAA CGAACTTTCT GCTGAATTAA TGGTAATAAA ACTCTGGGTG 1140 TTTTTCAAAA AAAAAAAAAA AAA 1163 Seq ID NO: C89 DNA Sequence 55 Nucleic Acid Accession #: BC022542 Coding sequence: 274..927 21 31 60 ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC CCTTCCTGCG TCCGCACCTG GCCCCGCGCG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC TGGCGGCTCG GGTGGCGGCG GTTCGGGCGG CCGCCTGGCT GCTCCTCGGG GCGCGACGG 180 GGCTCACGCG CGGGCCCGCC ACGGCCTTCA CCGCCGCGCG CTCTGACGCC GGCATAAGGG 240 CCATGTGTTC TGAAATTATT TTGAGGCAAG AAGTTTTGAA AGATGGTTTC CACAGAGACC 65 TTTTAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA TTAAACAGGA CATTCCTGCA GGACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAATTT TGATATAGAG GCCCCTAACT 360 420 480 ATTIGICCAA GGAGICIGAA GIICICATII AIGCCAGACG AGAIICACAG IGCAIIGACI GTTTTCAAGC CTTTTTGCCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTTGATGTT TTGTGACCAA GAGTTCCCGA 600 70 660 TTTTGAAATG CTGGGCTCAC TCAGAAGTGG CAGCCCCTTG TGCTTTGGAT AATGAGGATA 720 TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC
TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAATATGG CCATTTTTCC CTATAAGTTT 840 900 75 TATGTAGTTA AATGCTTCCT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960 TTCTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC TAGAGGAAAT TIGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTCTGC TAAATTAATG 1080 1140 TTTATTTGT GAGAAGTGAC TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200 80 GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCAATT TAAGCTACAA ATTGAGAAAA 1260 CCGTTATAAA TAAGAATAAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCCAGCAC 1320 TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380 ACCCTGTCTC TACTAAAAAT ACAAAAGTTA GCTGGGGGCTG GTGGTGGGCA TCTGTAGTCC CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500

| 5   | GGAAAAACAA<br>ATGTCATGAG<br>CTAAGAAATT<br>ACGCACTCCA<br>GGACTTGATG | AAAAGAAGAA<br>ACTATTAAAG<br>AATATTAATA<br>TTCTCCTTTT<br>AAACTGAGTA | TAAAATAATT<br>ATGTGCCAGA<br>TAAAAATTAT<br>ACATTTTATC<br>CTAAGATTTG | TGGGCGACAG<br>TGGATGAAAA<br>GTTTCAATGA<br>TGATAATCTT<br>ATGTTTCTTT<br>GTACAGAGTA<br>AAAAAAAAAA | TCATGTTTAT AAATCATTAA AAATTATTGA TGAATATATG TGTCAGGAAG | TTAAATAGTA<br>AGTAGGACAG<br>TTATTCCTTA<br>AATTGGCAAA | 1560<br>1620<br>1680<br>1740<br>1800<br>1860<br>1906 |
|-----|--|--|--|--|--|--|--|
| 10  | Nucleic Aci  | C90 DNA Sec<br>d Accession<br>mence: 202                           | #: NM_0049   | 994  |  |  |  |
|     | 1  | 11   | 21   | 31   | 41   | 51   |  |
| 15  | AGACACCTCT   | CCCTCACCA  | ן  | GCAGCCCCTG   | GTCCTCGTGC   | TOTTECTOOT   | 60   |
| 10  |  |  |  | CCAGTCCACC   |  |  | 120  |
|     |  |  |  | GGCAGAGGAA   |  |  | 180  |
|     |  |  |  | GAAATCTCTG<br>TGAGCTGGAT   |  |  | 240<br>300   |
| 20  |  |  |  | GGGCAGATTC   |  |  | 360  |
|     | CAAGTGGCAC   | CACCACAACA   | TCACCTATTG   | GATCCAAAAC   | TACTCGGAAG   | ACTTGCCGCG   | 420  |
|     |  |  |  | CTTCGCACTG   |  |  | 480  |
|     |  |  |  | AGACATCGTC<br>GGACGGGCTC   |  |  | 540<br>600   |
| 25  |  |  |  | CGACGATGAC   |  |  | 660  |
|     |  |  |  | CGCAGATGGC   |  |  | 720  |
|     |  |  |  | CACCACCGAC<br>CGACGACCGG   |  |  | 780<br>840   |
| 20  | GAGACTCTAC   | ACCCGGGACG   | <b>GCAATGCTGA</b>  | TGGGAAACCC   | TGCCAGTTTC   | CATTCATCTT   | 900  |
| 30  |  |  |  | GGACGGTCGC   |  |  | 960  |
|     |  |  |  | GCTCTTCGGC<br>GGAGCTGTGC   |  |  | 1020<br>1080   |
|     |  |  |  | GGGCCGCGGA   |  |  | 1140   |
| 35  |  |  |  | GTGGGGCTTC   |  |  | 1200   |
| 22  |  |  |  | CCACGCGCTG   |  |  | 1260<br>1320   |
|     |  |  |  | TCCTCGCCCT   |  |  | 1380   |
|     |  |  |  | CCCGACGGTC   |  |  | 1440   |
| 40  |  |  |  | CCCCACAGGT   |  |  | 1500<br>1560   |
| 10  |  |  |  | CGCGGAGATT   |  |  | 1620   |
|     |  |  |  | GGGCAGGGGG   |  |  | 1680   |
|     |  |  |  | CCGCAAGCTG   |  |  | 1740<br>1800   |
| 45  |  |  |  | GGGCCTGGGA   |  |  | 1860   |
|     |  |  |  |  |  | GCCTCTGGAG   | 1920   |
|     |  |  |  | CCGGAGCGCC   |  |  | 1980<br>2040   |
|     |  |  |  | CCGGAGTGAG   |  |  | 2100   |
| 50  | GGGCTACGTG   | ACCTATGACA   | TCCTGCAGTG   | CCCTGAGGAC   | TAGGGCTCCC   | GTCCTGCTTT   | 2160   |
|     |  |  |  |  |  | TTGCCGGATA   | 2220<br>2280   |
|     |  |  |  | ATAAACTTGG   |  |  | 2334   |
| 55  | Sec ID NO.   | C91 Sequen   | C0   |  |  |  |  |
|     |  | id Accessio  |  | 213  |  |  |  |
|     | Coding seq   | puence: 188.   | 5656   |  |  | •  |  |
|     | 1  | 11   | 21   | 31   | 41   | 51   |  |
| 60  | Ī  | ì  | 1  | 1  | 1  | 1  |  |
|     |  |  |  |  |  | CAGTCCCTGC<br>GAGCGAGTCC                             | 60   |
|     |  |  |  |  |  | GAGCGAGICC   | 120<br>180   |
| CE  | GAAGAGGATG   | GCAGGGCCAC   | GCCCCAGCCC   | ATGGGCCAGG   | CTGCTCCTGG   | CAGCCTTGAT   | 240  |
| 65  |  |  |  |  |  | TGAAGAGCTG<br>TGTTCAGGGA                             | 300<br>360   |
|     |  |  |  |  |  | AGAGCATCGT   | 420  |
|     | GGTCATGGAG   | AGCAGCTTCC   | AAATCACAGA   | GGAGACCCAG   | ATTGACACCA   | CCCTGCGGCG   | 480  |
| 70  |  |  |  |  |  | AGCGGCATTT   | 540  |
| , 0 |  |  |  |  |  | TCATGGACTT ACCTGGCTCG                                | 600<br>660   |
|     | GGTCCTGAGG   | CAGCTCACC  | GCGACTACAC   | TATTGGATTT   | GGCAAGTTTC   | TGGACAAAGT   | 720  |
|     |  |  |  |  |  | CCAACAGTGA   | 780  |
| 75  |  |  |  |  |  | G GCTTCGGAA  | 840<br>900   |
|     | CATCCTGCAC   | ACAGCTGTGT   | GCACGAGGG  | CATTGGCTGG   | CGCCCGGAC  | GCACCCACCT   | 960  |
|     |  |  |  |  |  | ACGTGCTGGC   | 1020   |
|     |  |  |  |  |  | CCTACACCCA CCAAGCACAA                                | 1080<br>1140   |
| 80  | CATCATCCC  | ATCTTTGCT  | TCACCAACT  | CTCCTATAG  | TACTACGAGA   | AGCTTCACAC   | 1200   |
|     | CTATTTCCC  | r GTCTCCTCA  | TGGGGGTGCT   | GCAGGAGGA  | TOGTOCAACA   | TCGTGGAGCT   | 1260   |
|     |  |  |  |  |  | TAGACAGCCC<br>CTGGGTCCTT                             | 1320<br>1380   |
|     |  |  |  |  |  | TTGAGCACGT   | 1440   |
|     |  |  |  |  |  |  |  |

|         | GGATGGGACG | CACGTGTGCC        | AGCTGCCGGA               | GGACCAGAAG       | GGCAACATCC  | ATCTGAAACC   | 1500         |
|---------|------------|-------------------|--------------------------|------------------|-------------|--------------|--------------|
|         | TTCCTTCTCC | GACGGCCTCA        | AGATGGACGC               | GGGCATCATC       | TGTGATGTGT  | GCACCTGCGA   | 1560         |
|         |            |                   | CAGCTCGCTG               |                  |             |              | 1620         |
| 5       |            |                   | GGAGTGGCCA               |                  |             |              | 1680         |
| 5       |            |                   | GGGAGGGCGA               |                  |             |              | 1740         |
|         |            |                   | GCTACGGCGA<br>GCACTTCCGG |                  |             |              | 1800         |
|         |            |                   | AGCCTGGTTG               |                  |             |              | 1860<br>1920 |
|         |            |                   | GCAATGGGGG               |                  |             |              | 1980         |
| 10      |            |                   | AGCAGTCGCT               |                  |             |              | 2040         |
|         |            |                   | TCTGCGAGGA               |                  |             |              | 2100         |
|         |            |                   | GGCGCACGTG               |                  |             |              | 2160         |
|         |            |                   | AGGAGGTGGT               |                  |             |              | 2220         |
| 15      |            |                   | CCATGGAAGG               |                  |             |              | 2280         |
| 13      |            |                   | ACTGCCCTCC               |                  |             |              | 2340         |
|         |            |                   | TGGCCCTGCT               |                  |             |              | 2400<br>2460 |
|         |            |                   | GGGAGAACCT               |                  |             |              | 2520         |
|         |            |                   | AGGCCGTGA                |                  |             |              | 2580         |
| 20      |            |                   | CTCATGCCGC               |                  |             |              | 2640         |
|         |            |                   | CCCGCCTTTG               |                  |             |              | 2700         |
|         |            |                   | AGGAGGTGGA               |                  |             |              | 2760         |
|         |            |                   | AGCAGACCAA               |                  |             |              | 2820         |
| 25      |            |                   | ACACAGTGCT               |                  |             | AGCCGGCCCT · | 2880<br>2940 |
| 25      |            |                   | CAGACCAGGA               |                  |             |              | 3000         |
|         |            |                   | GGGTGCCCCT               |                  |             |              | 3060         |
|         |            |                   | TCGACGTGCC               |                  |             |              | 3120         |
| 20      |            |                   | AGGAGCAAGC               |                  |             |              | 3180         |
| 30      |            |                   | ACCAGGTGGC               |                  |             |              | 3240         |
|         |            |                   | CCTACCGCAC               |                  |             |              | 3300         |
|         |            |                   | AGCTGCTGTT<br>AAGAAGTTGA |                  |             |              | 3360<br>3420 |
|         |            |                   | ACCCTAAGTT               |                  |             |              | 3480         |
| 35      |            |                   | CAGATGAACT               |                  |             |              | 3540         |
|         |            |                   | GCGACCTGGG               |                  |             |              | 3600         |
|         |            |                   | TCAACTGGCT               |                  |             |              | 3660         |
|         |            |                   | GCGACTCCGA               |                  |             |              | 3720         |
| 40      |            |                   | ACCTGTACCC               |                  |             |              | 3780         |
| 70      |            |                   | GTCTGGCCTT               |                  |             |              | 3840<br>3900 |
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| 45      |            |                   | GCTGGGGGCC               |                  |             |              | 4140         |
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|         |            |                   | TGCGGCGCGT               |                  |             |              | 4380         |
| 50      |            |                   | GGCGCTCCTC               |                  |             |              | 4440         |
|         |            |                   | GGGCGGCAGC               |                  |             |              | 4500         |
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|         |            |                   |                          |                  |             | TGTTCTCTGC   | 4800         |
|         |            |                   |                          |                  |             | GGCCGCTGCA   | 4860         |
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| 60      |            |                   | TGGTGGTGGA               |                  |             |              | 4980         |
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|         |            |                   | GCCCGCTGGT               |                  |             |              | 5100<br>5160 |
|         |            |                   | GGAGGCCCAA               |                  |             |              | 5220         |
| <i></i> |            |                   | GGCCAGCCAC               |                  |             |              | 5280         |
| 65      |            |                   | GCCTCAGCGA               |                  |             |              | 5340         |
|         |            |                   | GGCCAGAGCG               |                  |             |              | 5400         |
|         |            |                   | TGGGCAGCCG               |                  |             |              | 5460         |
|         |            |                   | CCACCCACAC               |                  |             |              | 5520         |
| 70      |            |                   |                          |                  |             | TGGACCAACA   | 5580<br>5640 |
|         |            |                   |                          |                  |             | GGCGTCCTCC   | 5700         |
|         |            |                   |                          |                  |             | GGCCCAGCCC   | 5760         |
|         | ACCCGCATGC | ACAGAGCAGG        | GGCTAGGTGT               | CTCCTGGGAG       | GCATGAAGGG  | GGCAAGGTCC   | 5820         |
| 75      |            |                   |                          |                  |             | AAGGACCCAG   | 5880         |
| 13      |            |                   |                          |                  |             | AAAAAAAA     | 5940         |
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|    |             |             | CTTGCCGGTG |            |            |                          | 420          |
|    |             |             | GTGGATCTTC |            |            |                          | 480          |
|    |             |             | GGTTGCAGAC |            |            |                          | 540          |
| 10 |             |             | TGGACCTTGG |            |            |                          | 600          |
| 10 |             |             | CATGTATACT |            |            |                          | 660          |
|    |             |             | TGTTTGGGTG |            |            |                          | 720          |
|    |             |             | AACAGAGGAC |            |            |                          | 780          |
|    |             |             | TACGGCAGTC |            |            |                          | 840<br>900   |
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|    |             |             | AAGCCGAAAG |            |            |                          | 1020         |
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|    |             |             | AGATGAATCT |            |            |                          | 1140         |
|    |             |             | GTGTAATGTT |            |            |                          | 1200         |
| 20 | TGTAGGTCAT  | TTTCAAGAAG  | GCTGTTCAAA | AAATCAAATA | TCAGAACCAG | GAGTGAAAGC               | 1260         |
|    |             |             | GAGAAGATCG |            |            |                          | 1320         |
|    | GTGTAGGCCT  | TTTATTGTTT  | GTTGGAATCG | ATATGTACAA | AGTGTAAATA | AATGTTTCTT               | 1380         |
|    | TTCATTATCC  | AAAAAAATT   | AA         |            |            |                          | 1402         |
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| 25 |             | C93 DNA Sec |            |            |            |                          |              |
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| 35 |             |             | CTGGGCTATG |            |            |                          | 240          |
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| 55 |             |             |            |            |            | GGACCCTCCT               | 1500         |
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|    |             |             |            |            |            | ATCTTTCCTT               | 3060         |
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|    |             |             |            |            |            | J                        | ~270         |

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        AATACAGTTT CTATAACAGA ATATGAGGAG GAGAGTTTAT TGACCAGTTT CAAGCTTGAT
                                                                                      1740
        ACTGGAGCTG AAGATTCTTC AGGCTCCAGT CCCGCAACTT CTGCTATCCC ATTCATCTCT
                                                                                      1800
        GAGAACATAT CCCAAGGGTA TATATTTTCC TCCGAAAACC CAGAGACAAT AACATATGAT GTCCTTATAC CAGAATCTGC TAGAAATGCT TCCGAAGATT CAACTTCATC AGGTTCAGAA
                                                                                      1860
                                                                                      1920
        GAATCACTAA AGGATCCTTC TATGGAGGGA AATGTGTGGT TTCCTAGCTC TACAGACATA
                                                                                      1980
65
        ACAGCACAGC CCGATGTTGG ATCAGGCAGA GAGAGCTTTC TCCAGACTAA TTACACTGAG
                                                                                      2040
        ATACCTGTTG ATGAATCTGA GAAGACAACC AAGTCCTTTT CTGCAGGCCC AGTGATGTCA CAGGGTCCCT CAGTTACAGA TCTGGAAATG CCACATTATT CTACCTTTGC CTACTTCCCA
                                                                                      2100
                                                                                      2160
        ACTGAGGTAA CACCTCATGC TTTTACCCCA TCCTCCAGAC AACAGGATTT GGTCTCCACG
                                                                                      2220
        GTCAACGTGG TATACTCGCA GACAACCCAA CCGGTATACA ATGAGGCCAG TAATAGTAGC
CATGAGTCTC GTATTGGTCT AGCTGAGGGG TTGGAATCCG AGAAGAAGGC AGTTATACCC
                                                                                      2280
70
                                                                                      2340
        CTTGTGATCG TGTCAGCCCT GACTTTTATC TGTCTAGTGG TTCTTGTGGG TATTCTCATC
                                                                                      2400
        TACTGGAGGA AATGCTTCCA GACTGCACAC TTTTACTTAG AGGACAGTAC ATCCCCTAGA
                                                                                      2460
        GTTATATCCA CACCTCCAAC ACCTATCTTT CCAATTTCAG ATGATGTCGG AGCAATTCCA
                                                                                      2520
        ATAAAGCACT TTCCAAAGCA TGTTGCAGAT TTACATGCAA GTAGTGGGTT TACTGAAGAA
TTTGAGGAAG TGCAGAGCTG TACTGTTGAC TTAGGTATTA CAGCAGACAG CTCCAACCAC
                                                                                      2580
75
                                                                                      2640
        CCAGACAACA AGCACAAGAA TOGATACATA AATATOGTTG CCTATGATCA TAGCAGGGTT
                                                                                       2700
        AAGCTAGCAC AGCTTGCTGA AAAGGATGGC AAACTGACTG ATTATATCAA TGCCAATTAT
GTTGATGGCT ACAACAGACC AAAAGCTTAT ATTGCTGCCC AAGGCCCACT GAAATCCACA
                                                                                      2760
                                                                                      2820
        GCTGAAGATT TCTGGAGAAT GATATGGGAA CATAATGTGG AAGTTATTGT CATGATAACA
                                                                                      2880
80
        AACCTOGTGG AGAAAGGAAG GAGAAAATGT GATCAGTACT GGCCTGCCGA TGGGAGTGAG
        GAGTACGGGA ACTITCTGGT CACTCAGAAG AGTGTGCAAG TGCTTGCCTA TTATACTGTG
                                                                                      3000
        AGGAATTTTA CTCTAAGAAA CACAAAAATA AAAAAGGGCT CCCAGAAAGG AAGACCCAGT
                                                                                      3060
        GGACGTGTGG TCACACAGTA TCACTACACG CAGTGGCCTG ACATGGGAGT ACCAGAGTAC
        TCCCTGCCAG TGCTGACCTT TGTGAGAAAG GCAGCCTATG CCAAGCGCCA TGCAGTGGGG
                                                                                      3180
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|     |              | •            |            |              |             |                          |      |
|-----|--------------|--------------|------------|--------------|-------------|--------------------------|------|
|     | CCTGTTGTCG   | TCCACTGCAG   | TGCTGGAGTT | GGAAGAACAG   | GCACATATAT  | TGTGCTAGAC               | 3240 |
|     |              |              | ACACGAAGGA |              |             |                          | 3300 |
|     |              |              |            |              |             |                          |      |
|     |              |              | TTTGGTACAA |              |             |                          | 3360 |
| _   | ACACTGGTTG   | AGGCCATACT   | TAGTAAAGAA | ACTGAGGTGC   | TGGACAGTCA  | TATTCATGCC               | 3420 |
| 5   | TATGTTAATG   | CACTCCTCAT   | TCCTGGACCA | GCAGGCAAAA   | CAAAGCTAGA  | GAAACAATTC               | 3480 |
| •   |              |              |            |              |             |                          |      |
|     |              |              | TATACAGCAG |              |             |                          | 3540 |
|     | AACAGGGAAA   | AGAATCGAAC   | TTCTTCTATC | ATCCCTGTGG   | AAAGATCAAG  | GGTTGGCATT               | 3600 |
|     | TCATCCCTGA   | GTGGAGAAGG   | CACAGACTAC | ATCAATGCCT   | CCTATATCAT  | GGGCTATTAC               | 3660 |
|     |              |              |            |              |             |                          |      |
| 10  |              |              | TACCCAGCAC |              |             |                          | 3720 |
| 10  | AGGATGATAT   | GGGACCATAA   | TGCCCAACTG | GTGGTTATGA   | TTCCTGATGG  | CCAAAACATG               | 3780 |
|     | GCAGAAGATG   | ATTTGTTTA    | CTGGCCAAAT | AAAGATGAGC   | OTTAGAGTATO | TGAGAGCTTT               | 3840 |
|     |              |              |            |              |             |                          |      |
|     |              |              | AGAACACAAA |              |             |                          | 3900 |
|     | CAGGACTTTA   | TCTTAGAAGC   | TACACAGGAT | GATTATGTAC   | TTGAAGTGAG  | GCACTTTCAG               | 3960 |
|     | TGTCCTAAAT   | GGCCAAATCC   | AGATAGCCCC | ATTAGTAAAA   | CTTTTGAACT  | TATAAGTGTT               | 4020 |
| 15  |              |              |            |              |             |                          |      |
| IJ  |              |              | TAGGGATGGG |              |             |                          | 4080 |
|     | GTGACGGCAG   | GAACTTTCTG   | TGCTCTGACA | ACCCTTATGC   | ACCAACTAGA  | AAAAGAAAAT               | 4140 |
|     | TOTCGTGGATG  | TTTACCAGGT   | AGCCAAGATG | ATCAATCTGA   | TGAGGCCAGG  | AGTCTTTGCT               | 4200 |
|     |              |              | TCTCTACAAA |              |             |                          |      |
|     |              |              |            |              |             |                          | 4260 |
| • • | GAAGAGAATC   | CATCCACCTC   | TCTGGACAGT | AATGGTGCAG   | CATTGCCTGA  | TGGAAATATA               | 4320 |
| 20  | GCTGAGAGCT   | TAGAGTCTTT   | AGTTTAA    |              |             |                          | 4347 |
|     |              |              |            |              |             |                          |      |
|     |              |              |            |              |             |                          |      |
|     | Seq ID NO:   | C97 DNA Sec  | quence     |              |             |                          |      |
|     | Nucleic Ac:  | ld Accession | #: XM 0313 | 379          |             |                          |      |
|     |              | ence: 148.   |            |              |             |                          |      |
| 25  | couring sequ | Telles: T40. | . 1095     |              |             |                          |      |
| 23  |              |              |            |              |             |                          |      |
|     | 1            | 11           | 21         | 31           | 41          | 51                       |      |
|     | ï            | ī            | 1          | Ī            | ï           | 1                        |      |
|     | <u> </u>     | 1            | 1          | !            | 1           | 1                        |      |
|     |              |              | CTCACTTCGA |              |             |                          | 60   |
|     | CAAAAAAAAC   | ATTTCCTTCG   | CTCCCCCTCC | CTCTCCACTC   | TGAGAAGCAG  | AGGAGCCGCA               | 120  |
| 30  |              |              | TCTGGAAATG |              |             |                          | 180  |
| 50  |              |              |            |              |             |                          |      |
|     | CAGCTCCTCT   | GTGTTTGCCG   | CCTGGATTGG | GCTAATGGAT   | ACTACAGACA  | ACAGAGAAAA               | 240  |
|     | CTTGTTGAAG   | AGATTGGCTG   | GTCCTATACA | GGAGCACTGA   | ATCAAAAAA   | TTGGGGAAAG               | 300  |
|     |              |              | CCCAAAACAA |              |             |                          | 360  |
|     |              |              |            |              |             |                          |      |
| 25  |              |              | GAAACTTAAA |              |             |                          | 420  |
| 35  | AACACATTCA   | TTCATAACAC   | TGGGAAAACA | GTGGAAATTA   | ATCTCACTAA  | TGACTACCGT               | 480  |
|     |              |              | AATGGTGTTT |              |             |                          | 540  |
|     |              |              |            |              |             |                          |      |
|     | AAATGCAATA   | TGTCATCTGA   | TGGATCAGAG | CATAGTTTAG   | AAGGACAAAA  | ATTTCCACTT               | 600  |
|     | GAGATGCAAA   | TCTACTGCTT   | TGATGCGGAC | CGATTTTCAA   | GTTTTGAGGA  | AGCAGTCAAA               | 660  |
|     |              |              | TTTATCCATT |              |             |                          |      |
| 40  |              |              |            |              |             |                          | 720  |
| 40  | GATTTCAAAG   | CGATTATTGA   | TGGAGTCGAA | AGTGTTAGTC   | GTTTTGGGAA  | GCAGGCTGCT               | 780  |
|     | TTAGATCCAT   | TCATACTGTT   | GAACCTTCTG | CCAAACTCAA   | CTGACAAGTA  | TTACATTTAC               | 840  |
|     |              |              |            |              |             | TTTTAAAGAT               |      |
|     |              |              |            |              |             |                          | 900  |
|     | ACAGTTAGCA   | TCTCTGAAAG   | CCAGTTGGCT | GTTTTTTGTG   | AAGTTCTTAC  | AATGCAACAA               | 960  |
|     | TCTGGTTATG   | TCATCCTCAT   | GCACTACTTA | CAAAACAATT   | TTCGAGAGCA  | ACAGTACAAG               | 1020 |
| 45  |              |              |            |              |             |                          |      |
| 73  |              |              |            |              |             | AGCAGTTTGT               | 1080 |
|     | AGTTCAGAAC   | CAGAAAATGT   | TCAGGCTGAC | CCAGAGAATT   | ATACCAGCCT  | TCTTGTTACA               | 1140 |
|     | TOCCADAGAC   | CTCCACTCCT   | TTATCATACC | ATCATTCACA   | ACTUTYCCACT | TTTGTACCAG               | 1200 |
|     |              |              |            |              |             |                          |      |
|     |              |              |            |              |             | TCAAGACTTG               | 1260 |
|     | GGTGCTATTC   | TCAATAATTT   | GCTACCCAAT | ATGAGTTATG   | TTCTTCAGAT  | AGTAGCCATA               | 1320 |
| 50  | TGCACTAATG   | GCTTATATGG   | AAAATACAGC | GACCAACTGA   | TTGTCGACAT  | GCCTACTGAT               | 1380 |
|     |              |              |            |              |             |                          |      |
|     |              |              |            |              |             | CAAGGAGGAG               | 1440 |
|     | GAAGAGGGAA   | AAGACATTGA   | AGAAGGCGCT | ATTGTGAATC   | CTGGTAGAGA  | CAGTGCTACA               | 1500 |
|     | AACCAAATCA   | GGAAAAAGGA   | ACCCCAGATT | TCTACCACAA   | CACACTACAA  | TCGCATAGGG               | 1560 |
|     |              |              |            |              |             | ATTCTCTGGA               | 1620 |
| 55  |              |              |            |              |             |                          |      |
| 55  |              |              |            |              |             | TAAATTAGCC               | 1680 |
|     | ACAGAAAAAG   | ATATTTCCTT   | GACTTCTCAG | ACTGTGACTG   | AACTGCCACC  | TCACACTGTG               | 1740 |
|     |              |              |            |              |             | TCCACATATG               | 1800 |
|     |              |              |            |              |             |                          |      |
|     |              |              |            |              |             | TGAGGAGGAG               | 1860 |
|     | AGTTTATTGA   | CCAGTTTCAA   | GCTTGATACT | GGAGCTGAAG   | ATTCTTCAGG  | CTCCAGTCCC               | 1920 |
| 60  |              |              |            |              |             | ATTTTCCTCC               | 1980 |
|     |              |              |            |              |             |                          |      |
|     |              |              |            |              |             | AAATGCTTCC               | 2040 |
|     | GAAGATTCAA   | CTTCATCAGG   | TTCAGAAGAA | TCACTAAAGG   | ATCCTTCTAT  | GGAGGGAAAT               | 2100 |
|     |              |              |            |              |             | AGGCAGAGAG               | 2160 |
|     |              |              |            |              |             |                          |      |
| 65  |              |              |            |              |             | GACAACCAAG               |      |
| 65  | TCCTTTTCTG   | CAGGCCCAGT   | GATGTCACAG | GGTCCCTCAG   | TTACAGATCT  | GGAAATGCCA               | 2280 |
|     |              |              |            |              |             | TACCCCATCC               |      |
|     |              |              |            |              |             |                          |      |
|     |              |              |            |              |             | AACCCAACCG               |      |
|     | GTATACAATC   | GTGAGACACC   | TCTTCAACCI | ' TCCTACAGTA | GTGAAGTCTT  | TCCTCTAGTC               | 2460 |
|     |              |              |            |              |             | AAGTAGTGAT               |      |
| 70  |              |              |            |              |             |                          |      |
| 70  |              |              |            |              |             | ATCCATCCTG               |      |
|     | TCTTCCTATC   | ATGGTGCACC   | TTTGCTTCCA | TTTTCCTCTG   | CTTCCTTCAG  | TAGTGAATTG               |      |
|     |              |              |            |              |             | TACCGAGAGT               |      |
|     |              |              |            |              |             |                          | 2700 |
|     | GATAAGGTGC   | CCTTGCATGC   | TTCTCTGCCA | GTGGCTGGGG   | GTGATTTGCT  | ATTAGAGCCC               | 2760 |
|     |              |              |            |              |             | GACGCTGGAA               |      |
| 75  |              |              |            |              |             |                          |      |
| 13  |              |              |            |              |             | TGAACCACCC               |      |
|     | AGCAGTGATC   | CCATGATGC    | TGCACGTTC1 | TCAGGGCCTG   | AACCTTCTTA  | TGCCTTGTCT               | 2940 |
|     |              |              |            |              |             | ACCTGTGCAT               |      |
|     |              |              |            |              |             |                          |      |
|     |              |              |            |              |             | TATACCAATA               |      |
|     | CCTAAGTCTT   | CGTTAATAAC   | CCCAACTGC  | TCATTACTCC   | AGCCTACTCA  | TGCCCTCTCT               |      |
| 80  |              |              |            |              |             |                          |      |
| 00  |              |              |            |              |             | TGACACAGAT               |      |
|     | GGGCTGACAC   | CCCTTAACA1   | TTCTTCACCT | GTTTCTGTAG   | CTGAATTTAC  | ATATACAACA               | 3240 |
|     | TCTGTGTTT    | GTGATGATAL   | TARGECTE   | TCTALLACTO   | AAATAATAT   | TGGAAATGAG               | 3300 |
|     |              | . GIGUIGUIM  |            |              |             |                          |      |
|     |              |              | - mmma     |              |             |                          |      |
|     | ACTGAACTG    | AAATTCCTT    | TTTCAATGAC |              |             |                          |      |
|     | ACTGAACTG    | AAATTCCTT    |            |              |             | CACAGTCATG<br>CTCTGTTTCC |      |

|     |             |                          |             |            | ATACCACCAC               |                          | 3480         |
|-----|-------------|--------------------------|-------------|------------|--------------------------|--------------------------|--------------|
|     |             |                          |             |            | TTCAACCTAC               |                          | 3540         |
|     |             |                          |             |            | CTCAGCTCTT               | AGAGCCAGCA               | 3600<br>3660 |
| 5   |             |                          |             |            |                          | TTCTGATGTT               |              |
|     |             |                          |             |            | ATCCAATATT               |                          | 3780         |
|     |             |                          |             |            |                          | TTCTGCTTCA               |              |
|     |             |                          |             |            |                          | TACTTCTCAT               |              |
| 10  |             |                          |             |            | CAAGTGAGAA               | TATGAACCA<br>TAATGATGAG  | 3960<br>4020 |
|     |             |                          |             |            | CCCCAAAAGG               |                          | 4080         |
|     |             |                          |             |            | CACTAATAAA               |                          | 4140         |
|     |             |                          |             |            | CTGGTAAGGT               |                          | 4200         |
| 15  |             |                          |             |            | ATTCTGTTCC               |                          | 4260         |
| 13  |             |                          |             |            | GTGCCAAATC               | CTCAACAAAG               | 4320<br>4380 |
|     |             |                          |             |            |                          | TGATGATGAC               |              |
|     | AGAGGTAGTG  | ATGGCTTATC               | CATTCATAAG  | TGTATGTCAT | GCTCATCCTA               | TAGAGAATCA               | 4500         |
| 20  |             |                          |             |            |                          | TCAGAATAAT               | 4560         |
| 20  |             |                          |             |            | ATAGAGTCAC               |                          | 4620         |
|     |             |                          |             |            | CACCATCAGC               | TGCTCTGCTT               | 4680<br>4740 |
|     |             |                          |             |            | GTGATGAAGA               |                          | 4800         |
| 25  |             |                          |             |            | CCACAGATTT               |                          | 4860         |
| 25  |             |                          |             |            |                          | AATAACTCCT               |              |
|     |             |                          |             |            |                          | GTTCCACGTT<br>TGAGGGGTTG |              |
|     |             |                          |             |            |                          | TTTTATCTGT               |              |
| 20  |             |                          |             |            |                          | TGCACACTTT               |              |
| 30  |             |                          |             |            | CTCCAACACC               |                          | 5220         |
|     |             |                          |             |            | CAAAGCATGT               |                          | 5280         |
|     |             |                          |             |            |                          | CCAGGAAGTG<br>AGACAACAAG |              |
|     |             |                          |             |            | GCAGGGTTAA               |                          | 5460         |
| 35  | CTTGCTGAAA  | AGGATGGCAA               | ACTGACTGAT  | TATATCAATG | CCAATTATGT               | TGATGGCTAC               | 5520         |
|     |             |                          |             |            |                          | TGAAGATTTC               |              |
|     |             |                          |             |            |                          | CCTCGTGGAG<br>GTACGGGAAC |              |
|     |             |                          |             |            | ATACTGTGAG               |                          | 5700<br>5760 |
| 40  |             |                          |             |            |                          | ACGTGTGGTC               |              |
|     |             |                          |             |            |                          | CCTGCCAGTG               |              |
|     |             |                          |             |            |                          | TGTTGTCGTC               |              |
|     |             |                          |             |            |                          | TATGTTGCAG<br>CCGTTCACAA |              |
| 45  |             |                          |             |            |                          | ACTGGTTGAG               |              |
|     |             |                          |             |            |                          | TGTTAATGCA               | 6180         |
|     |             |                          |             |            |                          | GCTCCTGAGC               |              |
|     |             |                          |             |            |                          | CAGGGAAAAG<br>ATCCCTGAGT | 6300<br>6360 |
| 50  |             |                          |             |            |                          | GAGCAATGAA               |              |
|     | TTCATCATTA  | CCCAGCACCC               | TCTCCTTCAT  | ACCATCAAGG | ATTTCTGGAG               | GATGATATGG               | 6480         |
|     |             |                          |             |            |                          | AGAAGATGAA               |              |
|     |             |                          |             |            |                          | GGTCACTCTT<br>GGACTTTATC | 6600<br>6660 |
| 55  |             |                          |             |            |                          | TCCTAAATGG               |              |
|     |             |                          |             |            |                          | AAAAGAAGAA               |              |
|     |             |                          |             |            |                          | GACGGCAGGA               |              |
|     |             |                          |             |            |                          | CGTGGATGTT               | 6900<br>6960 |
| 60  |             |                          |             |            |                          | AGAGAATCCA               |              |
| •   | TCCACCTCTC  | TGGACAGTAA               | TGGTGCAGCA  | TTGCCTGATG | GAAATATAGC               | TGAGAGCTTA               | 7080         |
|     |             |                          |             |            | ATCTGAGCAT               |                          | 7140         |
|     |             |                          |             |            | CTGTTGATTT<br>ATATCATTAA |                          | 7200<br>7260 |
| 65  |             |                          |             |            | AAAATGATTG               |                          | 7320         |
|     |             |                          |             |            | ATTTTAACAG               |                          | 7380         |
|     |             |                          |             |            | TTTTTAGTGT               |                          | 7440         |
|     |             |                          |             |            | CTTTTAATAC               |                          | 7500         |
| 70  |             |                          |             |            | CTCCATGGAC               |                          | 7560<br>7620 |
|     |             |                          |             |            | TTTTCTAGTT               |                          | 7680         |
|     | GTTTAGTTTA  | ATGACGTAGT               | TCATTAGCTG  | GTCTTACTCT | ACCAGTTTTC               | TGACATTGTA               | 7740         |
|     |             |                          |             |            | TTTAACTTTT               |                          | 7800         |
| 75  |             |                          |             |            | ACCTTACCAA<br>ATTGCCATTA |                          | 7860<br>7920 |
| , , |             | AAAAAAAAA                |             | AMIAIAMI   | AIIOCCAIIA               | AUTO DO TOTAL            | 7944         |
|     |             |                          |             |            |                          |                          |              |
|     |             | C98 DNA Se               |             |            |                          |                          |              |
| 80  |             | id Accessio<br>uence: 77 | n #: NM_002 | 851        |                          |                          |              |
| 00  | couring seq | concer //                | 4210        |            |                          |                          |              |
|     | 1           | 11                       | 21          | 31         | 41                       | 51                       |              |
|     |             |                          |             |            | 1                        | 1                        | <b>C</b> 2   |
|     | CACACATACG  | CACGCACGAT               | CTCACTTCGA  | TCTATACACT | GGAGGATTAA               | AACAAACAAA               | 60           |

|     | CAAAAAAAC ATTTCCTTCG CTCCCCCTCC CTCTCCACTC TGAGAAGCAG AG   | CACCCCCA                 | 120          |
|-----|--|--------------------------|--------------|
|     | CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCCT CG  | CTTGCATT                 | 180          |
|     | CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA AC  | AGAGAAAA                 | 240          |
|     | CTTGTTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAAA TT  | GGGGAAAG                 | 300          |
| 5   | AAATATCCAA CATGTAATAG CCCAAAACAA TCTCCTATCA ATATTGATGA AG  | ATCTTACA                 | 360          |
|     | CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC AT  | CATTGGAA                 | 420          |
|     | AACACATTCA TICATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TG  | ACTACCGT                 | 480          |
|     | GTCAGCGGAG GAGTTTCAGA AATGGTGTTT AAAGCAAGCA AGATAACTTT TC  | ACTGGGGA                 | 540          |
| 10  | AAATGCAATA TGTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA AT  | CACTCAAA                 | 600<br>660   |
| 10  | GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AG<br>GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AG | STTTAGE                  | 720          |
|     | GAAAAGGGA AGTTAAGAGC TTTATCCATT TIGTTIGAGG TIGGGACAGA AG<br>GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GC  | 'AGGCTGCT                | 780          |
|     | TTAGATCCAT TCATACTGTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TT  | ACATTTAC                 | 840          |
|     | AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TT  | TTAAAGAT                 | 900          |
| 15  | ACACTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTTGTG AAGTTCTTAC AA  | <b>TGCAACAA</b>          | 960          |
|     | TCTGGTTATG TCATGCTGAT GGACTACTTA CAAAACAATT TTCGAGAGCA AC  | CAGTACAAG                | 1020         |
|     | TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAAGGAAG AGATTCATGA AG  | CAGTTTGT                 | 1080         |
|     | AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TC  | TTGTTACA                 | 1140         |
| 20  | TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TT  | TGTACCAG                 | 1200         |
| 20  | CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTTGA CAGATGGCTA TO  | CANGACTIG                | 1260<br>1320 |
|     | GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AC TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GC    | TAGCCAIA                 | 1380         |
|     | AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAACTG AAGAAATAAT C   | AAGGAGGAG                | 1440         |
|     | GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CA  | AGTGCTACA                | 1500         |
| 25  | AACCAAATCA GGAAAAAGGA ACCCCAGATT TCTACCACAA CACACTACAA TC  | CGCATAGGG                | 1560         |
|     | ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCCAACAA GAGGAAGTGA AT  | <b>PTCTCTGGA</b>         | 1620         |
|     | AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAGTCAC TA  | AAATTAGCC                | 1680         |
|     | ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TO  | CACACTGTG                | 1740         |
| 20  | GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAAACTG TTCTTAGATC TC  | CCACATATG                | 1800         |
| 30  | AACTTGTCGG GGACTGCAGA ATCCTTAAAT ACAGTTTCTA TAACAGAATA TO  | JAGGAGGAG                | 1860         |
|     | AGTTTATTGA CCAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG C   | TCCAGTCCC                | 1920<br>1980 |
|     | GCAACTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT AT GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AA    | AATGCTTCC                | 2040         |
|     | GAAAACCCAG AGACAATAAC ATATGATGIC CITATACCAG AATCTGCTAG AG<br>GAAGATTCAA CITCATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT G  | GAGGGAAAT                | 2100         |
| 35  | GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AC  | GGCAGAGAG                | 2160         |
| 55  | AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTTGATG AATCTGAGAA G   | ACAACCAAG                | 2220         |
|     | TCCTTTCTG CAGGCCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT G  | GAAATGCCA                | 2280         |
|     | CATTATTCTA CCTTTGCCTA CTTCCCAACT GAGGTAACAC CTCATGCTTT T   | ACCCCATCC                | 2340         |
| 40  | TCCAGACAC AGGATTTGGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC A  | ACCCAACCG                | 2400         |
| 40  | GTATACAATG CAGAGGCCAG TAATAGTAGC CATGAGTCTC GTATTGGTCT A   | GCTGAGGGG                | 2460         |
|     | TTGGAATCCG AGAAGAAGGC AGTTATACCC CTTGTGATCG TGTCAGCCCT G   | ACTTTTATC                | 2520         |
|     | TGTCTAGTGG TTCTTGTGGG TATTCTCATC TACTGGAGGA AATGCTTCCA G   | ACTGCACAC                | 2580<br>2640 |
|     | TTTTACTTAG AGGACAGTAC ATCCCCTAGA GTTATATCCA CACCTCCAAC A CCAATTTCAG ATGATGTCGG AGCAATTCCA ATAAAGCACT TTCCAAAGCA T      | CCIMICILI                | 2700         |
| 45  | TTACATGCAA GTAGTGGGTT TACTGAAGAA TTTGAGACAC TGAAAGAGTT T   | TACCAGGAA                | 2760         |
| 73  | GTGCAGAGCT GTACTGTTGA CTTAGGTATT ACAGCAGACA GCTCCAACCA C   | CCAGACAAC                | 2820         |
|     | AAGCACAAGA ATCGATACAT AAATATCGTT GCCTATGATC ATAGCAGGGT T   | AAGCTAGCA                | 2880         |
|     | CAGCITGCIG AAAAGGATGG CAAACTGACT GATTATATCA ATGCCAATTA T   | CTTGATGGC                | 2940         |
|     | TACAACAGAC CAAAAGCTTA TATTGCTGCC CAAGGCCCAC TGAAATCCAC A   | GCTGAAGAT                | 3000         |
| 50  | TTCTCGAGAA TGATATGGGA ACATAATGTG GAAGTTATTG TCATGATAAC A   | <b>LAACCTCGTG</b>        | 3060         |
|     | GAGAAAGGAA GGAGAAAATG TGATCAGTAC TGGCCTGCCG ATGGGAGTGA G   | GAGTACGGG                | 3120         |
|     | AACTITCTGG TCACTCAGAA GAGTGTGCAA GTGCTTGCCT ATTATACTGT G   | AGGAATTTT                | 3180<br>3240 |
|     | ACTOTAGAA ACACAAAAAT AAAAAAGGGC TOCCAGAAAG GAAGACCCAG T  | TCCCTCCCA                | 3300         |
| 55  | GTCACACAGT ATCACTACAC GCAGTGGCCT GACATGGGAG TACCAGAGTA C<br>GTGCTGACCT TTGTGAGAAA GGCAGCCTAT GCCAAGCGCC ATGCAGTGGG G   | CCTGTTGTC                | 3360         |
| 55  | GTCCACTGCA GTGCTGGAGT TGGAAGAACA GGCACATATA TTGTGCTAGA C   | CAGTATGTTG               | 3420         |
|     | CAGCAGATTC AACACGAAGG AACTGTCAAC ATATTTGGCT TCTTAAAACA (   | CATCCGTTCA               | 3480         |
|     | CAAGAAATT ATTTGGTACA AACTGAGGAG CAATATGTCT TCATTCATGA 1  | PACACTGGTT               | 3540         |
|     | GAGGCCATAC TTAGTAAAGA AACTGAGGTG CTGGACAGTC ATATTCATGC (   | CTATGTTAAT               | 3600         |
| 60  | GCACTCCTCA TTCCTGGACC AGCAGGCAAA ACAAAGCTAG AGAAACAATT (   | CAGCTCCTG                | 3660         |
|     | AGCCAGTCAA ATATACAGCA GAGTGACTAT TCTGCAGCCC TAAAGCAATG   | CAACAGGGAA               | 3720<br>3780 |
|     | AAGAATCGAA CITCTICTAT CATCCCIGTG GAAAGATCAA GGGTTGGCAT   | CCACACCCAAT              | 3840         |
|     | AGTGGAGAAG GCACAGACTA CATCAATGCC TCCTATATCA TGGGCTATTA ( GAATTCATCA TTACCCAGCA CCCTCTCCTT CATACCATCA AGGATTCTG (       | CAGGATGATA               | 3900         |
| 65  | TGGGACCATA ATGCCCAACT GGTGGTTATG ATTCCTGATG GCCAAAACAT   | GGCAGAAGAT               | 3960         |
| 05  | GAATTIGTIT ACTGGCCAAA TAAAGATGAG CCTATAAATT GTGAGAGCTT   | TAAGGTCACT               | 4020         |
|     | CTTATGGCTG AAGAACACAA ATGTCTATCT AATGAGGAAA AACTTATAAT   | TCAGGACTTT               | 4080         |
|     | ATCTTAGAAG CTACACAGGA TGATTATGTA CTTGAAGTGA GGCACTTTCA   | GTGTCCTAAA               | 4140         |
| -   | TGGCCAAATC CAGATAGCCC CATTAGTAAA ACTTTTGAAC TTATAAGTGT   | TATAAAAGAA               | 4200         |
| 70  | GAAGCTGCCA ATAGGGATGG GCCTATGATT GTTCATGATG AGCATGGAGG   | AGTGACGGCA               | 4260         |
|     | GGAACTITCT GTGCTCTGAC AACCCTTATG CACCAACTAG AAAAAGAAAA   | TTCCGTGGAT               | 4320         |
|     | GTTTACCAGG TAGCCAAGAT GATCAATCTG ATGAGGCCAG GAGTCTTTGC   | TGACATTGAG               | 4380         |
|     | CAGTATCAGT TTCTCTACAA AGTGATCCTC AGCCTTGTGA GCACAAGGCA CCATCCACCT CTCTGGACAG TAATGGTGCA GCATTGCCTG ATGGAAATAT          | ACCACACACA<br>CAMPONONNE | 4440<br>4500 |
| 75  | TTAGAGTCTT TAGTTTAACA CAGAAAGGGG TGGGGGGACT CACATCTGAG   | CATTGTTTTC               | 4560         |
| , 5 | CTCTTCCTAA AATTAGGCAG GAAAATCAGT CTAGTTCTGT TATCTGTTGA   | TTTCCCATCA               | 4620         |
|     | CCTGACAGTA ACTITICATGA CATAGGATIC TGCCGCCAAA TITATATCAT  | TAACAATGTG               | 4680         |
|     | TGCCTTTTG CAAGACTTGT AATTTACTTA TTATGTTTGA ACTAAAATGA  |                          | 4740         |
|     | CAGTATTTCT AAGAATGGAA TTGTGGTATT TTTTTCTGTA TTGATTTTAA   | CAGAAAATTT               | 4800         |
| 80  | CAATTTATAG AGGTTAGGAA TICCAAACTA CAGAAAATGT TIGTTITTAG   |                          |              |
|     | TTAGCTGTAT TTGTAGCAAT TATCAGGTTT GCTAGAAATA TAACTTTTAA   | TACAGTAGCC               | 4920         |
|     | TGTAAATAAA ACACTCTTCC ATATGATATT CAACATTTTA CAACTGCAGT   | ATTCACCTAA               | 4980         |
|     | AGTAGAAATA ATCTGTTACT TATTGTAAAT ACTGCCCTAG TGTCTCCATG ATATTTATAA TTGTAGATTT TTATATTTTA CTACTGAGTC AAGTTTTCTA          | CHACCHARTIL              | 5040<br>5100 |
|     | ALALIMAN LIGHMANTI TIMINITIN CINCIANGIC ANGITTICA  |                          |              |

| 5   | GTATTGTGTT<br>ATAGAAATAC<br>TCAAATGGTT | TTAATGACGT<br>ACCTAAGTCA<br>CTTCATTTTG<br>TTTATCCAAG<br>AAAAAAAAA | TTAACTTTGT<br>AAAGAAGTTT<br>GAATTGCAAA | TTCAGCATGT<br>TTATGAGAAT | AATTTTAACT<br>AACACCTTAC | TTTGTGGAAA<br>CAAACATTGT | 5160<br>5220<br>5280<br>5340<br>5367 |
|-----|--|---|--|--------------------------|--------------------------|--------------------------|--------------------------------------|
| 10  | Nucleic Act                            | C99 DNA Sec<br>ld Accession<br>Lence: 501                         | #: Eos sec                             | quence                   |                          |                          |                                      |
| 10  | 1                                      | 11  | 21                                     | 31                       | 41                       | 51                       |                                      |
|     | Ī                                      | î   | ī                                      | ĩ                        | Ĩ.                       | Ĩ                        |                                      |
|     | CACACATACG                             | CACGCACGAT  | CTCACTTCGA                             | TCTATACACT               | GGAGGATTAA               | AACAAACAAA               | 60                                   |
| 1.5 |  | ATTTCCTTCG  |  |                          |                          |                          | 120                                  |
| 15  |  | CCGCAGACCG  |  |                          |                          |                          | 180                                  |
|     |  | GTGTTTGCCG  |  |                          |                          |                          | 240                                  |
|     |  | AGATTGGCTG<br>ATGTAATAGC  |  |                          |                          |                          | 300<br>360                           |
|     |  | GAATCTTAAG  |  |                          |                          |                          | 420                                  |
| 20  |  | TCATAACACT  |  |                          |                          |                          | 480                                  |
| -   |  | AGTTTCAGAA  |  |                          |                          |                          | 540                                  |
|     |  | GTCATCTGAT  |  |                          |                          |                          | 600                                  |
|     |  | CTACTGCTTT  |  |                          |                          |                          | 660                                  |
| 25  |  | GTTAAGAGCT  |  |                          |                          |                          | 720                                  |
| 43  |  | GATTATTGAT  |  |                          |                          | TACATTTACA               | 780<br>840                           |
|     |  | GACATCTCCT  |  |                          |                          |                          | 900                                  |
|     |  | CTCTGAAAGC  |  |                          |                          |                          | 960                                  |
| 20  |  | CATGCTGATG  |  |                          |                          |                          | 1020                                 |
| 30  |  |   |  |                          |                          | GCAGTTTGTA               | 1080                                 |
|     |  |   |  |                          |                          | CTTGTTACAT               | 1140                                 |
|     |  |   |  |                          |                          | TTGTACCAGC<br>CAAGACTTGG | 1200<br>1260                         |
|     |  | CAATAATTTG  |  |                          |                          |                          | 1320                                 |
| 35  |  |   |  |                          |                          | CCTACTGATA               | 1380                                 |
|     | ATCCTGAACT                             | TGATCTTTTC  | CCTGAATTAA                             | TTGGAACTGA               | AGAAATAATC               | AAGGAGGAGG               | 1440                                 |
|     |  |   |  |                          |                          | AGTGCTACAA               | 1500                                 |
|     |  |   |  |                          |                          | CGCATAGGGA               | 1560                                 |
| 40  |  |   |  |                          |                          | TTCTCTGGAA<br>AAATTAGCCA | 1620                                 |
| 40  |  |   |  |                          |                          | CACACTGTGG               | 1680<br>1740                         |
|     |  |   |  |                          |                          | CCACATATGA               | 1800                                 |
|     |  |   |  |                          |                          | GAGGAGGAGA               | 1860                                 |
| 45  |  |   |  |                          |                          | TCCAGTCCCG               | 1920                                 |
| 45  |  |   |  |                          |                          | TTTTCCTCCG               | 1980                                 |
|     |  |   |  |                          |                          | AATGCTTCCG<br>GAGGGAAATG | 2040<br>2100                         |
|     |  |   |  |                          |                          | GGCAGAGAGA               | 2160                                 |
| 50  | GCTTTCTCCA                             | GACTAATTAC  | ACTGAGATAC                             | GTGTTGATGA               | ATCTGAGAAG               | ACAACCAAGT               | 2220                                 |
| 50  |  |   |  |                          |                          | GAAATGCCAC               | 2280                                 |
|     |  |   |  |                          |                          | ACCCCATCCT               | 2340                                 |
|     |  |   |  |                          |                          | ACCCAACCGG               | 2400<br>2460                         |
|     |  |   |  |                          |                          | TTTATCTGTC               | 2520                                 |
| 55  |  |   |  |                          |                          | GCACACTTTT               | 2580                                 |
|     |  |   |  |                          |                          | ATCTTTCCAA               | 2640                                 |
|     |  |   |  |                          |                          | GCAGATTTAC               | 2700                                 |
|     |  |   |  |                          |                          | CAGGAAGTGC               | 2760<br>2820                         |
| 60  |  |   |  |                          |                          | CTAGCACAGC               | 2880                                 |
|     |  |   |  |                          |                          | GATGGCTACA               | 2940                                 |
|     | ACAGACCAAA                             | AGCTTATATI  | GCTGCCCAAG                             | GCCCACTGAA               | ATCCACAGCT               | GAAGATTTCT               | 3000                                 |
|     |  |   |  |                          |                          | CTCGTGGAGA               | 3060                                 |
| 65  |  |   |  |                          |                          | TACGGGAACT               | 3120                                 |
| 05  |  |   |  |                          |                          | COTOTOCTC                |                                      |
|     |  |   |  |                          |                          | CTGCCAGTGC               | 3300                                 |
|     |  |   |  |                          |                          | GTTGTCGTCC               |                                      |
| 70  |  |   |  |                          |                          | ATGTTGCAGC               | 3420                                 |
| 70  |  |   |  |                          |                          | CGTTCACAAA               |                                      |
|     |  |   |  |                          |                          | CTGGTTGAGG<br>GTTAATGCAC | 3540<br>3600                         |
|     |  |   |  |                          |                          | CTCCTGAGCC               |                                      |
|     |  |   |  |                          |                          | AGGGAAAAGA               |                                      |
| 75  |  |   |  |                          |                          | TCCCTGAGTG               |                                      |
|     | GAGAAGGCAG                             | CAGACTACATO   | AATGCCTCCT                             | TATATCATGG               | CTATTACCAG               | AGCAATGAAT               | 3840                                 |
|     |  |   |  |                          |                          | ATGATATGGG               |                                      |
|     |  |   |  |                          |                          | GAAGATGAAT<br>GTCACTCTTA |                                      |
| 80  |  |   |  |                          |                          | GICACICITA               |                                      |
|     |  |   |  |                          |                          | CCTAAATGGC               |                                      |
|     | CAAATCCAG                              | A TAGCCCCAT   | AGTAAAACTT                             | TTGAACTTA                | AAGTGTTATA               | AAAGAAGAAG               | 4200                                 |
|     | CTGCCAATA                              | G GGATGGGCC   | T ATGATTGTT                            | ATGATGAGC                | TGGAGGAGT                | ACGGCAGGAA               | 4260                                 |
|     | CTTTCTGTG                              | TCTGACAAC   | CTTATGCAC                              | : AACTAGAAA              | A AGAAAATTCC             | GTGGATGTTT               | 4320                                 |
|     |  |   |  |                          | _                        | 0.50                     |                                      |

| 5          | ATCAGTTTCT<br>CCACCTCTCT                             | CAAGATGATC<br>CTACAAAGTG<br>GGACAGTAAT<br>TTAACACAGA               | ATCCTCAGCC<br>GGTGCAGCAT                             | TTGTGAGCAC<br>TGCCTGATGG                             | AAGGCAGGAA<br>AAATATAGCT                             | GAGAATCCAT<br>GAGAGCTTAG                             | 4380<br>4440<br>4500<br>4560         |
|------------|--|--|--|--|--|--|--------------------------------------|
| 5          | ACAGTAACTT<br>TTTTTGCAAG<br>ATTTCTAAGA               | AGGCAGGAAA<br>TCATGACATA<br>ACTTGTAATT<br>ATGGAATTGT<br>TAGGAATTCC | GGATTCTGCC<br>TACTTATTAT<br>GGTATTTTT                | GCCAAATTTA<br>GTTTGAACTA<br>TCTGTATTGA               | TATCATTAAC<br>AAATGATTGA<br>TTTTAACAGA               | AATGTGTGCC<br>ATTTTACAGT<br>AAATTTCAAT               | 4620<br>4680<br>4740<br>4800<br>4860 |
| 10         | CTGTATTTGT<br>AATAAAACAC<br>GAAATAATCT<br>TTATAATTGT | AGCAATTATC<br>TCTTCCATAT<br>GTTACTTATT<br>AGATTTTTAT               | AGGTTTGCTA<br>GATATTCAAC<br>GTAAATACTG<br>ATTTTACTAC | GAAATATAAC<br>ATTTTACAAC<br>CCCTAGTGTC<br>TGAGTCAAGT | TTTTAATACA<br>TGCAGTATTC<br>TCCATGGACC<br>TTTCTAGTTC | GTAGCCTGTA<br>ACCTAAAGTA<br>AAATTTATAT<br>TGTGTAATTG | 4920<br>4980<br>5040<br>5100         |
| 15         | TGTGTTACCT<br>AAATACCTTC<br>ATGGTTTTTA               | TGACGTAGTT AAGTCATTAA ATTTTGAAAG TCCAAGGAAT AAAAAAAAA              | CTTTGTTTCA<br>AAGTTTTTAT<br>TGCAAAAATA               | GCATGTAATT<br>GAGAATAACA                             | TTAACTTTTG<br>CCTTACCAAA                             | TGGAAAATAG<br>CATTGTTCAA                             | 5160<br>5220<br>5280<br>5340<br>5363 |
| 20         | Nucleic Aci  | C100 DNA Se<br>d Accession<br>ence: 148                            | #: Eos sec   | quence   |  |  |                                      |
| 25         | 1  | 11   | 21   | 31   | 41   | 51   |                                      |
|            |  | CACGCACGAT   |  |  |  |  | 60                                   |
|            |  | ATTTCCTTCG   |  |  |  |  | 120                                  |
|            |  | CCGCAGACCG   |  |  |  |  | 180<br>240                           |
| 30         |  | AGATTGGCTG   |  |  |  |  | 300                                  |
|            |  | CATGTAATAG   |  |  |  |  | 360                                  |
|            |  | TGAATCTTAA<br>TTCATAACAC   |  |  |  |  | 420<br>480                           |
|            |  | GAGTTTCAGA   |  |  |  |  | 540                                  |
| 35         | AAATGCAATA   | TGTCATCTGA   | TGGATCAGAG   | CATAGTTTAG   | AAGGACAAAA   | ATTTCCACTT   | 600                                  |
|            |  | TCTACTGCTT   |  |  |  |  | 660                                  |
|            |  | CGATTATTGA   |  |  |  | _  | 720<br>780                           |
| 40         | TTAGATCCAT   | TCATACTGTT   | GAACCTTCTG   | CCAAACTCAA   | CTGACAAGTA   | TTACATTTAC   | 840                                  |
| 40         |  | TGACATCTCC   |  |  |  |  | 900                                  |
|            |  | GTCATGCTGA   |  |  |  | CAATGCAACA   | 960<br>1020                          |
|            |  | CAGGTGTTTT   |  |  |  |  | 1080                                 |
| 45         |  | CCAGAAAATG   |  |  |  |  | 1140                                 |
| 43         |  | CCTCGAGTCG   |  |  |  | TTTTGTACCA   | 1200<br>1260                         |
|            |  | CTCAATAATT   |  |  |  |  | 1320                                 |
|            |  |  |  |  |  | TGCCTACTGA   | 1380                                 |
| 50         |  |  |  |  |  | TCAAGGAGGA<br>ACAGTGCTAC                             | 1440<br>1500                         |
|            | AAACCAAATC   | AGGAAAAAGG   | AACCCCAGAT   | TTCTACCACA   | ACACACTACA   | ATCGCATAGG   | 1560                                 |
|            |  |  |  |  |  | AATTCTCTGG   | 1620                                 |
|            |  |  |  |  |  | CTAAATTAGC   | 1680<br>1740                         |
| 55         |  |  |  |  |  | CTCCACATAT   | 1800                                 |
|            |  |  |  |  |  | ATGAGGAGGA   | 1860                                 |
|            |  |  |  |  |  | GCTCCAGTCC<br>TATTTTCCTC                             | 1920<br>1980                         |
| <b>C</b> O | CGAAAACCCA   | GAGACAATAA   | CATATGATGT   | CCTTATACCA   | GAATCTGCTA   | GAAATGCTTC   | 2040                                 |
| 60         |  |  |  |  |  | TGGAGGGAAA   | 2100                                 |
|            |  | CAGACTAATT   |  |  |  | CAGGCAGAGA<br>AGACAACCAA                             | 2160<br>2220                         |
|            |  |  |  |  |  | TGGAAATGCC   |                                      |
| 65         |  |  |  |  |  | TTACCCCATC   |                                      |
| 05         | GGTATACAAT   | GAGGCCAGTA   | ATAGTAGCCA   | TGAGTCTCGT   | ATTGGTCTAG   | CIGAGGGGTT   | 2400<br>2460                         |
|            | GGAATCCGAG   | AAGAAGGCAG   | TTATACCCCT   | TGTGATCGTG   | TCAGCCCTGA   | CTTTTATCTG   | 2520                                 |
|            | TCTAGTGGTT   | CTTGTGGGTA   | TTCTCATCTA   | CTGGAGGAAA   | TGCTTCCAGA   | CTGCACACTT   | 2580                                 |
| 70         | AATTTCAGAT   | GACAGIACAI   | CAATTCCAAT   | ' AAAGCACTT'   | CCAAAGCATG   | CTATCTTTCC   | 2700                                 |
|            |  |  |  |  |  | TTGCAGATTT<br>ACCAGGAAGT                             |                                      |
|            |  |  |  |  |  | CAGACAACAA   |                                      |
|            |  |  |  |  |  | AGCTAGCACA   |                                      |
| 75         | AACAGACCAA   | AAGCTTATAT   | TGCTGCCCA  | GGCCCACTG  | AATCCACAGO   | TGAAGATTTC<br>CCTCGTGGAG                             | 3000                                 |
|            |  |  |  |  |  |  |                                      |
|            | AAAGGAAGGA   | GAAAATGTGA   | TCAGTACTG  | CCTGCCGATC   | GGAGTGAGGA   | GTACGGGAAC<br>GAATTTTACT                             | 3120                                 |
| 00         | CTAAGAAACA   | CAAAAATAAA   | AAAGGGCTCC   | CAGAAAGGA  | A GACCCAGTGG   | ACGTGTGGTC   | 3240                                 |
| 80         |  |  |  |  |  | CCTGCCAGTG<br>TGTTGTCGTC                             |                                      |
|            | CTGACCTTTG   | TGAGAAAGG  | AGCCTATGC  | AAGCGCCATC   | CAGTGGGGCC   | TGTTGTCGTC   | 3360                                 |
|            | CAGATTCAAC   | CACGAAGGAAG  | TGTCAACAT  | TTTGGCTTC  | TAAAACACAT   | TATGTTGCAG<br>CCGTTCACAA                             | 3480                                 |
|            |  |  |  |  |  | ACTGGTTGAG   |                                      |
|            |  |  |  |  |  |  |                                      |

|  | GCCATACTTA  | GTAAAGAAAC   | TGAGGTGCTG   | GACAGTCATA   | TTCATGCCTA   | TGTTAATGCA  | 3600  |
|--|---|--|--|--|--|---|---|
|  | CTCCTCATTC  |  |  |  |  |   | 3660  |
|  | CTGTCACCCA  |  |  |  |  |   | 3720  |
| _  | GGCTTAACTG .  |  |  |  |  |   | 3780  |
| 5  | TCAAATATAC .  |  |  |  |  |   | 3840  |
|  | CGAACTTCTT  |  |  |  |  |   | 3900  |
|  | GAAGGCACAG  |  |  |  |  |   | 3960  |
|  | ATCATTACCC CATAATGCCC   |  |  |  |  |   | 4020<br>4080  |
| 10   | GTTTACTGGC  |  |  |  |  |   | 4140  |
|  | GCTGAAGAAC  |  |  |  |  |   | 4200  |
|  | GAAGCTACAC  |  |  |  |  |   | 4260  |
|  | AATCCAGATA  |  |  |  |  |   | 4320  |
| 1.5  | GCCAATAGGG  |  |  |  |  |   | 4380  |
| 15   |   |  | TATGCACCAA   |  |  |   | 4440  |
|  |   |  | TCTGATGAGG   |  |  |   | 4500  |
|  |   |  | CCTCAGCCTT   |  |  |   | 4560  |
|  |   |  | TGCAGCATTG<br>GGGGTGGGGG   |  |  |   | 4620  |
| 20   |   |  | CAGTCTAGTT   |  |  |   | 4680<br>4740  |
| 20   |   |  | ATTCTGCCGC   |  |  |   | 4800  |
|  |   |  | CTTATTATGT   |  |  |   | 4860  |
|  |   |  | TATTTTTTC  |  |  |   | 4920  |
| ~~   | ATAGAGGTTA  | GGAATTCCAA   | ACTACAGAAA   | ATGTTTGTTT   | TTAGTGTCAA   | ATTTTTAGCT  | 4980  |
| 25   |   |  | GTTTGCTAGA   |  |  |   | 5040  |
|  |   |  | TATTCAACAT   |  |  |   | 5100  |
|  |   |  | AAATACTGCC   |  |  |   | 5160  |
|  |   |  | TTTACTACTG   |  |  |   | 5220  |
| 30   |   |  | TTAGCTGGTC<br>TTGTTTCAGC   |  |  |   | 5280<br>5340  |
| 50   |   |  | GTTTTTATGA   |  |  |   | 5400  |
|  |   |  | CAAAAATAAA   |  |  |   | 5460  |
|  | AAAAAAAAA   |  |  |  | •  |   | 5481  |
| ~ =  |   |  |  |  |  | •   |   |
| 35   | Seq ID NO:  | C101 DNA S   | equence  |  |  |   |   |
|  |   |  | n #: Eos se  | Ineuce   |  |   |   |
|  | Coding sequ   | ence: 13   | 340  |  |  |   |   |
|  |   | ••   |  |  | 43   | E3  |   |
| 40   | 1   | 11   | 21   | 31   | 41   | 51<br>I   |   |
| -10  | DTGCGAATCC  | TANACCETTE   | CCTCGCTTGC   | ATTCAGCTCC   | TOTAL  | CCCCCTCGAT  | 60  |
|  |   |  | ACAACAGAGA   |  |  |   | 120   |
|  |   |  | AAATTGGGGA   |  |  |   | 180   |
|  | CAATCTCCTA  | TCAATATTGA   | TGAAGATCTT   | ACACAAGTAA   | ATGTGAATCT   | TAAGAAACTT  | 240   |
| 45   |   |  | AACATCATTG   |  |  |   | 300   |
|  |   |  | TAATGACTAC   |  |  |   | 360   |
|  |   |  |  |  | <b>האדמידיניודינידיניי</b>   | TGATGGATCA  | 420   |
|  |   |  |  |  |  |   |   |
|  | GAGCATAGTT  | TAGAAGGACA   | AAAATTTCCA   | CTTGAGATGC   | AAATCTACTG   | CTTTGATGCG  | 480   |
| 50   | GAGCATAGTT<br>GACCGATTTT  | TAGAAGGACA<br>CAAGTTTTGA   | AAAATTTCCA<br>GGAAGCAGTC   | CTTGAGATGC<br>AAAGGAAAAG   | AAATCTACTG<br>GGAAGTTAAG   | CTTTGATGCG<br>AGCTTTATCC  | 540   |
| 50   | GAGCATAGTT<br>GACCGATTTT<br>ATTTTGTTTG  | TAGAAGGACA<br>CAAGTTTTGA<br>AGGTTGGGAC   | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAT   | CTTGAGATGC<br>AAAGGAAAAG<br>TTGGATTTCA   | AAATCTACTG<br>GGAAGTTAAG<br>AAGCGATTAT   | CTTTGATGCG<br>AGCTTTATCC<br>TGATGGAGTC  | 540<br>600  |
| 50   | GAGCATAGTT<br>GACCGATTTT<br>ATTTTGTTTG<br>GAAAGTGTTA  | TAGAAGGACA<br>CAAGTTTTGA<br>AGGTTGGGAC<br>GTCGTTTTGG   | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAT<br>GAAGCAGGCT   | CTTGAGATGC<br>AAAGGAAAAG<br>TTGGATTTCA<br>GCTTTAGATC   | AAATCTACTG<br>GGAAGTTAAG<br>AAGCGATTAT<br>CATTCATACT   | CTTTGATGCG<br>AGCTTTATCC<br>TGATGGAGTC<br>GTTGAACCTT  | 540   |
| 50   | GAGCATAGTT GACCGATTTT ATTTTGTTTG GAAAGTGTTA CTGCCAAACT  | TAGAAGGACA<br>CAAGTTTTGA<br>AGGTTGGGAC<br>GTCGTTTTGG<br>CAACTGACAA   | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAT<br>GAAGCAGGCT<br>GTATTACATT   | CTTGAGATGC<br>AAAGGAAAAG<br>TTGGATTTCA<br>GCTTTAGATC<br>TACAATGGCT   | AAATCTACTG<br>GGAAGTTAAG<br>AAGCGATTAT<br>CATTCATACT<br>CATTGACATC   | CTTTGATGCG<br>AGCTTTATCC<br>TGATGGAGTC  | 540<br>600<br>660   |
|  | GAGCATAGTT GACCGATTTT ATTTTGTTTG GAAAGTGTTA CTGCCAAACT ACAGACACAG   | TAGAAGGACA<br>CAAGTTTTGA<br>AGGTTGGGAC<br>GTCGTTTTGG<br>CAACTGACAA<br>TTGACTGGAT   | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAT<br>GAAGCAGGCT<br>GTATTACATT<br>TGTTTTTAAA   | CTTGAGATGC<br>AAAGGAAAAG<br>TTGGATTCA<br>GCTTTAGATC<br>TACAATGGCT<br>GATACAGTTA  | AAATCTACTG<br>GGAAGTTAAG<br>AAGCGATTAT<br>CATTCATACT<br>CATTGACATC<br>GCATCTCTGA   | CTTTGATGCG<br>AGCTTTATCC<br>TGATGGAGTC<br>GTTGAACCTT<br>TCCTCCCTGC  | 540<br>600<br>660<br>720  |
| 50<br>55   | GAGCATAGTT GACCGATTTT ATTITGTTTG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTTT TTACAAAACA   | TAGAAGGACA<br>CAAGTTTTGA<br>AGGTTGGGAC<br>GTCGTTTTGG<br>CAACTGACAA<br>TTGACTGGAT<br>GTGAAGTTCT<br>ATTTTCGAGA   | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAT<br>GAAGCAGGCT<br>GTATTACATT<br>TGTTTTTAAA<br>TACAATGCAA<br>GCAACAGTAC   | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCTCTA  | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT  | CTTTGATGCG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC   | 540<br>600<br>660<br>720<br>780   |
|  | GAGCATAGTT GACCGATTTT ATTTTGTTTG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTTT TTACAAAACA ACTGGAAAGG  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACA TTGACTGGAT GTGAAGTTCT ATTTTCGAGA AAGAGATTCA  | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAT<br>GAAGCAGGCT<br>GTATTACAAA<br>TGCAATGCAA   | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCTCTA TGTAGTTCAG   | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA   | CTTTGATGCG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT  | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960  |
|  | GAGCATAGTT GACCGATTTT ATTTGTTTA CTGCCAAACT ACAGACACAG GCTGTTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGG   | TAGAAGGACA CAAGTITITGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGATTCT ATTTTCGAGA ATTATACCAG ATTATACCAG  | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAA<br>GAAGCAGGCT<br>GTATTACATT<br>TGTTTTTAAA<br>TACAATGCAA<br>CACAGCAGTAC<br>TGAAGCAGTT<br>CCTTCTTGTT  | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCTCTA TGTAGTTCAG ACATGGGAAA  | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT  | CTTTGATGCG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TCTTCAGGCT CGTTTATGAT   | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960  |
|  | GAGCATAGTT GACCGATTITI ATTITIGITG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGATT GTGAAGTTCT ATTTTCGAGA AAGAAGATTCA ATTATACCAG AGAAGTTTGC  | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAAT<br>GAAGCAGGCT<br>GTATTACAAT<br>TGTTTTTAAA<br>TACAATGCAA<br>GCAACAGTAC<br>TGAAGCAGTAC<br>CCTTCTTGTT<br>AGTTTTGTAC   | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCACT TGTAGTTCAG ACATGGGAAA CAGCAGTTGG  | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA AGCCTCGAGT ATGGAGAGGA   | CTTTGATGCG AGCTTTATCC TCATGGACTC GTTGAACCTT TCCTCCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TCTTCAGGCT TCGTTTATGAT CCTAAACCAAG  | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020  |
| 55   | GAGCATAGTT GACCGATTITT ATTITGITTG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG CATGAATTG  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGGAT ATTTTCGAGA AAGAGATTCA ATTATACCAG AGAAGTTTCA AGAAGTTTCA TGACAGATGGAT TGACAGATGGAT   | AAAATTTCCA<br>GGAAGCAGTC<br>AGAAGAAAAT<br>GAAGCAGGCT<br>GTATTACATT<br>TGTTTTTAAA<br>TACAATGCAA<br>GCAACAGTAC<br>TGAAGCAGTT<br>CCTTCTTGTT<br>AGTTTTGTAC   | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCTCTA TGTAGTTCAG ACATGGGAAA CAGCAGTTGG TTGGGTGCTA  | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAGAGGA TTCTCAATAA  | CTTTGATGCG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CCTTTATGAT CCAAACCAAG TTTGCTACCC   | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140  |
|  | GAGCATAGTT GACCGATTIT ATTITITITG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTTT AATATGAGTT AATATGAGTT  | TAGAAGGACA CAAGTTTTGA AGGTTGGAAC GTCGTTTTGG CAACTGACAA TTGACTGGAT GTGAAGTTCT ATTTTCGACA AAGAGATTCA ATTATACCAG AGAAGTTTTG TGACAGATGC TGACAGATGC ATGTTCTTCA  | AAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC TGAAGCAGTTC CCTTCTTGTT AGTTTTGTAAA CTATCAAGC GTATCAAGC GATAGTAGCC  | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT CAATCTGGTT AAGTTCTCTA TGTAGTTCAG ACATGGGAAA CAGCAGTTGG TTGGGTGGTA ATATGGGTGGTA ATATGCACTA   | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTGATACT CATTGACATC GCATCTCTGA ATGTCATCCT GACAGGTGTT AACCAGAAAA GACCTCGACT ATGGAGAGGA ATGTCAATAA ATGGCTTATA   | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACC TGGAAACTAC  | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140  |
| 55   | GAGCATAGTT GACCGATTIT ATTITIGTTG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGA GCACCAGAGA ACCATGATTG CATGAATTTT AATATAGGTT AAGCACCAAC  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGGAT ATTTTCGACA AAGAGATTCA ATTATACCAG AGAAGTTTGC TGACAGATTG TGACAGATTG TGACAGATTG TGACAGATTG TGATGTTCTTCA TGATTGTCAT  | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGGCT GTATTACATT TGTTTTTAAA TACAATCCAA GCAACAGTAC TGAAGCAGTTAC CCTTCTTGTT AGTTTTTAAC CTTACAAGAC CTATCAAGAC CGATAGTACC CATGCCTACT   | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCAC TGTAGTTCAG TGTAGTTCAG TGTAGTTCAG TCAGCAGTTGG TTGGGTGCTA ATATGCACTA GATAATCCTG  | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGATGT AACCAGAAAA ATGGCATGAT ATGGAGAGGA TTCTCAATAA ATGGCTATTA AGGCCAGTAA  | CTTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCC TGGAAAATAC TAGTAGCCAT   | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140  |
| 55   | GAGCATAGTT GACCGATTAT ATTITITITG GAAAGTGTTA CTGCCAAACT ACAGCACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCAGAATGT CATGAATTT AATATGAGTT AGCGACCAAC GAGTCTCGTA GTGATCGTAT  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GTCATTTTGGACA TTGACTGACAA ATTATCGACA ATTATACCAG AGAAGTTTCA ATTATACCAG AGAAGTTTCT TGATTGTCAA ATTATGTCAA TTGATTGTCAA TTGGTCTAGC CAGCCCTGAC CAGCCTCTCTCTCCTCTC  | AAATTTCCA GGAGCAGTC AGAAGAAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC TGAAGCAGTTC CCTTCTTGTT AGTTTTAAA CTAACAGAC CATACCTACC CATGCCTACT TGAGGGGTTC TTAACGGGGTTC  | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCACTA ACATGGGTA ACATGGGAAA CAGCAGTTGG TTGGGTGCTA ATATCCACTA GATAATCCTG GATAATCCTG GATACCGAGA CTAGTGGTTC  | AARTCHACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAGAGGA TTCTCAATAA ATGGCTTATA AGGCCAGTAA AGAAGCAGT TTGTGGGTAT   | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGGT CGTTTATGAT CCAAACCAAG TTTGCTCACC TGGAAAATAC TAGTAGCCAT TATIACCCTT TCTCATCTC   | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200  |
| .60  | GAGCATAGTT GACCGATTITI ATTITISTITG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG AACATGATTG AATATAGATT AGGGACCAAC GAGTCTGTAA GTGATCGTAT  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGGAAT ATTATACCAG AGAAGTTTCA AGAAGTTTCT TGACAGATTCCA TGACAGATTCCA TGACAGATTCCA TGACTGTTCTCA TGATTGTCTCA TGATTGTCAG GCTTCCAGAC GCTTCCAGAC GCTTCCAGAC GCACCCTGACA  | AAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCCT GTATTACATT TGTTTTTAAA TACAATCCAA GCAACAGTAC CCTTCTTGTT AGTTTTTAAC CCTTCTTGTT CCTTCTTGTT CGTTCATGAC CATCACAGCAC CTATCAAGCAC CTATCAAGCAC CTTCATCATCCT TGAGGGGTTG TTTTATCTGT TGCACACTTT  | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT CAATCTGGTT AAGTTCAC TGTAGATCAG CAGTCAG CAGTCAG CAGTCAG CAGTCAG CAGTCAG TTGGGTGCT TAGTTCAG GAATCCAGAA ATATGCACTA GATAATCCTG GAATCCAGAGA CTAGTGGTTC TACTTAGAGG  | AATCTACTE GGAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTGAGT ATGGAGAGGA TTCTCAATAA ATGGCTATT AGGCCAGTAA AGAAGGCAGT TTGTGGGTAT ACAGTACATCA  | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCG TGGAAAATAC TAGTAGCCAT TATACCCCTT TCTCATCAC CCCTAGAGTT  | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1260<br>1320<br>1380<br>1440  |
| 55   | GAGCATAGTT GACCGATTITI ATTITITITE GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG ACCATGATTG CATGAATGT AATATAGTT AAGGACCAAC GAGTCTCGTA GTGATCCTT TGGAGGAAAT ATATCAACA  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGGAT TTGACTGGAT ATTTTCGAGA AAGAGATTCA AATTATACCAA AGAAGTTTGT TGACAGATGG TTGATTGTCTCA TGATTGTCAGC CAGCCCTGAC CAGCCCTGAC CTCCAACACC CTCCAACACCC   | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGGCT GTATTACAAT TGCAACCAGA GCAACAGTAC TGAAGCAGTT AGTTTTTAAC CCTTCTTGTT AGTTTTTTAC CATACTAAGAC CATACTACCC CATACCACCC TGAAGCGTTC TGAGGGGTTC TGAGGGGTTC TGAGGGGTTC TTTTATCTGT TGCACACTT  | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT AAGTTCTCTA TGTAGTTCA AAGTTCTCTA TGTAGTTCAG TGGGGGAA CAGCAGTTGG TTGGGTGCTA ATATGCACTA GATAATCCTG GAATCCGAGA CTAGTGGTTCT TGTAGTTCAGAGA ATATGCACTA TGTAGTTCAGAGA CTAGTGGTTC TACTTAGAGG ATTTCAGATG  | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA ATGGCATATA ATGGCATATA AGGCCAGTAA AGGCCAGTAA AGAAGGCAGT ATTGGGGTATT AGCAGTACATC ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGA ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC ATGTCGGAGC   | CTTGATGGG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TCTTCATAC TCTTCATAGAT CCAAACCAAG TTTGCTACCC TGGAAAATAC TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGGTT AATTCCAATA   | 540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1260<br>1320<br>1380<br>1440<br>1500  |
| .60  | GAGCATAGTT GACCGATTATT ATTITITITE GAAAGTGTTA CTGCCAAACT ACAGCACAG GCTGTTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCAGAATGT CATGAATTT AGTGACCAAC GAGTCTCGTA GTGATCGTA TGGAGGAAAAT ATATCCACAG AAGCACTTTC  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GTCATTTTGG GTCATTTCGACA ATTATACCAG AGAAGTTTCA ATTATACCAG AGAAGTTTCT TGATTGTCAA ATTATACCAG AGAAGTTCT TGATTGTCAA ATTATGCAG CTCCAACACC CAAAGCATTC   | AAATTTCCA GGAGCAGTC AGAAGAAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CCTTCTTGTT AGTTTTAGA CCTACTAGAC CATGCCTACT TGAGGGGTTG TGAGGGGTTG TTTATCTAC TTTATCTTCT TGCACACTTT TTTATCTTCCAC TGCAGGATTTA   | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCACTA ACATGGGTA ACATGGGTA ACATGGGAAA CAGCAGTTGG TTGGGTGCTA ATATCCACTA GATAATCCTG GATAATCCTG TACTTGAGGG ATTTCAGAGA ATTTCAGAGA ATTTCAGATG ATTTCAGATG ATTTCAGATG ATTTCAGATG ATTTCAGATG ATTTCAGATG ATTTCAGATG  | AARTCHACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAAGAGA TTCTCAATAA ATGGCTTATA AGGCCAGTAA AGAAGCAGT TTGTGGGTAA ACAGTACATC ATGTCAGTAC ATGTCAGTTATA ATGTTCAGAGC ATGTCAGTTATA ATGTTCAGAGC ATGTTCAGTTATA ATGTTCAGAGC ATGTTCAGTTTAC ATGTTCAGTTTTAC ATGTTCAGTTTAC ATGTTCAGTTTTAC ATGTTCAGTTTAC ATGTTCAGTTACAC ATGTTCAGTTCA  | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGGT CGTTTATGAT CCAAACCAAG TTGGTACCA TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGCATTA AATTCCAATT TGAAGAATTT TGAAGAATTT   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500   |
| .60  | GAGCATAGTT GACCGATATTT ATTITITTEG GAAAGTGTTA CTGCCAAACTT ACAGCACAGG GCTGTTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG AATTAGATTA AATATGAGTT AGGACCAAC GAGTCTGTA TGGAGGAAAT ATATCCACAC AAGCACTTCC AAGCACTTCC AAGCACTTCC   | TAGAAGGACA CAAGTITIGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGACAA ATTATACCAG AGAATTCT ATTATACCAG AGAAGTTCT TGACGATTCT TGACGATTCC TGACAGATCCT TGACTCTCAC TGACTCTCAC CAGCCCTGAC GCTTCCAGAC CTCCAACAC CAAAGCATGTT AAGAGTTTTA   | AAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCCT GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CTTCTTGTT CCTTCTTGTT CTTATCAAGC GATAGTAGCC CATGCCTACT TGAGGGGTTG TTGACACT TTCCACACT TGCACACTT CCAGGAAGTC  | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC TACAATGGCT CAATCTGGTT AAGTTCACTA TGTAGTTCAG ACATCAGGTA CAGCAGTTAG CAGCAGTTAG CAGCAGTTCAG ATATCCAGAA ATATCCAGAA CAGCAGTTCAG GAATCCAGGA CTAGGTGTCT TACTTAGAGG ATTTCAGATG CATGCAAGTA CAGAGTAGCAAGTA CAGAGCTGTA  | AATCTACTE GGAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAGAA GACCTGGAGT ATGGAGAGGA TTCTCAATAA ATGGCTTATA AGGCCAGTAA AGAAGCAGT TTGTGGGTAT ACAGTACATC ATGTCGGAGC GTGGGTTTAC CTGTTGACTT   | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCC TGGAAAATAC TAGTAGCCAT TATTACCCCTT TCTCATCTAC CCCTAGAGTT AATTCCAATA TGAAGAATTT AAGTATTCAATA  | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560<br>1620   |
| .60  | GAGCATAGTT GACCGATTITI ATTITISTITG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG CATGAATGT AATATAGGTT AAGTACAGACACG GAGTCTGTA GTGATCCTGTA GTGATCCTGTA GGAGCACTTTG GAGCACTTTG GAGCACCTTG GCAGCACCGCT  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACA TTGACTGGAT ATTTTCGAGA AAGAGATTCA ATTATACCAG AGAAGTTTGT TGACAGATGG TTGACTGTTTTCTCAGA AGAGTTCTTCAGC AGCCCTGAC CACCCCTGAC CTCCAACACC CAAAGCATGT AAGAGTTTTC CAAACCATGT AAGAGTTTTC CCAACCACCC CCAACCACCC CCAACCCCCCCC   | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGGCT GTATTACATT TGTTTTTAAA TACAATACAA   | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT AAGTTCATTCAG CAATCTGGTT AAGTTCCTA TGTAGTTCAG CAGCAGTTGG TTGGGTGCTA ATATGCACTA GATAATCCTG GAATCCGAGA CTAGTGGT TACTTAGAGG ATTTCAGAGG ATTTCAGATG ATTTCAGATG CAGAGCTGTA CAGAGATTG   | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA ATGGCATATA ATGGCAGCATTAT AGGCCAGTATA AGGACAGTATA AGAAGGCAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT AGGAAGGCAGT AGGAAGGCAGT AGGAAGGCAGT AGGTTACATC ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGT ATGTCGGAGC GTGGTTTAC ATGTTGACTT GATACATAAA   | CTTGATGGG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TCTTCATAC TCTTCATAC TCTTCATAC TGTTATGAT CCAAACCAAG TTTGCTACCC TGGAAATAC TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGGTT AATTCCAATA TGAAGAATT AGGTATACA TAGGTATACA TATACGTTGCC   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1320<br>1380<br>1500<br>1500<br>1620<br>1680   |
| .60  | GAGCATAGTT GACCGATTITI GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG CATGAATTG CATGAATTG CATGAATTT AAGTACACA GAGTCTCGTA GTGATCCTTA TGAGGAAAT ATATCACTC AAGCACTTC GAGACACC AAGCACTTC GAGACACTC GAGACACTC GAGACACTC CAGACACC TATGATCATA  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGGAT ATTTTCGAGA AAGAGATTCA ATTATACAG AGAAGATTCT TGACAGATGC TGATGTTCTTCAGC CAGCCCTGAC GCTTCCAGAC CCTCCAACACC CAAAGCATTTA AAGAGTTTTT AAGAGATTTTTACAGACACC CCAACCACC CCAACCC CCAACCC CCAACCC CCAACCC CCAACCC CCACCGCCC CCACGGTTAA  | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGGCT GTATTACAAT TGTTTTTAAA GCAACAGTAC TGAAGCAGTT CCTTCTTGTT AGTTTTTAAC CTATCAAGAC CATGCCTACT TGAGGGGTTG TGAGGGGTTG TGAGGAGTTT TGCACACTTT TGCACACTTT TATCTTTCAC TGCACACTTT CAGGAAGTTA  | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC GATACAGTTA CAATCTGGTT AAGTTCTCTA TGTAGTTCAG ACATGGGAAA CAGCAGTTGG TTGGGTGCTA ATATGCACTA GGAATCCGAGA CTAGTGGTCTC GAATCCGAGA CTAGTGGTTC CTACTTAGAGG ATTTCAGATG CATGAAGTA CAGAGCTGTA  | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC CATTGACATC GACAGGTGTT AACCAGAAAA AGGCCAGTAA AGGCCAGTAA AGGCCAGTAA AGAGCCAGTAA AGAGCCAGTAA ACAGTACATC ATTGCGGTATT ACCAGTACATC ATTGTCGGGTTTAC ATTGTCGGGTTTAC ATTGTCGGGTTTAC ATTGTCGGACC GTGGGTTTAC CTGTTGACTTT GGATACATC GATACATCAA AGGATGGCAA AGGATGGCAA   | CTTTGATGCG AGCTTTATCC TCATGGACTC TCCTCCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TTCCTCATAC TCTTCATAC TCTTCATAC TTTCTAGAT CCAAACCAAG TTTGCTACCC TCGAAAATAC TATTACCCCTT TCTCATCTCT TCTCATCTAC CCCTAGAGTT AATTCCAATA TGAAGAATTT AGGTATTACA TTAGAGATTT AGGTATTACCA TTAGAGATTT AGGTATTACCA TTAGAGAATTT AGGTATTACCA TTAGAGAATTT AGGTATTACCA TTATACGTTGCC ACTGACTGAT  | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1380<br>1380<br>1440<br>1500<br>1500<br>1620<br>1680<br>1740   |
| .60<br>.65   | GAGCATAGTT GACCGATTITT TATTITITTE GAAAGTGTTA CTGCCAAACT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTT AATATCACACA GAGTCTGTT AGGGACCAAC GAGTCTGTT TGGAGGAAAT ATATCCACAC GAGACATTT GAGACACTTT GAGACACTTT TGAGCACACT TATGATCATAT TTATATCATAT   | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GTCGTTTTGG GTCGTTTTGG GTCATGACA ATTATACCAG AGAAGTTCT ATTATACCAG AGAAGTTCT TGACAGATCG AGAAGTTCT TGACAGATCG TGACAGC CGCCTGAC GCTCCAACACC CCAACACCC CCAACACCAC GCAGGGTTAA CCAACATCG CCACACT CCACACCACC CCACACCACC CCACACCACC CCACACCAC  | AAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCCT GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CCTTCTTGTT CCTTCTTGTT CGTTCTTGTT CGTTCTTGTT CTTATCAAGC CATGCCTACT TGAAGGATTA TGCACACTTT TGCACACTTT CTACAGGATT CCAGGAAGTT CCAGGAAGTT CCAGGAAGTT CCAGGAAGTC AGACAACAAC AGACAACAAC AGCTAGCCCAC TGCAGAACAAC CTGACGACTAC TGCAGAACTAC TGCAGAACAAC AGCTAGCCCAC TGATAGCACCAC  | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT CAATCTGGTT AAGTTCACT ACATCTGGT ACATCAGTA CAATCTGGT ACATCAGTA ACATCAGTA CAGCAGTTGG ACATCAGAAA CAGCAGTAGA CTAGTGCTCA ATATCCACTA GATAATCCTA GATAATCCTAGATG CATGCAAGTA CAGAGCTGTA CAGAGAGTC CATGCAAGTA CAGAGCTGTA CAGAGAGATC CTTGCTGAAA AACAGACCAA  | AATCTACTE GGAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAGAGGA TTCTCAATAA AGGCCAGTAA AGGACGCAGTAA AGGACGCAGT ACGGGTAA ACGATCACAC CTGGTTATA ACGTTCACAC ATGTCCGACC GTGGGTTTAC CTGTTGACTT GATACATAAA AGGATGGCAA AAGCTACTATA   | CTTGATGGG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TCTTCATAC TCTTCATAC TCTTCATAC TGTTATGAT CCAAACCAAG TTTGCTACCC TGGAAATAC TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGGTT AATTCCAATA TGAAGAATT AGGTATACA TAGGTATACA TATACGTTGCC   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1620<br>1620<br>1680   |
| .60<br>.65   | GAGCATAGTT GACCGATTITT ATTITITTE GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG CATGAATGT AATATGAGTT AGCGACCAAC GAGTCTCGTA GTGATCCTGT TGGAGGAAAT ATATCACTG AGCACTTTC GAGCACTTC GAGCACTGT TATGATCATA TATATCATG GCCCACTG TATGATCATG GCCCACTG GCCCACTG   | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACAA TTGACTGGAT TTGACTGAAT ATTTTCGAGA AAGAATTCCA AGAAGTTTG TGACAGATGC TGACAGATGC TGACAGATGC CAGCCCTGAC CCAACACC CAAAGCATGT AAGGTTTTA AAGGTTTTA AAGGTTTTA AAGGTTTTA CAATTATGC GCAGGGTTAA CCAACTACC GCAGGGTTAA CCAACTACC TCCAACACC TCCAACCC TCCAACACC TCCAACCC TCCAACCC TCCAACACC TCCAACCC TCCAACCACC TCCAACCC TCCAACCACC TCCAACCACCACC TCCAACCACC TCCAACCACCACC TCCAACCACCACC TCCAACCACCACCACC TCCAACCACCACCACCACCACCACCACCACCACCACCACC                                   | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGGCT GTATTACAAT TGCAACAGTAC GCAACAGTAC GCAACAGTAC GATAGTAGCAGT CCTTCTTGTT AGTTTTGAAGCAGT CGATAGTAGC CTATCAAGAC CTATCAAGAC CTATCAAGAC TGAAGCGTTC TGAGGGGTTC TGCACACTT TATCTTTCCA TGCAGATTTC CAGGAGATTAC CAGGAGAGAGAGAC CAGGAGAGAGAGAGAGAGAGAG  | CTTGAGATGC AAAGGAAAAC GCTTTAGATC GCTTTAGATC GCTTTAGATC GATACAGTTA CAATCTGGTT AAGTTCTCTA TGTAGTTCAG CAGCAGTTCG TTGGGTGCTA ATATGCACTC GAATCCAGAG CTAGCTGGTCTA ATATCCACTA GATATCCACTA GATATCCACTA GATATCCACTA GATATCCACTA CAAGCAGTGG ATTCCAGAGA CTAGCAGTA CAGAGCCTAA CACAGAATCC CTTGCTGAAA AAACGAACGA   | AAATCTACTG GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA ATGGCATGAT ATGGAAGGA ATTCTCAATAA AGGACAGTATA AGACGCAGTAT AGGCCAGTAA AGAAGCCAGT ATGTCGGACT ATGTCGGACT ATGTCGGACT ATGTCGGACT ATGTCGGACT ATGTCGGACT AGGATTGACTT GATACATCAAA AGGATTGCGAACA AAGCTTATAT ATGTGGGAACA AAGCTTATAT ATGTGGGAACA GAAAATGTGGAACA GAAAATGTGA  | CTTGATGGG AGCTTTATCC TGATGGAGTC GTTGAACCTT TCCTCCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TCTTCATAC TCTTCATAC TCTTTAGAT CCAAACCAAG TTTGCTACCA TGGAAAATAC TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGTT AATTCCAATA TGAAGAATT AGGTATACA TAGTGTGCC ACTGACTGAT TGCTGCCCAA TATTGTTGCC ACTGACTGAT TGCTGCCCAA TATTGTTGCA TGATGTTGCAT TGCTGCCCAA TATTGTTGCAT TGCTGCCCAA TAATGTTGGAA TCAGTACTGG   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1380<br>1380<br>1440<br>1500<br>1500<br>1620<br>1680<br>1740   |
| .60<br>.65   | GAGCATAGTT GACCGATTITT TATTITITTITG GAAAGTGTTA CTGCCAAACT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCCAGAGA ACCAGATTT AATATGAGTT AGGACCACA GAGTCTCGTA TGGAGGAAAT TGGAGCAACT TGGAGGAAAT TATATCCACAC AGCACTTGG GAGACACTGA GCAGACAGCT TATATCAATG GCAGACAGCT TATATCAATG GCAGACAGCT TATATCAATG GCCCACTGA GCCCACTGA GCCCACTGA CCCTGCCGATG CCTGCCGATG   | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GTCATTTTGGACA TTGACTGGAT ATTATACCAG AGAAGTTCT AATTATACCAG AGAAGTTCT TGACAGACT TTGGTCTAGC GCTCCAGAC CTCCAACACC CCAAGCACT CCAACACC CCAAGCATTACAA CCACACC CCAAGCATTAT AAGAGTTTTA AATACAAG GCAGTTAACAA AATCACAGC GCAGGTTAA CAATTATGT AATCACAGG GCAGTTAACAAG GGAGTTAACAAG GGAGTTAACAAG GGAGTGAGGG GGAGTGAGG GGAGTGAGGG GGAGTGAGG GGAGTGAGG GGAGTGAGG GGAGTGAGG GGAGTGAGGG GGAGTGAGG GGAGG GGAGTGAGG GGAGGAGG GGAGGAGG GGAGGAGG GGAGGAGG   | AAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CTTCTTGTT AGTTTTTACA CTTATCAAGAC AGAAGCAGTAC CTATCATCAC CTATCACAC CTACACAC CTACACAC CTACACAC CTACACAC CTACACAC CTACACAC CTACACACAC   | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCCTA ACATGGGTA ACATGGAAAA CAGCAGTTCG TTGGGTGCTA ATATCCACTA GATAATCCTG GATAATCCTG TACTTGAGAGA CTAGTGGTTC TACTTAGAGG ATTTCAGATG CATGCAAGTA CAGAGCTGTA CAGAGCAGTA CAGAGCAGTA CAGAGACCAA AAAGGAACCAA TGGAGAATGAA AAAGGAACGAA TTTCTGGTCACA  | AATCTACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAGAGA ATGGCTATA AGGCCAGTAA AGGACCAGTAA AGGACCAGTAA AGGACCAGTAA AGGACCAGTAA AGGACCAGT TGTGGGGAC CTGGTTACATC GATACATC AATGTCGGAC ATGTCGAGC CTGGTTTAC CTGTTGACTT GATACATCAA AGGATGGCAA AAGCTTATAT TAGGGAACA CTCAGAAGAG CTCAGAAGAGC CTCAGAAGAGC   | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCC TGGAAAATAC TAGTACCCTT TCTCATCTAC CCCTAGAGTT AATTCCATAT AGGTATTACA TAGAGATTT AGGTATTACA TATAGTTGCT ACTGCCCAA TAATGTGGAA TCAGTACTGG TGTGCCCAA TAATGTGGAA TCAGTACTGG TGTGCCCAA TCAGTACTGG TGTGCCCAA TCAGTACTGG TGTGCCCAA TCAGTACTGG TGTGCCCAA   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1620<br>1620<br>1620<br>1740<br>1800<br>1860<br>1920<br>1980   |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GAGCATAGTT GACCGATTATT ATTITISTITG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG AATATGATTA AGTGATAGTT AGGACCAAC GAGTCTGTA AGTGATCGTA ATATCCACAC AAGCACTTC GAGACACTGA GCAGCACTCG GCAGACAGCT TATGATCATA GCCCCACTGA GCCCCCTGA GCTTATTTCTCA CCTGCCCATG  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GTCGTTTTGG CAACTGACAT ATTGACTGGAT ATTTTCGACA AAGAGTTCT ATTTTCGACA AAGAGTTCT TGACAGATTCC TGACAGATTCG TGATTGTCAG GCTTCCAGAC CTCCAACACC CAAAGCATTTT CCAACACC CCAGGGTTAA AAGAGTTTT CCAACACC CCAGGGTTAA AAGAGTTTT CCAACACC CCAGGGTTAA CCAATTATGT AATCCACAGC TGATTACCAGAG TGATTACCAGAG TGATTACCACAG GGAGTGAGGG ATTACTCACAG   | ARATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCCT GTATTACATT TGTTTTTAAA TACAATCCAA GCAACAGTAC CTATCATGTT CCTTCTTGTT CATTTATAA TACAATGCAA CCATCCTACT TGAAGCAGTT TGAAGCAGTT TGAAGCAGTT TGAAGCAGTT TGAAGCACTACT TGAAGCATTT CATCATCACACT TGCAGATTTACAGCACACACACACACACACACACACACAC   | CTTGAGATGC AAAGGANAAG TTGGATTTCA GCTTTAGATC GCTTTAGATC GATACAGTTA CAATCTGGTT AAGTTCAC TGAGATCA TGTAGTTCAG ACATCGGTTA GATACAGTAC GATACTCGT TGGGTGCTA GATACCTAG GATACCTAG GATACCTAG GATACCTAG CTAGTGTTC TACTTAGATG CATGCAAGTA CAGAGCTGTA CAGAGATCA CAGAGATCA TGGAGAATCA TGGAGAATCA TGGAGAATCA TGGAGAATCA TTCTCGTTCA CTAAGAAACCA TTTCTGGTCAC CTTAGAAGAACCA TTTCTGGTCAC CTTAGAAAACA  | AATCTACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTTAT AACCAGAAAA GACCTCGAGT ATGGAGAGA ATGGCTATA AGGAGAGGA TTCTCAATAA AGGACTATA AGGACGAGT ATGGGTATA AGAAGGCAGT ATGTCGGAGA ATGGGTTACA ATGTCGGAGA AGAAGGAATT AAGTTACAT GATACATCAGAGAGA GAAAAATGAG CAAAAATGAG CAAAAATGAG AAGCTACAT  | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCCTGG AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCCT TGGAAAATAC TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGTT AATTCCAATA TATACAATA TGAAGAATTT AAGTATTACA TATCGTTGCC ACTGACTTT TGCTCCCAA TAATGTGGAA TTAATGTGGAA TAATGTGGAA TAATGTGAAT TAATGTCCAA TAATGTGAA TAATGTGAA TAATGTGAA TAATGTCAATA TAATGTGAA TAATGTCAATA TAATGTGAA TAATGTGAA TAATGTCAATA TAATGTCAATA TAATGTCAATA TAATGTCAATA TAATGTCAATA TAATGTCAATA TAATGTCAATA TAATGTCAATA TAATGTCAATA                 | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1320<br>1320<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040   |
| .60<br>.65   | GAGCATAGTT GACCGATTIT ATTITISTITG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGA ACCATGATTG CATGAAAGT ACATGAATGT AATATGAGTT AATATGAGTT AGGACCAAC GAGTCTGTAT TGGAGGAAAT ATATCACAC AAGCACTTTC GAGACACTGA GCAGACAGCT TATGATCATA TATATCAATC TATATCAATC GGCCCACTGA GGCCCACTGA GCCCCACTGA CCTGCCCATG CCTGCCCATTC CCTGCCCATTC CTAGAAAGGAA  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACA TTGACTGGAT ATTATCCAG AGAAGTTCT ATTTTCGACA AGAAGTTCT TGACAGATTCT TGACTGATT TGATTGTCTCT TGATTGTCAGC CACCCCTGAC CCCAACACC CCAAGACC CCAACACC CCAACACC CCAACACC GCAGGTTTA CCAACTATCT AATCCACACC GCAGGTTAACA TGATTATCACAG TGATTATCACAG TGATTATCACAG AATCCACACC GCAGGTTAACAA GAAGTGAGGA GACCAGTCG GAACCACCC GCAGGTTAACAA GGAGTGAGGA AACCACTGCACCC CCAACCACCC CCAACCACCC CCAACCACCC CCAACCACC  | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGGCT GTATTACATT TGTTTTTAAA TACAATACAA   | CTTGAGATGC AAAGGAAAAA TTGGATTTCA GCTTTAGATC GCTTTAGATC GATACAGTTA CAATCTGGTT AAGTTCTA TGTAGTTCA CAGCAGTTGG TTGGGTGCTA CAGCAGTTGG TTGGGTGCTA GATACCTAG GATAATCCTG GATATCCAGA CTAGCAGTTG CAGCAGTTG CAGCAGTTG CAGCAGTTG CAGCAGTTA CAGCAGTAG CAGCAGTTAG CAGAGATGA CAGAGATGA CAGAGATGA AACAGACCAA TTGCTGGTGT AACAGACCAA AACAGAAACA CTAAGAAACA CACAGTATC CACAGTATC   | AATCTACTE GGAAGTTAAG AAGCGATTAT CATTCATACT CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA ATGGCATATA AGAAGGCAGT ATGGCAGTATA AGAAGGCAGT ATGTCAGTATA AGAAGGCAGT ATGTCAGTATA AGAAGGCAGT ATGTCAGAGA AGATTACAT ATGTCAGAGA AGATTACAT GATACATAAA AAGATTACAT TATGGGAACA GAAAATGAA CCAAAAATAAA ACTACACAGC   | CTTTGATGGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT TCGTTATGAT CCAAACCAAG TTTGCTACCC TGGAAAATAC TAATACCCCTT TCTCATCTAT CCCTTAGGGTT AATTCCATTA TGAAGAATTT AAGTATTACA TATGGTTGCC ACTGACTGA TGTTGCCCAA TGTTGCCCTA TGTTGCCCTA TGTTGCCCTA TGTTGCCCTA TGTTGCCCTA TGTTGCCCTA TGTTGCCCAA TGTGCCTGAGTT TGTTGCCCAA TGTGCCTGAGTT AAGTACTGGT TGTGCCAAGTG TGTGCAAGTG TGTGCAAGTG TGTGCCAACTG AAAGGGCTCC  | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1320<br>1380<br>1560<br>1560<br>1680<br>1740<br>1880<br>1740<br>1860<br>1920<br>1980<br>2040<br>2100                                 |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GAGCATAGTT GACCGATTTT TATTITITTEG GAAAGTGTTA CTGCCAAACT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCCAGAGA ACCATGATTTT AATATGAGTT AGGACCAAC GAGTCTCGTA GTGATCGTA GTGATCGTA GTGATCGTA TGGAGAAAGG GACACTGA TTATGATCATA TATATCACACA GAGACACTCC GAGACACTCC TATGATCATA TATATCATA TATATCATA TATATCATA TATATCATA TATATCATA TATATCATA CCTGCCGATG CTTGCCTATT CAGAAAGGAA ATGGGATAC  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGGGAC GTCGTTTTGGGAC GTGAAGTTCT ATTTTCGACA ATTATACCAG AGAAGTTCC AGACTCT TGATTGTCAACACC CCAAGCATTCAACACC CCAAGCATTCA AGAGTTTC CAACCACCC CCAGGGTTAA CCAAGCATGA CCAAGTTATGA AATCCACAGC CAAGCTGAGG ATACTTGAC CAACCACCC CAGGGTGAGG ATACTTGAC CAACCACCC CAGGGTGAGG ATACTTGAC CAACCACCC CAGGCTCATGAC CACCACTCC CAGGCTCATGAC CACCACTCC CAGGCTCATGAC CACCACTCC CAGGCTCATGAC CACCACTCC CAGGCTCATGAC CACCACTCC CACCACTC CACCACT CACCACTC CACC | AAATTTCCA GGAAGCAGTC AGAAGCAGTC AGAAGCAGTC AGAAGCAGTC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CTTCTTGTT AGTTTTATAA CTACAATGCAC AGAAGCAGTAC CTATCTTGTT TGAGGGTTG TTATCTATC TGAGGGTTG TTATCTCAC TGAGGAGTTC TGAGGAGTTC TGAGGATTTA CCAGGAAGTC AGCACACAC TGAAGACCAC TGAAGATTTC TGAAGATTTC TGAAGATTTC TGAAGATTTA CCTGTGGGAA GTACGGGAAC TGATGGCACAC TGATGCACAC TGATGCAC TGATGCACAC TGATGCACAC TGATGCACAC TGATGCACAC TGATGCACAC TGA | CTTGAGATGC AAAGGAAAAA TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCATA ACATGGAAAA ACACAGAAAAAA AAACAGAAGAAAAAAAAAA   | AATCTACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAGAGAA ATGGCTTATA AGGCCAGTAA AGGACCAGTAA AGGACCAGTAA AGGATCACAC ATGTCAGAAA ATGGCTATA AGGACCAGT ACAGTACAT ACAGTACAT ACAGTACAT ACAGTACAT CTGTTGACT GATACATAAA AGGATGGCAA AAGCTTATAT TATGGGAAC CAAAAATAAA ACTACACCC TGAGAAAGGC TCAGAAAGGC TCAGAAAGAGC TCAGAAAGAGC TCAGAAAGAGC TCAGAAAGAGC TCAGAAAGAGAAAAAAAAAA  | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGGT CGTTTATGAT CCAAACCAAG TTGGTACCCT TAGTAACCAG TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGTT AATTCCATAT AGGTATTACA TATGGTTACC TGGAAACTAT TGATGGTCAC TGGAGTT TGTATCGTTCCC ACTGACTGAT TGTATGGTACC TGGAGTT TGTGGTACC TGGAGTT TGGAGAGTT TGATGGTACC TGGAGAGTT TGTGGTACC TGGAGAGTT TGTGGCCAA TAATGTTGGA TGGTGCCAA TAATGTGGAA TCAGTACTGG TGGCAGCTGAC AAGCGCTCG GTGGCCTGAC AGCCTTATCCC   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1380<br>1380<br>1440<br>1500<br>1500<br>1620<br>1680<br>1740<br>1800<br>1920<br>1980<br>2040<br>2100<br>2160                         |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GAGCATAGTT GACCGATTITT TATTITITTE GAAAGTGTTA CTGCCAAACTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG AACAGACGCCAAGCT AACAGACGAGA ACCATGATTG AGGACCAAC GAGTCTGTA TGGAGGAAAT ATATCCACAC GAGACACTTC GAGACACTT TATGATCATA GCCCCATGA GCCCCATGA GCCCCATGA GCCCCATGA GCCCCATGA GCTTATTGTCA CCTGCCCATG CCTGCCCATG CTTGCCTATT CAGAAAGGAA ATGGAAAGGAA ATGGAAAGGAA ATGGAAAGGAA ATGGGAGTAC AAGCGCCATG   | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GTCGTTTTGG GTCGTTTTGG GTCGTTTTGGGAT ATTTGACGA ATTGACTGGAT ATTTTCGACA AGAAGTTCT AGATTCCA AGAAGTTCT TGACGATTCCA TGACAGATCCA CAGCCTGAC GCTCCAGAC CTCCAACACC CCAACACCAC GCAGGGTTAT AGAGGTTTT AATCCACAGC TGATAACAAG GCAGGGTTAA AGAGTTTTG CAACCACCC GCAGGGTTAA GCAGGGTTATG AATCCACAGC TGATAACAAG GAGTAGGGAGGGAGGAGC CCAATAACAAG GCAGCCCAGTGC CAGCCCAGTGC GCAGGGTCC CAGGGTGC CAGGGTGC CAGGGGTCC CAGGGGGTCC CAGGGGGTCC CAGGGGGTCC CAGGGGGTCC CAGGGGGTCC CAGGGGGCC CAGGGGCC CAGGGCC CAGGGGCC CAGGGGCC CAGGGCC CAGGCC CAGCC CAGCC CAGGCC CAGCC  | AAATTTCCA GGAAGCAGTC AGAAGAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CTTCTTGTT CCTTCTTGTT CAGTTTTTAAC TTATCAATGCAA CCATCCTACT CTATCAAGCA CTATCAAGCAC CTATCACAGC CTATCACAGC CTATCACAGC CTATCACACT CTGAGGGTTTC CTGCAGATTTACACACC CTGCAGAACTACACC CTGCAGAACTACC CTGAGGAACTACC CTGCCAGCACC CTGCCAGCC CTGCCAGCC CTGCCAGCC CTGCCAGCC CTGTCCAGCC CTGTCCAGCC CTGCCAGCC CTGTCCAGCC CTGTCCAGCC CTGTCCAGCC CTGTCCAGCC CTGCCAGCC CTGTCCAGCC CTGTCCAGCC CTGTCCAGCC CTGCCAGCC CTGCCAGC CTGCCAGCC CTGCCAGC CTGCCAGCC CTGCCAGCC CTGCCAGCC CTGCCAGCC CTGCCAGCC CTGCCAGCC CTGCCAGC CTGCCAGC CTGCCAGC CTGCCAGC CTGCCAGC CTGCCAGC CTGCCAGC CTGCCACC CTGCCAGC CTGCCACC CTGCCAGC CTGCCAGC CTGCCAGC C | CTTGAGATGC ANAGGANAAG TTGGATTTCA GCTTTAGATC GCATTTAGATC GATACAGTTA CAATCTGGTT AAGTTCACTA TGTAGTTCAG ACATCGGTTA GCATTCAGATA CAGCAGTTAG CAGCAGTTAG TTGGGTGCTA ATATCCACTA GATACTCAG TACTTAGATG CAGCAGTAG CAGCAGTAG CAGCAGTAG CAGCAGTAT CAGAGATCC TTGCTGAAA TTCTGGTGCA TTGAGAGATCA CAGAGAATCA CAGAGATCA CACAGTATC CTTAGAGAACA TTCTGGTCA CTAGAGAACA CTAGAGAACA CTAGAGAACA CTAGAGAACA CTAGAGAACA CTAGAGAACA CTAAGAAACA CTAGAGAACA CTAGAGAACA CTAGAGAACA CTAGAGAACA CTAAGAAACA CACAGTATC CTAGCCTTTC CACTGCAGTGC   | AATCTACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTAA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAAGGA TTCTCAATAA ATGGCTTATA AGGCCAGTAA AGAAGGCAGT ATGTCAGTAT ACAGTACATC GTGGTTTATA AGGATGCAA AGGATGCAA AAGAATGTACA CAAAAATAAA CAAAAATAAA CAAAAATAAA CTACAAGGA CAAAAATAAA CTACAAGGA CTACAAGAG CTACAAGAGC CTACAAGAGC CTACAAGAAGC CTACAAGAAGC CTAGAAGAGC CTAGAAAGCC TTGAGAAAGCC TTGAGAAGCC TTGAGAAAGCC TTGAGAAAGCC   | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGC AGCCAGTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCT TGGAAACTAC TAGTACCCAT TATTACCCCTT TCTCATCTC CCCTAGAGTT AAATCCATAC TCCTAGAGTT AAATCCATAC TATTACACCT ACTACTACC ACGAGTT AATTCCAATA TGATGCCCAA TAATGTTGCC ACTGACTGAT TGCTGCCCAA TAATGTGCC ACGACTGAC TGGCCCAA TAATGTGCC AGCGCCTGAC AGCCCTGAC AGCCCTATGCC    | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1800<br>1980<br>2040<br>2160<br>2220   |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GAGCATAGTT GACCGATTATT ATTITISTITG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG ATTGAAATTT ATTACAAACAG GAGTCTGTA AGCGACCAAC GAGTCTGTT TGGAGGAAAT ATATCACAC GAGACACTGA GCAGACAGC TATGATCATA TATATCAATG GCCCACTGA GCCCACTGA GTTATTGTCA CCTTGCCCATC CAGAAAGGAA ATGGGATTAT CAGAAAGGAA ATGGGATTAC CAGAAAGGAA ATGGGATTAC AAGGGCCATTA CAGAAAGGAA ATGGGATTAC AAGGGCCATTA ACATATATTTCC CATTATTATTATCATAC AAGGGCCATTAC ACATATATTTCC ACATATATTCC ACATATATTTCC ACATATATTTCC ACATATATTTCC ACATATATTTCC ACATATATTCC ACATATATTTCC ACATATATTTCC ACATATATTTCC ACATATATTTCC ACATATATTCC ACATATATTCC ACATATATTCC ACATATATTCC ACATATATTCC ACATATATTCC ACATATATTCC ACATATATTCC ACATATATAT  | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG CAACTGACA TTGACTGACA TTGACTGACA AGGAGTTCT ATTTTCGACA AGGAGTTCT ATTTTCGACA AGGAGTTCT TGACAGATTCC TGACAGATTCC TGACAGATTCC TGACTGCTAGC GCTTCCAGAC CTCCAACACC CAAACCACT CCAACACC CCAGGGTTAA CAACTACT AATCACACAC GCAGGTTAAC AATCACTACAC TGATAACAAC TGATAACAAC CGAGTTAACCAC CCAGGGTTAAC CAACCACC CCAGCGCTCAC CCAGCGCTCAC CCAGCGCTCAC CCAGCGCTCAC CCAGCGCTCC CCAGCTCCC CCACCACCC CCAGCTCCC CCACCACC CCAGCTCCC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC CC | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGTT TGTTTTTAAA TACAAT TGAAGCAGTT CCTTCTTGTT AGTTTTTAAA TCAATACAAT CCATCATACAC CTATCAAGAC CTATCAAGAC CTATCAAGAC TTATCATACAC CTATCAAGAC TTATCATACAC CTATCAAGAC CTATCACAC TGAAGGATTC TGCAGATTT CCAGGAAGTAC AGCAGACACAC CTAGCACACAC CTAGCACATT CCAGGAAGTAC CCAGGAAGTAC CCTGCAGATTT CCAGGATTTCCAC CCTGCCAGTAC CCTGCCAGTAC CCTGCCAGTAC CTGTTGTCGCC CTTGTTGTCGCC CTTGTTGTCGTCCAGTAC CTGTTGTCGTCCAGTAC CTGTTGTCGTCCAGTAC CTGTTGTTCGTCCAGTAC CTGTTGTTGTTCCACTAC CTGTTGTTGTCAC CTGTTGTTGTTCCACTAC CTGTTGTTGTTCCACTAC CTGTTGTTGTCCACTAC CTGTTGTTGTTCCACTAC CTGTTGTTGTTCCACTAC CTGTTGTTGTTCCACTAC CTGTTGTTGTCCACTAC CTGTTGTTGTTCCACTAC CTGTTGTTGTTCCACTAC CTGTTGTTGTTCCACTACACTA  | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC GCTTTAGATC GATACAGTTA CAATCTGGTT AAGTTCAC CAGTCAC CAGCAGTTAG CAGCAGTTAG CAGCAGTTAG CAGCAGTTAG GATAATCCTG GATAATCCTG GATAATCCTG GATAATCCTG GATAATCCTG GAATCCAGGA CTAGCAGTTC TACTTAGAGG ATTTCAGATG CACAGAGATCA CACAGGAATGA AACAGAACAA TTGAGAAGAA TTCTGGTCAC CTTGCTGAAAA AACAGAACAA CTGACCTTTC CTGACCTTTC CTGACCTTTC CTGACCTTTC CACAGGAACA CACAGAACA CACAGGAACA CACAGGAACA CACAGGAACA CACAGGAACA CACAGGAACA CACAGAACA CACAGGAACA CACAGAACA CACAGA | AATCTACTE GGAAGTTAAG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GACAGGAGTAA AGCAGAGAA ATGCTTATA AGGAGAGA ATGGCTATA AGGACAGTAA AGAAGGCAGTAA AGAATGACTTACATCA ATGTCATACA ATGTCATACA AGATGCAGAA AGATTACATC GATACATCA AGATGCAGAA AGCTTATA AGAGTACATC CTCAGAAGAA CCAAAAATGAA ACTACACCC TGAGAAAGGC CAAAAATGAA CCAGAAAAGAC CAAAAATGAA CCAGAAAAGAC CAAAAATGAA CCAGAAAAGAC CCAGAAAAGAC CCAGAAAATGAA CCACAGAAGAGC CCAGAAAATGAA CCACAGAAGAGC CCAGAAAATGAA CCAAAAATGAA CCACAGAAGAGC CCAGAAAAGCAC CCAGAAAAGAC CCAGAAAAGAC CCAGAAAAGAC CCAGAAAAGAC CCAGAAAAGAC CCAGAAAAGAC CCAGAAAAGAC CCAGAAAAATGAA CCACAGAAGAGC CCAGAAAAGAC CCAGAAAGAGAAC CCAGAAAGAGAAC CCAGAAAAGAAGAAC CCAGAAAGAGAAC CCAGAAAGAGAAC CCAGAAAGAGAAC CCAGAAAGAGAAC CCAGAAGGAAC CCAGAAGGAAC CCAGAAGGAAC CCAGAAGGAAC CCAGAAGGAAC CCAGAGGAAC CCAGAAGGAAC CCAGAAGGAAC CCAGAGGAAC CCAGAGAAC CCAGAGGAAC CCAGAGAAC CCAGAGGAAC CCAGAGAAC CCAGAGAAC CCAGAGAAC CCAGAGAAC CCAGAGAAC CCAGAGAAC CCAGAGAAC CCAGAGAAC CCAGAGAAC CCAGAGAC CCAGACAC C | CTTGATGGG AGCTTTATCG GTTGAACCTT TCCTCCTGGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCTT CCTATAC TGTTAGGACTAC TGTTAGGACTAC TGTTAGGACTAC TAGTAGCCAT TATACACCAT TATACCCCTT TCTCATCTAC TCCTCATCTAC TAGTAGCCAT TATACCCCTT TCTCATCTAC TAGTAGCAT AATTCCAATAA TGAAGAATTA TGAAGAATTT TGCTGCCCAA TATAGTGGGA TGTGCAAGGG TGTGCAAGGGC AGGGCCTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AAGAACAGGC TGTCAACATA   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1380<br>1380<br>1560<br>1560<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2160<br>2280   |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GAGCATAGTT GACCGATTATT TATTITITITE GAAAGTGTTA CTGCCAAACT TTACAAAACA ACTGGAAAGG GCTGTTTTTT TTACAAAACA ACTGGAAAGG ACCCAGAGA ACCAGAGA ACCGAGAAGG ACCAGAGA ACTGGATTTT AGTGATCTGTA GGGACCAAC GAGCACTGA TTATGATCATA TATATCACAG GCAGACAGCT TATGATCATA TATATCATA CCTTGCCGATG CTTGCCTATT CAGAAAGGAA ATGGGATTAC AAGCGCCATTG AAGCGCCTTCT TTTGGCTTCT TTTGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGCTTCT TTTGCTTCT TTTGGCTTCT TTTGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGGCTTCT TTTGCTTCT TTTTTCT TTTTTTCT TTTTTTTCT TTTTTTT | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGGGAC GTCGTTTTGGGAC GTCGTTTTGGGAC ATTTTGACAG ATTATACCAG AGAAGTTCA ATTATACCAG AGAAGTTCA ATTATACCAG AGAAGTTCA ATTATACCAG AGACTCTCAACACC CCAAGACATTCA CCAACACCC CCAAGCATTA AGAGTTTA CCAACACCC CCAGGCTTAA CCACACCC CCAGGCTTAA CCAAGCATGA GAGTTATGC AATCACAGC CCAGGCTTAA CCAAGCATCT CCAATTATGT AATCCACAGC CCAGGCTTAA CCAGTCAGC CAGGCTTACAC CCAGTCAGC CAGGCTACAC CCAGTCAGC CAGGCTACT CCAGTCGC CAGTGGGGC CCAGTGGGGC TACACACAC TACACACC TACACACC TACACAC TACACACC TACACAC TACACACC CAGTGGGGC TCCAGTCGC TCCAGTCGC TCCAGTCGC TCCAGTCGC TCCAGTCGC TACACACC TACACC TACACACC TACACC  | AAATTTCCA GGAACAGTC AGAAGAAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CTTCTTGTT AGTTTTATAA CCTTCTTGTT CTTATCAAGAC AGATCACCACCACCACCACCACCACCACCACCACCACCACCA  | CTTGAGATGC AAAGGAAAAA TTGGATTTCA GCTTTAGATC TACAATGGCT GATACAGTTA CAATCTGGTT AAGTTCATA ACATGGTT ACATCGGTG ACATGGAAAA ACAGAGATAC CAGAGTTCAG GATACCGAGA CTAGTTGCATA ATATCCACTA GATAATCCTG GATATCCAGAGA CTAGTGGTTC TACTTAGAGG ATTTCAGATG CATGCAAGAAT CAGAGACCAA AACAGAACCA TTGAGAAACA AAACAGAAGAA TTTCTGGTCA CTTAGAAACA AAACAGAACAC CCTAGCATTCC CTAGAAAACA CACACGATTCC CCACGCTTTCC CACTGCAGTTCC CCACGCTTTCC CACTGCAGTTCAAAACA ACACAGTATC CCACGCTTTCC CACTGCAGTTCC CACTGCAGTTTCAAAACAA AACACAGTATCC CCACGCTTTCC CACTGCAGTTTCC CACTGCAGTTCC CACTGCAGTTTCAACA AGAAATTATT   | AATCTACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTAA ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGTCATATA ATGCCTTATA ATGCCTTATA AGGCCAGTAA AGGCCAGTAA AGGACCAGTAA AGGATACAT CCGTACATA AGGATACAT ACTGTACATA AGGTTATA AGGTTACAT ACTGTACATA AGGATTACAT AGGTTACAT AGGTTACAT AGGTTACAT AGGTTACAT AGGTTACAT AGGTTACAT CCGTACATA AGGATTACAT AGGATCACAT CCGAAAATAAA AGGATGGCAA CCAAAAATAAA ACTACACGC CTGGAGTTGC CTGGAGTTGC ACGAAAGGGC CTGGAAGGAC CTGGAAGGAC TGGAAGAGGAC TGGAAGAGGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAGAC TGGAAGAAGAC TGGAAGAAAC TGGAAGAAAC TGGAAGAAC TGGAAGAAAC TGGAAGAAC TGGAAGAAC TGGAAGAAAC TGGAAGAAC TGGAACACAC TGCACACAC TGGAACACAC TGCACACACAC TGCACACACAC TGCACACACACAC TGCACACACACACA | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGGT CGTTTATGAT CCAAACCAAG TTGCTACCC TGGAAAACTAC TAGTAGCCAT TATACCCCTT TCTCATCTAC CCCTAGAGTT AATTCCAATA TAGTAGCCAT TGAAGAATTAC TAGTATCCAA TATCGTTACC ACTGACTGAT TGATGGTAT TGATGCCAA TAATGTTGCC ACTGACTGAT TGATGCCCAA TAATGTTGCC ACTGACTGAT CGTGCCCAA TAATGTTGCC ACTGACTGAT CGTGCCCAA TAATGTTGCC ACTGACTGAT CGTGCCCAA TAATGTTGCC ACTGACTGAT TGATGCCCAA TGATGCCCAA TGATCTGCC AGCCTTGCC AGCCTTGCC TGTCAACTAT TGAGGAGCAA                             | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1680<br>1740<br>1800<br>1980<br>2040<br>2160<br>2160<br>2220<br>2280<br>2340                 |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | GAGCATAGTT GACCGATTATT TATTITITTEG GAAAGTTAT CTGCCAAACTT TTACAAAACCA ACTGGAAAGG GACCCAGAGA ACCATGATTG CATGATATTC AGAGCCAAGC AGCCACAGC GAGTCTGTT TGGAGGAAAT TGGAGGAAAT TGGAGCAAC GAGTCTGTA TGGAGGAAAT ATATCCACAC GAGACACTTC GAGACACTTC GAGACACTTC GAGACACTT TATGATCATA TATATCAATA GCCCACTGA GCTATTTCTCCCCATG CTTGCCCTATT CAGAAAGGGAA ATGGAGAGTAC AAGCACTTCT CAGAAAGGAA ATGGAGAGTAC AAGCGCATG AAGCGCATG ACATATATTTC TTTGCCTTCT TATGTCTTCT TATGTCTTCT TATGTCTTCT   | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GCACTGACAA TTGACTGGAT ATTTTCGACA AAGATTCTCA ATTATACCAG AGAATTCTC TGACAGATTCT TGACTGACACACC CTCCAACACC CTCCAACACC GCAGGGTTAT AAGACATGT AATCCACAGG TGATAACAAA TGACTACCC CACACCC CCAAGACCC CCAAGCACCC CCAAGCACC CCAAGCACCC CCAAGCACCC CCAAGCACCC CCAGGTTAACAAA TGATAACAAC TGATAACAACACAC TGATAACAACA TTAAAACACAC TTAAAACACAC TTAAAACACAC TTAAAAACACAC TTAAAACACAC TTAAAACACACT TTAATGATAACACACT TTAATGATAACT TTATTATGATAACACACT TTAATGATACT TTATTATGATAACACACT TTAATGATAACACACT TTAATGATACT TTATTATGATAACACACT TTATTATGATAACACACT TTATTATGATAACACACT TTATTATTATTATTATTATTATTATTATTATTATTATT   | AAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CCTTCTTGTT CCTTCTTGTT CATTCAAGCAC CATGCCTACT TGAAGGATTA CCAGGAAGTAC TGAAGGATTA CCAGGAAGTAC TGAAGGATTA CCAGGAAGTTA CCAGGAAGTTA CCAGGAAGTTA CCAGGAAGTTA CCAGGAAGTTA CCAGGAAGTGA TGAAGATTTA CCAGGAAGTGA CCTCGTTGGAC GTATGCCCAGC TGATGCCCAGC TGATGCCCAGC TGATGTGCCC CCTCCCAGGAAGTGGAC CCTCGTTGGAC CCTCCCAGGAAGTGGAC CCTCGTTGGAC CCTCCCAGGAAGTGGAC CCTCGTTGGAC CCTCCCAGGAAGTGGAC CCTCGTTGACAC CCTCCCAGCAC CCTCCCAGCAC CCTCCCAGCAC CCTCCCAGCAC CCTCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCCACAC CCTCCCACAC CCTCCCCACAC CCTCCCCCACAC CCTCCCCCACAC CCTCCCCCCACAC CCTCCCCCCCACAC CCCCCCCC   | CTTGAGATGC ARAGGANAAG TTGGATTTCA GCTTTAGATC TACAATGGCT CAATCTGGTT AAGTTCATCAT ACATCGGTT AAGTTCAG ACATCGGTT AGATCCAGA ACATCTGGTT ATTTCAGTGCTA ATATCGCTGCTA ATATCGATGC TACTTAGATGC TACTTAGATGC CATGCAAGTA CAGAGCTGTA CAGAGCTGTA AACAGACCAA TTCCTGAAA AAAGAACGA CTAGGAGATCAC CTTAGATGG CTTAGATGG CTTAGATGG CTTAGATGG CTTAGATGG CTTAGATGG CTTAGATGG CTTAGATGG CTTAGATGG CTTAGATGATGC CTTAGAGAACA CTAGAGAACTATC CACAGGTTCAG CACAGTTATC CACTGCAGTG CACTGCAGTAG CACTGCAGTG CACTGCAGTG CACTGCAGTG CACTGCAGTG CACTGCAGTAG CACTGCAG CACTAC CACTGCAG CACTCCAG CACTGCAG CACTCCAG CACTCCAG CACTCCAG CACTCCAG CACTCCAG CACTCCAG CACTCCAG CACTCCAG CACTCAG CA | AATCTACTE GGAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GCAGGTGTT AACCAGAGAGA ATGGAGAGGA TTCTCAATAA ATGGCTTATA AGGCCAGTAA AGAAGCAGT TTGTGGGTAT ACAGTACATC GTAGAGAAGA CTGTTAATA AGGATGCATA ATGTCAGAGC CTGTTACATAA AGGATGCATA ATGTCAGAGC CTGTAATAA AGGATGCAA AAGAATGTGA CTAAAAATAAA CGAAAGAAGC CTGAGAGGAC CTAAAAATAAA CTCAGAAGAG CTAGAAGAAG CTGGAGTTGC CTGGAGTACAAAC CTGAAAGAAAC CTGAAAGAAAC CTGAAAGAAAC CTGAAAGAAAC  | CTTGATGGG AGCTTTATCG GTTGAACCTT TCCTCCTGGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCTT CCTATAC TGTTAGGACTAC TGTTAGGACTAC TGTTAGGACTAC TAGTAGCCAT TATACACCAT TATACCCCTT TCTCATCTAC TCCTCATCTAC TAGTAGCCAT TATACCCCTT TCTCATCTAC TAGTAGCAT AATTCCAATAA TGAAGAATTA TGAAGAATTT TGCTGCCCAA TATAGTGGGA TGTGCAAGGG TGTGCAAGGGC AGGGCCTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AGGCCTTGAC AAGAACAGGC TGTCAACATA   | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1200<br>1380<br>1380<br>1560<br>1560<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2160<br>2280   |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | GAGCATAGTT GACCGATTITT TATTITGTTG GAAAGTGTTA CTGCCAAACT ACAGACACAG GCTGTTTTT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCATGATTG AATATAGATTA AGTGAACAGG GAGTCTGTA AGTGATCGTAA AGTGATCGTAA ATATCACACA AAGCACTTTG GAGACACTGA GCCCACTGA GTTATTGTCACA CCTGCCGATG CTTGCCTATT CAGAAAGGAA ATGGGCTATT CAGAAAGGAA ATGGGCTATT CAGAAAGGAA ATGGGCTATT CAGAAAGGAA ATGGGCTATT CAGAAAGGAA ATTGGCCTTCT CAGAAATTTTT TTTGGCTTTCT GACAGTCATA   | TAGAAGGACA CAAGTTTTGA AGGTTGGAA GTCGTTTTGG CAACTGACA ATTGACTGAAT ATTTTCGACA AAGAGTTCTCA AGAAGTTCTCA AGAAGTTCTCA TGACAGATTCCA TGACAGATCCA TGATTGTCAGC CACCCCTCAGAC CCACACACC CCAGAGCATTCT CCAACACC CCAGGGTTATA CCAATTATG AATCACAGC TGATAACAA CCAGTTATG CAACACC CCAGGGTTAAC CCAATTATG CAACACC CCAGGGTTAAC CCAATTATG CAACACC CCAGGGTTAAC CCAATTATG CAACACC CCAGGGTTAAC CCAATTATG CAACACC CCAGGGTTCAC CCAGTGC CCAGGGTCC CAGGGGCC TCATACACAC TCATTCTGAC TCATTCTGAC CAGTGGGGC TCATACACAC TAACACAC TAACACACA TAACACACA TAACACACA TAACACACA TAACACACA TAACACACA TAACACAC TAACACACAC   | AAAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGTC GTATTACATT TGTTTTTAAA TACAATCAA GCAACAGTAC CCTTCTTGTT AGTTTTTAAC CTATCAAGAGT CCTTCTTGTT CCTTCTTGTT AGTTTTTACA CTATCAAGAGT CTATCAAGAGT CTATCAAGAGT CTATCAAGAGT CTATCAAGAGT CTATCAAGAGT CTATCAGAGT CTACAGGAACT CCAGGAAGT CCAGGAACT CCAGCAGT CCAGTACAGG CCAGTCACAG ACTAGGTTGACA ACTGGTTGACA ACTGGTTGACA ACTGGTTGACA ACTGGTTGACA ACTGGTTGACAA  | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC GCTTTAGATC GATACAGTTA CAATCTGGTT AAGTTCAG CAGTCAG CAGCAGTTAG CAGCAGTTAG CAGCAGTTAG CAGCAGTTAG CAGCAGTTAG CAGCAGTTAG CAGCAGTAG CAGCAGTAG CAGCAGTAG CATTCAGATG CATCAGAGAA CAGAGAATCA CAGAGAATCA CAGAGAATCA CAGAGAATCA CAGAGAATCA CAGAGAATCA CAGAGATCA CAGAGAATCA CAGAGATCA CAGAGATCA CAGAGATCA CAGAGATCA CAGAGATCA CAGAGATCA CAGAGATCA CACAGGATCA CACAGGATTCA CACAGGATTCA CACAGGATTCA CACAGCATTCA CACAGCATTCA CACAGCATTCA CACAGCATTCA CACAGCATTCA CACAGCATTCA CACAGCATTCA CACAGCATCA CACAGCA CACAGCATCA CACAGCATC | AATCTACTE GGAAGTTAAG AAGCGATTAT CATTGACATC CATTGACATC GCATCTCTGA ATGTCATGCT GCAGGTGTT AACCAGAAAA GACCTGGACT ATGGAGAGA ATGGCTATA AGGAGAGAA ATGGCTATA AGGAGGACT ATGGGTATA AGAAGGCAGT ATGGGTATA AGAATGCTATA AGATTGCGAG GTGGTTACA ATGTCATAAA AGGATTGCA CTGTTGACTT CATACATCAC CAAAAATGAG CAAAAATGAG CCTAGAGAGG CCTAGAAGGAC CCTGGAGAGGAC CCTGGTGAACA CCTGGAGAGGC CCTGGAGAGGC CCTGAGAAGGC CCTGGAGAGGC CCTGGAGCAC CCTGGACGAAA CTGTACAAAA CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAAGAAAC CGTAAAACAAAC CGTACAACCAC CCTGGACCCAC CTGGACCCAC CTGCACCCAC CTCCACC CTCCACC CTCCACC CTCCACC CTGCACCCAC CTCCACC  | CTTGATGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCCTGG AGCCAGTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCA TAGTAGCCAT TATTACCCCTT AATTCCATAC CCCTAGAGTT AATTCCATAC CCCTAGAGTT AATTCCATAC TGTACTACC ACTGACTGAT TGATGCCCAA TAATGGTGCC ACTGACTGAT TGCTGCCCAA TAATGTGCCCAA TAATGTGCCCAA TAATGTGCCCAA TAATGTGCCCAA TAATGTCATGC ACTGACTGAT CGGCCTGAC AAGCGCTCC AAGCACTACCC AAGCACTATGCC AAGCACTACCC AAGCACTACCC AAGCACTACCC TGTCCAACATA TGAGGGCCAA TGAGGGCCAA TGAGGGAGCCAA TGAGGGAGCCAA TGAGGGAGCCAA TGAGGGAGCAA TGAGGGAGCAA | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1620<br>1740<br>1800<br>1980<br>2040<br>2160<br>2220<br>2280<br>2280<br>2400<br>2400 |
| <ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | GAGCATAGTT GACCGATTATT ATTITITITE GAAAGTGTTA CTGCCAAACT TTACAAAACA ACTGGAAAGG GACCCAGAGA ACCAGAGA ACCAGAGA ACCAGAGTATTT AATATCAGATTA AGGACCAAC GAGTCTGTT TGAGGAAAT ATATCACACA GAGTCTGTT TGAGGACACTGA GCAGACACTGA GCAGACACTTA GAGACACTTTC GAGACACTTT CAGAAAGGAA ATTATCACAC CCTTGCCGATG CTTGCCGATG CTTGCCGATG CTTGCCGATG CTTGCCTATT CAGAAAGGAA ATGGGATTAC ATGGCTTCT CAGAAAGGAA ATGGGGTTAC TTTGGCTTCT TATGTCTCA CCTGCCTATT CAGAAAGGAA ATGGGGTTAC ACATATTTC TTTGCTTCA GACAGTCATA AAGCTAGAGA ACCAGCCTTAA   | TAGAAGGACA CAAGTTTTGA AGGTTGGGAC GTCGTTTTGG GTCGTTTTGG GTCGTTTTGG GTCGTTTTGG GTCATTTGACA ATTATACCAG AGAAGTTTCT TGACTAGACA AGAAGTTTG TGACTAGACA AGAAGTTTG TGACTAGACA AGAAGTTTG CAACACCC CCCAACACC GCAGGGTTAA GCAATGACA GGAGTTAACAA GGAGTTAACAA GGAGTTAACAA GGAGTTAGGA CACCAGTCC CAGACCAGCC CAGAGGTTA TCATACAA GCAGTTACAA TTCATACAA TTCATAGACA TTCATGACA TTCATGACA TTCATGACA TTCATGACA TTCATGACA TTCATGACA TTCATGACAA AACAATTCC AGCAATGCA AGCAATGCA AGCAATGCA ACCAATTCC AGCAATGCA TCATGACAATGCA ACCAATTCC AGCAATGCA TCATGACATACA TCATGACATACA ACCAATTCC ACCAATTC | AAATTTCCA GGAAGCAGTC AGAAGAAAAT GAAGCAGCC GTATTACATT TGTTTTTAAA TACAATGCAA GCAACAGTAC CCTTCTTGTT CCTTCTTGTT CTTATCAAGAC CATGCCTACT TGAAGCATTAC TTATCAAGAC CATGCCTACT TGAAGACTTAC CTTATCTTCTCT TTATCTTCTCT TTATCTTCTCT TTATCTTTCCACAC CAGGAAGTC CAGGAAGTCAC CAGTTCACAA CAGGAACAAC CAGGAAGTCAC CAGTTCACAA CAGGAAGTCAC CAGTTCACAA CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGGAAAAAC CAGGAAAAAC CAGGGAAAAAC CAGGAACAC CAGGAACC CAGGAACAC CAGGAACC CAGGAACAC CAGGAACC CAGGAACC CAGC | CTTGAGATGC AAAGGAAAAG TTGGATTTCA GCTTTAGATC GCTTTAGATC GATACAGTTA CAATCTGGTT AAGTTCATG ACATCGGTT AGATCCAGA ACATCAGTA ATGTAGTTCAG ACATCGGTGTA ATGTAGTTCAG ACATCAGAA CAGCAGTTGG GATACCAGA CAGCAGTAC CAGCAGTTCAGAGA CAGCAGTAGA CAGCAGTAGA CAGCAGTAGA CAGCAGTAGAACAGAGAC TTGGAGAATCA CACAGGAACAG CTTGCTGAAAA AAAGGAACGA TTTCTGGTCA CTTGCTCAAA CACAGTATC CTGAGATTCAGAG ACACAGTATC CAGCACTTTGG CACTGCAGTCAGAACAGAA   | AARTCHACTE GGAAGTTANG AAGCGATTAT CATTGACATC CATTGACATC GCATCCTGACAGCTGAT ATGTCATGCT GACAGGTGTT AACCAGAAAA GACCTCGAGT ATGGAGAGA ATGGCATAAA ATGGCTATAA AGGCCAGTAA AGGCCAGTAA AGGCCAGTAA AGGACAGAGCAGT CTGGTACATC CTGTTGACTT GATACATCAAAA AGGATGGCAA AAGCTTATAA TATGGGAACA CTAAAAATGGAAAA CTCAGAAGAG CTGGGTTGCAGCAGC CTGGACCAGC TTGGACCAGC CTTCATATCAT CTGGACCAGC CTTCAGCAGAG CTTCAGCAGCAGC CTTCAATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC   | CTTGATGGG AGCTTTATCG TGATGGAGTC GTTGAACCTT TCCTCCTGGC AAGCCAGTTG GATGGACTAC TTCCTCATAC TGTTCAGGCT CGTTTATGAT CCAAACCAAG TTTGCTACCCT TGGAAAATAC TAGTAGCCAT TATACCCCTT TCTCATCAT AATTCCAATA ATTCCAATA TGAAGAATT AAGGTATTACAATA TGAAGAATT AGGTACTGAT TGTGCCCAA TAATGTGGCA TAATGTGGAA TCAGTACTGA TGAGGACCAA CAGCCTATGCC AGGCCTGAC AGGCCTAGGCC AGGCCTAGCC AGGACCATA TGAGGACCAA TGAGGGGCCC AGGACAAACCA TGAGGGTGCC AGGGGTGCC AGGGCAAAACCA TGAGGGTGCC AGGCAAAACCA TGAGGGTGCC AGGCAAAACCA  | 540<br>600<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1220<br>1380<br>1500<br>1560<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2100<br>2220<br>2280<br>2340<br>2460                         |

| 5  | ACCATCAAGG<br>CCTGATGGCC<br>ATAAATTGTG<br>GAGGAAAAAC<br>GAAGTGAGGC<br>TTTGAACTTA<br>CATGATGAGC<br>CAACTAGAAG<br>AGGCCAGGAG<br>CTTGTGAGCA | GCTATTACCA ATTTCTGGAG AAACATGGC AGAGCTTTAA ACTTTCAGTG TAAGTGTTAT ATGGAGGAGT AAGAAAATTC TCTTTGCTGA CAAGGCAGGA GAAATATAGC | GATGATATGG AGAAGATGAA GGTCACTCTT GGACTTTATC TCCTAAATGG AAAAGAAGAA GACGGCAGGA CGTGGATGTT CATTGAGCAG AGAGAATCCA | GACCATAATG TTTGTTTACT ATGGCTGAAG TTAGAAGCTA CCAAATCCAG GCTGCCAATA ACTITCTGTG TACCAGGTTAG TATCAGGTTTC TCTACCTCTC | CCCAACTGGT<br>GGCCAAATAA<br>AACACAAATG<br>CACAGGATGA<br>ATAGCCCCAT<br>GGGATGGGCC<br>CTCTGACAAC<br>CCAAGATGAT<br>TCTACAAAGT | GGTTATGATT AGATGAGCCT TCTATCTAAT TTATGTACTT TAGTAAAACT TATGATTGTT CCTTATGCAC CAATCTGATG GATCCTCAGC | 2700<br>2760<br>2820<br>2880<br>2940<br>3000<br>3120<br>3180<br>3240<br>3340 |
|----|--|---|---|---|--|--|--|
| 15 | Seq ID NO:<br>Nucleic Aci  | C102 DNA Se<br>d Accession<br>mence: 144  | quence<br>  #: Eos seq  |   |  |  |  |
|    | 1  | 11  | 21  | 31  | 41   | 51   |  |
| 20 | TGGGCTAATG<br>ACAGGAGCAC   | TAAAGCGTTT<br>GATACTACAG<br>TGAATCAAAA  | ACAACAGAGA<br>AAATTGGGGA  | AAACTTGTTG<br>AAGAAATATC  | AAGAGATTGG<br>CAACATGTAA   | CTGGTCCTAT<br>TAGCCCAAAA   | 60<br>120<br>180   |
| 25 | AAATITCAGG<br>ACAGTGGAAA<br>TTTAAAGCAA   | TCAATATTGA<br>GTTGGGATAA<br>TTAATCTCAC<br>GCAAGATAAC<br>TAGAAGGACA  | AACATCATTG<br>TAATGACTAC<br>TTTTCACTGG  | GAAAACACAT<br>CGTGTCAGCG<br>GGAAAATGCA  | TCATTCATAA<br>GAGGAGTTTC<br>ATATGTCATC   | CACTGGGAAA<br>AGAAATGGTG<br>TGATGGATCA   | 240<br>300<br>360<br>420<br>480  |
| 30 | GACCGATTTT<br>ATTTTGTTTG<br>GAAAGTGTTA<br>CTGCCAAACT   | CAAGTTTTGA<br>AGGTTGGGAC<br>GTCGTTTTGG<br>CAACTGACAA  | GGAAGCAGTC<br>AGAAGAAAAT<br>GAAGCAGGCT<br>GTATTACATT  | AAAGGAAAAG<br>TTGGATTTCA<br>GCTTTAGATC<br>TACAATGGTT  | GGAAGTTAAG<br>AAGCGATTAT<br>CATTCATACT<br>CATTGACATC   | AGCTTTATCC<br>TGATGGAGTC<br>GTTGAACCTT<br>TCCTCCCTGC   | 540<br>600<br>660<br>720   |
| 35 | GCTGTTTTT<br>TTACAAAACA<br>ACTGGAAAGG  | TTGACTGGAT<br>GTGAAGTTCT<br>ATTTTCGAGA<br>AAGAGATTCA  | TACAATGCAA<br>GCAACAGTAC<br>TGAAGCAGTT  | CAATCTGGTT<br>AAGTTCTCTA<br>TGTAGTTCAG  | ATGTCATGCT<br>GACAGGTGTT<br>AACCAGAAAA   | GATGGACTAC<br>TTCCTCATAC<br>TGTTCAGGCT   | 780<br>840<br>900<br>960   |
|    | GACCCAGAGA<br>ACCATGATTG<br>CATGAATTTT   | ATTATACCAG<br>AGAAGTITGC<br>TGACAGATGG<br>ATGTTCTTCA  | CCTTCTTGTT<br>AGTTTTGTAC<br>CTATCAAGAC  | ACATGGGAAA<br>CAGCAGTTGG<br>TTGGGTGCTA  | GACCTCGAGT<br>ATGGAGAGGA<br>TTCTCAATAA   | CGTTTATGAT<br>CCAAACCAAG<br>TTTGCTACCC   | 1020<br>1080<br>1140<br>1200   |
| 40 | AGCGACCAAC<br>TTAATTGGAA<br>GCTATTGTGA   | TGATTGTCGA<br>CTGAAGAAAT<br>ATCCTGGTAG  | CATGCCTACT<br>AATCAAGGAG<br>AGACAGTGCT  | GATAATCCTG<br>GAGGAAGAGG<br>ACAAACCAAA  | AACTTGATCT<br>GAAAAGACAT<br>TCAGGAAAAA   | TTTCCCTGAA<br>TGAAGAAGGC<br>GGAACCCCAG   | 1260<br>1320<br>1380   |
| 45 | CGATCCCCAA<br>AATTCCACTT<br>CAGACTGTGA   | CAAGAGGAAG<br>CCCAACCAGT<br>CTGAACTGCC  | TGAATTCTCT<br>CACTAAATTA<br>ACCTCACACT  | GGAAAGGGTG<br>GCCACAGAAA<br>GTGGAAGGTA  | ATGTTCCCAA<br>AAGATATTTC<br>CTTCAGCCTC   | CTTGACTTCT<br>TTTAAATGAT   | 1440<br>1500<br>1560<br>1620   |
| 50 | AATACAGTTT<br>ACTGGAGCTG<br>GAGAACATAT   | CTATAACAGA<br>AAGATTCTTC<br>CCCAAGGGTA  | ATATGAGGAG<br>AGGCTCCAGT<br>TATATTTTCC  | GAGAGTTTAT<br>CCCGCAACTT<br>TCCGAAAACC  | TGACCAGTTT<br>CTGCTATCCC<br>CAGAGACAAT   | ATTCATCTCT AACATATGAT  | 1680<br>1740<br>1800<br>1860   |
|    | GAATCACTAA<br>ACAGCACAG  | AGGATCCTTC<br>CCGATGTTGG  | TATGGAGGGA<br>ATCAGGCAGA  | AATGTGTGGT<br>GAGAGCTTTC  | TTCCTAGCTC TCCAGACTAA  | : AGGTTCAGAA<br>: TACAGACATA<br>A TTACACTGAG<br>: AGTGATGTCA                                       | 1920<br>1980<br>2040<br>2100   |
| 55 | CAGGGTCCCT<br>ACTGAGGTAZ<br>GTCAACGTGC<br>CATGAGTCTC   | CAGTTACAGA<br>CACCTCATGO<br>TATACTCGCA<br>GTATTGGTCT  | TCTGGAAATG TTTTATCCCA GACAACCCAA AGCTGAGGGG   | CCACATTATT TCCTCCAGAC CCGGTATACA TTGGAATCC  | CTACCTTTGC ACAGGATTT ATGAGGCCAG AGAAGAAGGC   | CTACTTCCA<br>GGTCTCCACG<br>TAATAGTAGC<br>AGTTATACCC  | 2160<br>2220<br>2280<br>2340   |
| 60 | TACTGGAGG/<br>GTTATATCC/<br>ATAAAGCAC  | A AATGCTTCCA<br>A CACCTCCAAC<br>I TTCCAAAGCA  | GACTGCACAC<br>ACCTATCTT<br>TGTTGCAGAT   | TTTTACTTAC<br>CCAATTTCAC<br>TTACATGCAA  | AGGACAGTAC<br>ATGATGTCGC<br>AGTAGTGGGT   | TATTCTCATC ATCCCCTAGA AGCAATTCCA TACTGAAGAA  | 2400<br>2460<br>2520<br>2580   |
| 65 | ACAGCAGACI<br>GCCCATGATI<br>GATTATATC  | A GCTCCAACCA<br>C ATAGCAGGGT<br>A ATGCCAATTA  | A CCCAGACAA(<br>TAAGCTAGC)<br>A TGTTGATGG(  | AAGCACAAGA<br>A CAGCTTGCT(<br>C TACAACAGA(  | A ATCGATACAT<br>B AAAAGGATGC<br>C CAAAAGCTTA   | A CTTAGGTATT  CAAATATCGTT  CAAACTGACT  A TATTGCTGCC  | 2640<br>2700<br>2760<br>2820   |
| 70 | GAAGTTATT<br>TGGCCTGCO   | G TCATGATAA<br>G ATGGGAGTG  | C AAACCTCGTY<br>A GGAGTACGG   | GAGAAAGGA<br>AACTTTCTG  | A GGAGAAAAT<br>3 TCACTCAGA   | A ACATAATGTG  TGATCAGTAC  A GAGTGTGCAA  A AAAAAAGGGC   | 2880<br>2940<br>3000<br>3060   |
| _  | TCCCAGAAA<br>GACATGGGA<br>GCCAAGCGC  | G GAAGACCCAG<br>G TACCAGAGTA<br>C ATGCAGTGG   | G TEGACETETO<br>A CTCCCTECC<br>G GCCTGTTGT  | GTCACACAG<br>GTGCTGACC<br>GTCCACTGC   | r atcactaca<br>r ttgtgagaa<br>a gtgctggag  | C GCAGTGGCCT<br>A GGCAGCCTAT<br>T TGGAAGAACA<br>G AACTGTCAAC                                       | 3120<br>3180<br>3240<br>3300   |
| 75 | ATATTTGGC<br>CAATATGTC<br>CTGGACAGT  | T TCTTAAAAC<br>T TCATTCATG<br>C ATATTCATG   | A CATCOGTTO<br>A TACACTGGT<br>C CTATGTTAA   | A CAAAGAAAT<br>I GAGGCCATA<br>I GCACTCCTC   | I ATTTGGTAC<br>C TTAGTAAAG<br>A TTCCTGGAC  | A AACTGAGGAG<br>A AACTGAGGTG<br>C AGCAGGCAAA   | 3360<br>3420<br>3480   |
| 80 | ACAATCTCG<br>TCCCGAGTG<br>GCAGCCCTA  | G CTCACTGCA<br>G CTAGGACTA<br>A AGCAATGCA   | A CCTTCCTCT<br>T ACTCCTGAG<br>A CAGGGAAAA   | C CCTGGCTTA<br>C CAGTCAAAT<br>G AATCGAACT   | A CTGATCCTC<br>A TACAGCAGA<br>T CTTCTATCA  | A GTGCAGAGGC C TACCTCAGCC G TGACTATTCT T CCCTGTGGAA  | 3540<br>3600<br>3660<br>3720   |
|    | TATATCATG  | G GCTATTACC   | A GAGCAATGA   | A TTCATCATT   | A CCCAGCACC  | T CAATGCCTCC<br>C TCTCCTTCAT<br>T GGTTATGATT   | 3780<br>3840<br>3900   |

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CCTGATGGCC AAAACATGGC AGAAGATGAA TTTGTTTACT GGCCAAATAA AGATGAGCCT
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          TTTGAGACAC TGAAAGAGTT TTACCAGGAA GTGCAGAGCT GTACTGTTGA CTTAGGTATT
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         ACAGCAGACA GCTCCAACCA CCCAGACAAC AAGCACAAGA ATCGATACAT AAATATCGTT
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         GATTATATCA ATGCCAATTA TGTTGATGGC TACAACAGAC CAAAAGCTTA TATTGCTGCC CAAGGCCCAC TGAAATCCAC AGCTGAAGAT TTCTGGAGAA TGATATGGG ACATAATGTG
                                                                                          2820
 65
                                                                                          2880
          GAAGTTATTG TCATGATAAC AAACCTCGTG GAGAAAGGAA GGAGAAAATG TGATCAGTAC
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          TGGCCTGCCG ATGGGAGTGA GGAGTACGGG AACTTTCTGG TCACTCAGAA GAGTGTGCAA
                                                                                          3000
          GTGCTTGCCT ATTATACTGT GAGGAATTTT ACTCTAAGAA ACACAAAAAT AAAAAAGGGC
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          TCCCAGAAAG GAAGACCCAG TGGACGTGTG GTCACACAGT ATCACTACAC GCAGTGGCCT
                                                                                          3120
  70
          GACATGGGAG TACCAGAGTA CTCCCTGCCA GTGCTGACCT TTGTGAGAAA GGCAGCCTAT
                                                                                          3180
          GCCAAGCGCC ATGCAGTGGG GCCTGTTGTC GTCCACTGCA GTGCTGGAGT TGGAAGAACA
                                                                                          3240
          GGCACATATA TTGTGCTAGA CAGTATGTTG CAGCAGATTC AACACGAAGG AACTGTCAAC
ATATTTGGCT TCTTAAAACA CATCCGTTCA CAAAGAAATT ATTTGGTACA AACTGAGGAG
                                                                                          3300
                                                                                          3360
          CANTATGTCT TCATTCATGA TACACTGGTT GAGGCCATAC TTAGTAAAGA AACTGAGGTG
                                                                                          3420
  75
          CTGGACAGTC ATATTCATGC CTATGTTAAT GCACTCCTCA TTCCTGGACC AGCAGGCAAA
                                                                                          3480
                                                                                          3540
          ACARAGCTAG AGAAACAATT CCAGCTCCTG AGCCAGTCAA ATATACAGCA GAGTGACTAT
          TCTGCAGCCC TAAAGCAATG CAACAGGGAA AAGAATCGAA CTTCTTCTAT CATCCCTGTG
                                                                                          3600
          GAAAGATCAA GGGTTGGCAT TTCATCCCTG AGTGGAGAAG GCACAGACTA CATCAATGCC
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                                                                                          3720
          TCCTATATCA TGGGCTATTA CCAGAGCAAT GAATTCATCA TTACCCAGCA CCCTCTCCTT
  80
          CATACCATCA AGGATTTCTG GAGGATGATA TGGGACCATA ATGCCCAACT GGTGGTTATG
                                                                                           3780
          ATTCCTGATG GCCAAAACAT GGCAGAAGAT GAATTTGTTT ACTGGCCAAA TAAAGATGAG
                                                                                          3840
          CCTATAAATT GTGAGAGCTT TAAGGTCACT CTTATGGCTG AAGAACACAA ATGTCTATCT
                                                                                          3900
          AATGAGGAAA AACTTATAAT TCAGGACTTT ATCTTAGAAG CTACACAGGC ATGGAGGAGT
GACGGCAGGA ACTTTCTGTG CTCTGACAAC CCTTATGCAC CAACTAGAAA AAGAAAATTC
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```

| 5   | CATTGAGCAG<br>AGAGAATCCA | TACCAGGTAG<br>TATCAGTTTC<br>TCCACCTCTC<br>GAGTCTTTAG | TCTACAAAGT | GATCCTCAGC | CTTGTGAGCA | CAAGGCAGGA               | 4080<br>4140<br>4200<br>4220 |
|-----|--------------------------|--|------------|------------|------------|--------------------------|------------------------------|
| •   | Nucleic Aci              | Cl04 DNA Seid Accession<br>lence: 143                | 1#: XM_002 | 914.6      |            |                          |                              |
| 10  | 1                        | 11 .   | 21         | 31         | 41         | 51                       |                              |
| •   | AGGGAGAGAA               | TCGACATAGG<br>CCAGCACTTC                             | TGGGACGCAC | AGAGACCGTG | AAGATTCCAA | GTTCAGGAGA               | 60<br>120                    |
| 15  |                          | TGGAATGCCA<br>CCATGCATTC                             |            |            |            |                          | 180<br>240                   |
|     |                          | GCTTGAGTGC<br>CTGGGCTTTT                             |            |            |            |                          | 300<br>360                   |
|     | GTGGCCCACA               | AGAAGGGGGA   | GCTCTCAATG | GAAGACGTGT | GGTCTCTGTC | CAAGCACGAG               | 420                          |
| 20  |                          | TGAACTGCAG<br>CTGCTTCCCT                             |            |            |            |                          | 480<br>540                   |
|     | CTGTCCATCG               | TGTGCCTGAT   | GATCACGCAG | CTGGCTGGCT | TCAGTGGACC | AGCCTTCATG               | 600                          |
|     |                          | TCTTGGAGTA<br>GCCTCCTCCT                             |            |            |            |                          | 660                          |
| 0.5 |                          | ACCGAACCGG   |            |            |            |                          | 720<br>780                   |
| 25  | AAGATCCTTA               | AGTTAAAGAA   | CATTAAAGAG | AAATCCCTGG | GTGAGCTCAT | CAACATTTGC               | 840                          |
|     |                          | GGCAGAGAAT<br>CCATCTTAGG                             |            |            |            |                          | 900<br>960                   |
|     | CTGGGATCAG               | CTGTTTTTAT   | CCTCTTTTAC | CCAGCAATGA | TGTTTGCATC | ACGGCTCACA               | 1020                         |
| 30  |                          | GGAGAAAATG<br>ACATTAAATT                             |            |            |            |                          | 1080                         |
| 30  |                          | TCCGCGAGGA   |            |            |            |                          | 1140<br>1200                 |
|     |                          | GTGTGGCTCC   |            |            |            |                          | 1260                         |
|     |                          | TGGGCTTCGA<br>CTTTTGCTTT                             |            |            |            |                          | 1320<br>1380                 |
| 35  |                          | TTGACAGATT   |            |            |            |                          | 1440                         |
|     |                          | CCAGTCCTCA   |            |            |            |                          | 1500                         |
|     |                          | CCAGTATCCA<br>GGGGCAAGAA                             |            |            |            |                          | 1560<br>1620                 |
| 40  | GTGCTGGCAG               | AGCAGAAAGG   | CCACCTCCTC | CTGGACAGTG | ACGAGCGGCC | CAGTCCCGAA               | 1680                         |
| 40  |                          | GCAAGCACAT   |            |            |            | ACTGCACAGC<br>GGGAAGTGGA | 1740                         |
|     |                          | TCATTTCAGC   |            |            |            |                          | 1800<br>1860                 |
|     | ATCAGTGGAA               | CCTTCGCTTA   | TGTGGCCCAG | CAGGCCTGGA | TCCTCAATGC | TACTCTGAGA               | 1920                         |
| 45  |                          | TGTTTGGGAA<br>GGCCTGACCT                             |            |            |            |                          | 1980<br>2040                 |
|     |                          | ACCTGAGCGG   |            |            |            |                          | 2100                         |
|     |                          | GCATCTACAT   |            |            |            |                          | 2160                         |
|     |                          | TCAATAGTGC<br>TACAGTACCT                             |            |            |            |                          | 2220<br>2280                 |
| 50  | ATTACGGAAA               | GAGGCACCCA   | TGAGGAACTG | ATGAATTTAA | ATGGTGACTA | TGCTACCATT               | 2340                         |
|     |                          |  |            |            |            | AAAGGAAACC<br>AAAGAAGGAA | 2400<br>2460                 |
|     |                          |  |            |            |            | GCAGGGTTCA               | 2520                         |
| 55  |                          |  |            |            |            | GGCATTCCTG               | 2580                         |
| 55  |                          |  |            |            |            | CTGGTGGTTG               | 2640<br>2700                 |
|     | GTGAGTGACA               | GCATGAAGGA   | CAATCCTCAT | ATGCAGTACT | ATGCCAGCAT | CTACGCCCTC               | 2760                         |
|     |                          |  |            |            |            | CAAGGGCACG<br>AAGCCCTATG | 2820<br>2880                 |
| 60  | AAGTTTTTTG               | ACACGACCCC   | CACAGGGAGG | ATTCTCAACA | GGTTTTCCAA | AGACATGGAT               | 2940                         |
|     |                          |  |            |            |            | TATCCTGGTG               | 3000                         |
|     |                          |  |            |            |            | AGTGGGGCCC<br>GGAGCTGAAG | 3060<br>3120                 |
| 65  | CGTCTGGACA               | ATATCACGCA   | GTCACCTTTC | CTCTCCCACA | TCACGTCCAG | CATACAGGGC               | 3180                         |
| 03  |                          |  |            |            |            | CCAGGAGCTG<br>GCTGGCTGTG | 3240<br>3300                 |
|     | CGGCTGGACC               | TCATCAGCAT   | CGCCCTCATC | ACCACCACGG | GGCTGATGAT | CGTTCTTATG               | 3360                         |
|     |                          |  |            |            |            | CCAGTTAACG               |                              |
| 70  |                          |  |            |            |            | CACCTCGGTG<br>AATTAAGAAC | 3480<br>3540                 |
|     | AAGGCTCCCT               | CCCCTGACTG   | GCCCCAGGAG | GGAGAGGTGA | CCTTTGAGAA | CGCAGAGATG               | 3600                         |
|     | AGGTACCGAG               | AAAACCTCCC   | TCTCGTCCTA | AAGAAAGTAT | CCTTCACGAT | CAAACCTAAA               |                              |
|     |                          |  |            |            |            | GATGGCCCTC<br>AATCAGTGAT | 3720<br>3780                 |
| 75  | ATTGGCCTTG               | CCGACCTCCG   | AAGCAAACTC | TCTATCATTC | CTCAAGAGCC | GGTGCTGTTC               |                              |
|     |                          |  |            |            |            | CCAGATTTGG<br>GAAACTTGAA | 3900                         |
|     | TCTGAAGTGA               | TGGAGAATGG   | GGATAACTTC | TCAGTGGGGG | AACGGCAGCT | CTTGTGCATA               | 3960<br>4020                 |
| 80  | GCTAGAGCCC               | TGCTCCGCCA   | CTGTAAGATT | CTGATTTTAG | ATGAAGCCAC | AGCTGCCATG               | 4080                         |
| 00  |                          |  |            |            |            | AGACTGTACC               |                              |
|     | GCCCAGGGAC               | AGGTGGTGGA   | GTTTGACACC | CCATCGGTCC | TTCTGTCCAA | CGACAGTTCC               |                              |
|     | CGATTCTATC               | CCATGTTTGC   | TGCTGCAGAG | AACAAGGTCG | CTGTCAAGGG | CTAG                     | 4314                         |
|     |                          |  |            |            |            |                          |                              |

Seq ID NO: C105 DNA Sequence Nucleic Acid Accession #: NM\_005688.1 Coding sequence: 126..4439

| 5  | 1 :                      |                |             |              | 41          | 51                           |              |
|----|--------------------------|----------------|-------------|--------------|-------------|------------------------------|--------------|
|    | CCGGGCAGGT               | <br>GGCTCATGCT |             | TTGAGCGCC    | TGGCGCGGTT  | GTCCTGGAGC                   | 60           |
|    | AGGGGCGCAG               | GAATTCTGAT     | GTGAAACTAA  | CAGTCTGTGA   | GCCCTGGAAC  | CTCCGCTCAG                   | 120          |
|    | AGAAGATGAA               | GGATATCGAC     | ATAGGAAAAG  | AGTATATCAT   | CCCCAGTCCT  | GGGTATAGAA                   | 180          |
| 10 | GTGTGAGGGA               | GAGAACCAGC     | ACTTCTGGGA  | CGCACAGAGA   | CCGTGAAGAT  | TCCAAGTTCA                   | 240          |
|    | GGAGAACTCG               | ACCGTTGGAA     | TGCCAAGATG  | CCTTGGAAAC   | AGCAGCCCGA  | GCCGAGGGCC                   | 300          |
|    | TCTCTCTTGA               |                |             |              |             |                              | 360          |
|    | GAAAGTACCA               |                |             |              |             |                              | 420          |
| 15 | ACCCAGTGGA               |                |             |              |             |                              | 480          |
| 13 | CCCGTGTGGC<br>ACGAGTCTTC | CCACAAGAAG     | GGGGAGCTCT  | CAATGGAAGA   | CTCCCAACAA  | GACCTCAAGC                   | 540<br>600   |
|    | AAGTTGGGCC               |                |             |              |             |                              | 660          |
|    | TCATCCTGTC               | CATCGTGTGC     | CTGATGATCA  | CGCAGCTGGC   | TGGCTTCAGT  | GGACCAGCCT                   | 720          |
|    | TCATGGTGAA               | ACACCTCTTG     | GAGTATACCC  | AGGCAACAGA   | GTCTAACCTG  | CAGTACAGCT                   | 780          |
| 20 | TGTTGTTAGT               | GCTGGGCCTC     | CTCCTGACGG  | AAATCGTGCG   | GTCTTGGTCG  | CTTGCACTGA                   | 840          |
|    | CTTGGGCATT               | GAATTACCGA     | ACCGGTGTCC  | GCTTGCGGGG   | GGCCATCCTA  | ACCATGGCAT                   | 900          |
|    |                          |                |             |              |             | CTCATCAACA                   | 960<br>1020  |
|    |                          |                |             |              |             | CTGCTGGCTG<br>GGACCAACAG     | 1080         |
| 25 |                          |                |             |              |             | GCATCACGGC                   | 1140         |
|    |                          |                |             |              |             | CAGAAGATGA                   | 1200         |
|    | ATGAAGTTCT               | TACTTACATT     | AAATTTATCA  | AAATGTATGC   | CTGGGTCAAA  | GCATTTTCTC                   | 1260         |
|    |                          |                |             |              |             | GGGTACTTCC                   | 1320         |
| 20 |                          |                |             |              |             | GTGACCTTCT                   | 1380         |
| 30 |                          |                |             |              |             | GTGGTGACAG                   | 1440         |
|    |                          |                |             |              |             | TCCCTCTCAG<br>GTTCACATGA     | 1500<br>1560 |
|    |                          |                |             |              |             | ACCTTGGCAT                   | 1620         |
|    |                          |                |             |              |             | ATGAAAAAAG                   | 1680         |
| 35 |                          |                |             |              |             | ACTGAGCATC                   | 1740         |
|    |                          |                |             |              |             | OGGCCCAGTC                   | 1800         |
|    | CCGAAGAGGA               | AGAAGGCAAG     | CACATCCACC  | TGGGCCACCT   | GCGCTTACAG  | AGGACACTGC                   | 1860         |
|    |                          |                |             |              |             | AGTGTGGGAA                   | 1920         |
| 40 |                          |                |             |              |             | GAGGGCAGCA                   | 1980         |
| 40 |                          |                |             |              |             | AATGCTACTC                   | 2040<br>2100 |
|    | TGAGAGACAA               | CATCCIGITI     | CACCTCCCCA  | TTCTTCCCAC   | CACCCACCTC  | TCTGTGCTGA<br>ACGGAGATTG     | 2160         |
|    |                          |                |             |              |             | GCCCGGGCCT                   | 2220         |
|    |                          |                |             |              |             | GATGCCCATG                   | 2280         |
| 45 |                          |                |             |              |             | ACAGTTCTGT                   | 2340         |
|    | TTGTTACCCA               | CCAGTTACAG     | TACCIGGITG  | ACTGTGATGA   | AGTGATCTTC  | ATGAAAGAGG                   | 2400         |
|    | GCTGTATTAC               | GGAAAGAGGC     | ACCCATGAGG  | AACTGATGAA   | TTTAAATGGI  | GACTATGCTA                   | 2460         |
|    |                          |                |             |              |             | TCAAAAAAGG                   | 2520         |
| 50 |                          |                |             |              |             | TCAGTAAAGA<br>AAAGGGCAGG     | 2580<br>2640 |
| 50 |                          |                |             |              |             | CCCTTGGCAT                   | 2700         |
|    |                          |                |             |              |             | AGCACCTGGT                   | 2760         |
|    |                          |                |             |              |             | GGGAACGAGA                   | 2820         |
|    |                          |                |             |              |             | AGCATCTACG                   | 2880         |
| 55 |                          |                |             |              |             | TTTGTCAAGG                   | 2940         |
|    |                          |                |             |              |             | CTTCGAAGCC                   | 3000         |
|    |                          |                |             |              |             | TCCAAAGACA                   | 3060         |
|    |                          |                |             |              |             | G AACGTTATCC<br>C GTGGCAGTGG | 3120<br>3180 |
| 60 |                          |                |             |              |             | ATTCGGGAGC                   | 3240         |
| •  |                          |                |             |              |             | TCCAGCATAC                   | 3300         |
|    |                          |                |             |              |             | CAGATACCAGG                  | 3360         |
|    |                          |                |             |              |             | CCCTCCCTCC                   | 3420         |
| CF |                          |                |             |              |             | 3 ATGATCGTTC                 | 3480         |
| 65 |                          |                |             |              |             | GCTGTCCAGT                   | 3540         |
|    |                          |                |             |              |             | CGATTCACCT                   | 3600         |
|    |                          |                |             |              |             | r gccagaatta<br>r gagaacgcag | 3660<br>3720 |
|    |                          |                |             |              |             | C ACGATCAAAC                 | 3780         |
| 70 |                          |                |             |              |             | G CTGGGGATGG                 | 3840         |
|    |                          |                |             |              |             | A GTGAGAATCA                 | 3900         |
|    | GTGATATTG                | CCTTGCCGA      | CTCCGAAGC   | A AACTCTCTA  | T CATTCCTCA | A GAGCCGGTGC                 | 3960         |
|    |                          |                |             |              |             | T GAAGACCAGA                 | 4020         |
| 75 |                          |                |             |              |             | A CCTCTGAAAC                 | 4080         |
| 75 |                          |                |             |              |             | G CAGCTCTTGT                 | 4140         |
|    |                          |                |             |              |             | A GCCACAGCTG<br>A TTTGCAGACT | 4200<br>4260 |
|    |                          |                |             |              |             | T AGGATTATGG                 | 4320         |
|    |                          |                |             |              |             | G TCCAACGACA                 | 4380         |
| 80 |                          |                |             |              |             | C AAGGGCTGAC                 | 4440         |
|    | TCCTCCCTG                | T TGACGAAGT    | C TCTTTTCTT | T AGAGCATTG  | C CATTCCCTG | C CTGGGGCGGG                 | 4500         |
|    | CCCCTCATC                | G CGTCCTCCT    | A CCGAAACCT | T GCCTTTCTC  | G ATTTTATCT | T TCGCACAGCA                 | 4560         |
|    |                          |                |             |              |             | T TATTGTATTT                 | 4620         |
|    | ATTCCATAT                | T CATGTAAAC    | A AAATITAGT | T TITIGITCIT | A ATTGCACTO | T AAAAGGTTCA                 | 4680         |
|    |                          |                |             |              |             | 1265                         |              |

|    |             |             | TATCAGAGGC               |            |             |                          | 4740         |
|----|-------------|-------------|--------------------------|------------|-------------|--------------------------|--------------|
|    |             |             | TAGCCTATAT               |            |             |                          | 4800         |
|    |             |             | TAATAACAGT<br>TTTTGCTATT |            |             |                          | 4860         |
| 5  |             |             | GTGCCAGGTT               |            |             |                          | 4920<br>4980 |
|    |             |             | CCCCTCTGCC               |            |             |                          | 5040         |
|    |             |             | GACCATGCAG               |            |             |                          | 5100         |
|    |             |             | GTTTCTGTCA               |            |             |                          | 5160         |
| 10 |             |             | ATGGGGATCA<br>GCTGTTGTTT |            |             |                          | 5220<br>5280 |
| 10 |             |             | ATGGCTGGCC               |            |             |                          | 5340         |
|    |             |             | CCAACTGCTG               |            |             |                          | 5400         |
|    |             |             | CAGTGGCAGG               |            |             |                          | 5460         |
| 15 |             |             | GTCTCTCTCT               |            |             |                          | 5520         |
| 13 |             |             | CTCACACTGG<br>GTGTGGTTTG |            |             |                          | 5580<br>5640 |
|    |             |             | GCGTGGTCAC               |            |             |                          | 5700         |
|    | ATGTCGTGAC  | CAACTAGACA  | TTCTGTCGCC               | TTAGCATGTT | TGCTGAACAC  | CTTGTGGAAG               | 5760         |
| 20 |             |             | TAAAATTATT               | TTGGATTTTG | AAAAAAAA    | ААААААААА                | 5820         |
| 20 | алалалала   | AAAAAAA     |                          |            |             |                          | 5838         |
|    | Sea ID NO:  | C106 DNA S  | equence                  |            |             |                          |              |
|    |             |             | 1#: NM_005               | 62         |             |                          |              |
| 25 | Coding sequ | uence: 90   | 3671                     |            |             |                          |              |
| 25 | •           | ••          |                          |            | 43          | <b>5</b> 3               |              |
|    | 1<br>       | 11          | 21<br>                   | 31         | 41          | 51<br>I                  |              |
|    | ACAGCGGAGC  | GCAGAGTGAG  | AACCACCAAC               |            | GGCAGCGACC  | CCTGCAGCGG               | 60           |
| 20 |             |             | GGCACCGCCA               |            |             |                          | 120          |
| 30 |             |             | GCAGCCCGGG               |            |             |                          | 180          |
|    |             |             | ATCTTTGATC               |            |             |                          | 240<br>300   |
|    |             |             | AGGGACCGCT               |            |             |                          | 360          |
| 25 | CTCTTAGTGC  | TCGATGTGAC  | AACTCTGGAC               | GGTGCAGCTG | TAAACCAGGT  | GTGACAGGAG               | 420          |
| 35 |             |             | CCAGGCTTCC               |            |             |                          | 480          |
|    |             |             | AAGTGTGACT<br>AAGCCAGCTG |            |             |                          | 540<br>600   |
|    |             |             | GGGGGGAACC               |            |             |                          | 660          |
| 40 | GGCATTCAGC  | CAGCTGCCGC  | AGCTCTGCAG               | AATACAGTGT | CCATAAGATC  | ACCTCTACCT               | 720          |
| 40 |             |             | TGGAAGGCTG               |            |             |                          | 780          |
|    |             |             | GATGTGTTTA               |            |             |                          | 840          |
|    |             |             | CTTGGGAATC               |            |             |                          | 900<br>960   |
|    |             |             | GCTCCCTTGA               |            |             |                          | 1020         |
| 45 | TCACCAAGAC  | TTACACATTC  | AGGTTAAATG               | AGCATCCAAG | CAATAATTGG  | AGCCCCCAGC               | 1080         |
|    |             |             | AGGTTACTGC               |            |             |                          | 1140         |
|    |             |             | GGGTACATTG<br>TGGGTTGAAC |            |             |                          | 1200<br>1260 |
|    |             |             | TCTGGCTACA               |            |             |                          | 1320         |
| 50 |             |             | TGTCAAGGGG               |            |             |                          | 1380         |
|    |             |             | CCTGACATTG               |            |             |                          | 1440         |
|    |             |             | AGCTGCAAGC<br>GAGGTGGTGT |            |             |                          | 1500<br>1560 |
|    |             |             | GATGGCTACT               |            |             |                          | 1620         |
| 55 | TGAGGCCTTG  | TCAGCCCTGT  | CAATGCAACA               | ACAATGTGGA | CCCCAGTGCC  | TCTGGGAATT               | 1680         |
|    |             |             | TGTTTGAAGT               |            |             |                          | 1740         |
|    |             |             | TTCGGGGACC<br>ATGGGCTCAG |            |             | GACAAGTGTC               | 1800<br>1860 |
|    |             |             |                          |            |             | AGCTGTCCAG               | 1920         |
| 60 | CTTGCTATAA  | TCAAGTGAAG  | ATTCAGATGG               | ATCAGTTTAT | GCAGCAGCTT  | CAGAGAATGG               | 1980         |
|    |             |             | CAGGGTGGTG               |            |             |                          | 2040         |
|    |             |             |                          |            |             | CAGATTTCAG               | 2100<br>2160 |
|    |             |             |                          |            |             | CTGGGAAGTC               | 2220         |
| 65 |             |             |                          |            |             | CTGAGCCTGG               | 2280         |
|    |             |             |                          |            |             | TACGTGGGGC               |              |
|    |             |             |                          |            |             | CACGTTGAGT               |              |
|    |             |             |                          |            |             | CAAGCCCTCT               |              |
| 70 |             |             |                          |            |             | CAGCAGTTGA               |              |
|    | CAAGGGAGG   | CACTCAAGC   | GAAATTGAAG               | CAGATAGGTO | TTATCAGCAC  | AGTCTCCGCC               | 2640         |
|    |             |             |                          |            |             | GTGGAAGAAG               |              |
|    |             |             |                          |            |             | CATATGGATG<br>CAGCTCTTAC |              |
| 75 |             |             |                          |            |             | AATCTTGCTA               |              |
| -  | AAAGCAGAG   | CACAAGAAGC  | CTGAGTATGG               | GCAATGCCAG | TTTTTTATGAA | GTTGAGAGCA               | 2940         |
|    | TCCTTAAAAA  | CCTCAGAGAG  | TTTGACCTGC               | AGGTGGACA  | CAGAAAAGCA  | GAAGCTGAAG               | 3000         |
|    |             |             |                          |            |             | GACAAGACCC               |              |
| 80 |             |             |                          |            |             | AAGAATGGGG<br>CTGAACTTGG |              |
|    |             |             |                          |            |             | TCTCTGAAGA               |              |
|    | GTGAGATGAG  | G GGAAGTGGA | GGAGAGCTGG               | AAAGGAAGG/ | GCTGGAGTT   | GACACGAATA               | 3300         |
|    | TGGATGCAG:  | r acagatggt | ATTACAGAAG               | CCCAGAAGG1 | TGATACCAGA  | GCCAAGAACG               | 3360         |
|    | CIGGGGTTA   | : AATUCAAGA | . ACACTCAAC              | CATTAGACGO | CUTCCTGCAT  | ' CTGATGGACC             | 3420         |

|  | AGCCTCTCAG   | TGTAGATGAA   | GAGGGGCTGG   | TCTTACTGGA   | GCAGAAGCTT  | TCCCGAGCCA  | 3480  |
|--|--|--|--|--|---|---|---|
|  | AGACCCAGAT   | CAACAGCCAA   | CTGCGGCCCA   | TGATGTCAGA   | GCTGGAAGAG  | AGGGCACGTC  | 3540  |
|  | AGCAGAGGGG   |  |  |  |   |   | 3600  |
|  |  |  |  |  |   |   |   |
| 5  | AGAACTTGGA   |  |  |  |   |   | 3660  |
| 3  | AGCAACAGTG   | AAGCTGCCAT   | AAATATTTCT   | CAACTGAGGT   | TCTTGGGATA  | CAGATCTCAG  | 3720  |
|  | GGCTCGGGAG   | CCATGTCATG   | TGAGTGGGTG   | GGATGGGGAC   | ATTTGAACAT  | GTTTAATGGG  | 3780  |
|  | TATGCTCAGG   |  |  |  |   |   | 3840  |
|  |  |  |  |  |   |   |   |
|  | TGCACCATAC   |  |  |  |   |   | 3900  |
| 10   | ATGATCAAGG   | ATCTGGACCC   | CAAAGAATAG   | ACTGGATGGA   | AAGACAAACT  | GCACAGGCAG  | 3960  |
| 10   | ATGTTTGCCT   | CATAATAGTC   | GTAAGTGGAG   | TCCTGGAATT   | TGGACAAGTG  | CTGTTGGGAT  | 4020  |
|  | ATAGTCAACT   |  |  |  |   |   | 4080  |
|  |  |  |  |  |   |   |   |
|  | ATGAAATTCT   |  |  |  |   |   | 4140  |
|  | ACTATTGCCT   | CATATTGTCC   | TCTGCAAGCT   | TCTTGCTGAT   | CAGAGTTCCT  | CCTACTTACA  | 4200  |
|  | ACCCAGGGTG   | TGAACATGTT   | CTCCATTTTC   | AAGCTGGAAG   | AAGTGAGCAG  | TGTTGGAGTG  | 4260  |
| 15   | AGGACCTGTA   |  |  |  |   |   |   |
|  |  |  |  |  |   |   | 4320  |
|  | GTTCTGGACC   |  |  |  |   |   | 4380  |
|  | ATTTTTATTA   | AAGCATTTCC   | TACCAGCAAA   | GCAAATGTTG   | GGAAAGTATT  | TACTTTTTCG  | 4440  |
|  | GTTTCAAAGT   | GATAGAAAAG   | TGTGGCTTGG   | GCATTGAAAG   | AGGTAAAATT  | CTCTAGATTT  | 4500  |
|  | ATTAGTCCTA   |  |  |  |   |   | 4560  |
| 20   |  |  |  |  |   |   |   |
| 20   | ATCTTATTTT   |  |  |  |   |   | 4620  |
|  | CACACTTCAG   | CTGGGTCACA   | TCCATCCCTC   | CATTCATCCT   | TCCATCCATC  | TTTCCATCCA  | 4680  |
|  | TTACCTCCAT   |  |  |  |   |   | 4740  |
|  | GTGGGACAGT   |  |  |  |   |   |   |
|  |  |  |  |  |   |   | 4800  |
| 25   | AGCATTTTTA   |  |  |  |   |   | 4860  |
| 25   | GCAATAACCG   | CTTGGTTTGC   | AACCTCTTTG   | CTCAACAGAA   | CATATGTTGC  | AAGACCCTCC  | 4920  |
|  | CATGGGGGCA   | CTTGAGTTTT   | GGCAAGGCTG   | ACAGAGCTCT   | GGGTTGTGCA  | CATTTCTTTG  | 4980  |
|  | CATTCCAGCT   |  |  |  |   |   | 5040  |
|  |  |  |  |  |   |   |   |
|  |  |  | GGAGGAACCA   |  |   |   | 5100  |
| 20   | TGGTGCTGCC   | TTGCTTCTGT   | ATTTCCTTGG   | ATTTTCCTGA   | AAGTGTTTTT  | AAATAAAGAA  | 5160  |
| 30   | CAATTGTTAG   | ATGCC  |  |  |   |   | 5175  |
|  |  |  |  |  |   |   | 54.5  |
|  | O TD 110   |  |  |  |   |   |   |
|  | Seq ID NO:   |  |  |  |   |   |   |
|  | Nucleic Aci  | d Accession  | 1 #: NM_0213   | 101  |   |   |   |
|  | Coding sequ  | ence: 221  | . 856  |  |   |   |   |
| 35   |  |  |  |  |   |   |   |
| 55   | _  |  |  |  |   |   |   |
|  | 1  | 11   | 21   | 31   | 41  | 51  |   |
|  |  |  | 1  | 1  |   | 1   |   |
|  | GAATTCGGCA   | CGAGGCCTCG   | TGCCGGGGAG   | CAACCTCAGC   | TTCTAGTATC  | CAGACTCCAG  | 60  |
|  |  |  | CCAACCCCGA   |  |   |   |   |
| 40   |  |  |  |  |   |   | 120   |
| 40   |  |  | TTCCTCCGCG   |  |   |   | 180 .   |
|  | CCCACCTGCA   | AACTCTCCGC   | CTTCTGCACC   | TGCCACCCCT   | GAGCCAGCGC  | GGGCGCCCGA  | 240   |
|  |  |  |  |  |   |   |   |
|  | CHUATACTIT ATTA  | GLACAVAGAGG  | CCCTYCCACCT  | Charle Countries   | Publishing Annual V   | TOTALCONTO  | 300   |
|  |  |  |  |  |   | TCCTGGGATG  | 300   |
|  | GATCGGCGCC   | ATCGTCAGCA   | CTGCCCTGCC   | CCAGTGGAGG   | ATTTACTCCT  | ATGCCGGCGA  | 300<br>360  |
| 45   | GATCGGCGCC   | ATCGTCAGCA   |  | CCAGTGGAGG   | ATTTACTCCT  | ATGCCGGCGA  |   |
| 45   | GATCGGCGCC<br>CAACATCGTG   | ATCGTCAGCA<br>ACCGCCCAGG   | CTGCCCTGCC<br>CCATGTACGA   | CCAGTGGAGG<br>GGGGCTGTGG   | ATTTACTCCT<br>ATGTCCTGCG  | ATGCCGGCGA<br>TGTCGCAGAG  | 360<br>420  |
| 45   | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG   | ATCGTCAGCA<br>ACCGCCCAGG<br>ATCCAGTGCA   | CTGCCCTGCC<br>CCATGTACGA<br>AAGTCTTTGA   | CCAGTGGAGG<br>GGGGCTGTGG<br>CTCCTTGCTG   | ATTTACTCCT<br>ATGTCCTGCG<br>AATCTGAGCA  | ATGCCGGCGA<br>TGTCGCAGAG<br>GCACATTGCA  | 360<br>420<br>480   |
| 45   | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT   | ATCGTCAGCA<br>ACCGCCCAGG<br>ATCCAGTGCA<br>GCCTTGATGG   | CTGCCCTGCC<br>CCATGTACGA<br>AAGTCTTTGA<br>TGGTTGGCAT   | CCAGTGGAGG<br>GGGGCTGTGG<br>CTCCTTGCTG<br>CCTCCTGGGA   | ATTTACTCCT<br>ATGTCCTGCG<br>AATCTGAGCA<br>GTGATAGCAA  | ATGCCGCGA<br>TGTCGCAGAG<br>GCACATTGCA<br>TCTTTGTGGC   | 360<br>420<br>480<br>540  |
| 45   | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT<br>CACCGTTGGC   | ATCGTCAGCA<br>ACCGCCCAGG<br>ATCCAGTGCA<br>GCCTTGATGG<br>ATGAAGTGTA   | CTGCCCTGCC<br>CCATGTACGA<br>AAGTCTTTGA<br>TGGTTGGCAT<br>TGAAGTGCTT   | CCAGTGGAGG<br>GGGGCTGTGG<br>CTCCTGCTG<br>CCTCCTGGGA<br>GGAAGACGAT  | ATTTACTCCT<br>ATGTCCTGCG<br>AATCTGAGCA<br>GTGATAGCAA<br>GAGGTGCAGA  | ATGCCGGCGA<br>TGTCGCAGAG<br>GCACATTGCA<br>TCTTTGTGGC<br>AGATGAGGAT  | 360<br>420<br>480   |
| 45   | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT<br>CACCGTTGGC   | ATCGTCAGCA<br>ACCGCCCAGG<br>ATCCAGTGCA<br>GCCTTGATGG<br>ATGAAGTGTA   | CTGCCCTGCC<br>CCATGTACGA<br>AAGTCTTTGA<br>TGGTTGGCAT   | CCAGTGGAGG<br>GGGGCTGTGG<br>CTCCTGCTG<br>CCTCCTGGGA<br>GGAAGACGAT  | ATTTACTCCT<br>ATGTCCTGCG<br>AATCTGAGCA<br>GTGATAGCAA<br>GAGGTGCAGA  | ATGCCGGCGA<br>TGTCGCAGAG<br>GCACATTGCA<br>TCTTTGTGGC<br>AGATGAGGAT  | 360<br>420<br>480<br>540  |
|  | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT<br>CACCGTTGGC<br>GGCTGTCATT   | ATCGTCAGCA<br>ACCGCCCAGG<br>ATCCAGTGCA<br>GCCTTGATGG<br>ATGAAGTGTA<br>GGGGGCGCGA   | CTGCCCTGCC<br>CCATGTACGA<br>AAGTCTTTGA<br>TGGTTGGCAT<br>TGAAGTGCTT<br>TATTTCTTCT   | CCAGTGGAGG<br>GGGGCTGTGG<br>CTCCTTGCTG<br>CCTCCTGGGA<br>GGAAGACGAT<br>TGCAGGTCTG   | ATTTACTCCT<br>ATGTCCTGCG<br>AATCTGAGCA<br>GTGATAGCAA<br>GAGGTGCAGA<br>GCTATTTTAG  | ATGCCGGCGA<br>TGTCGCAGAG<br>GCACATTGCA<br>TCTTTGTGGC<br>AGATGAGGAT<br>TTGCCACAGC  | 360<br>420<br>480<br>540<br>600<br>660  |
|  | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT<br>CACCGTTGGC<br>GGCTGTCATT<br>ATGGTATGGC   | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGCGCGA AATAGAATCG   | CTGCCCTGCC<br>CCATGTACGA<br>AAGTCTTTGA<br>TGGTTGGCAT<br>TGAAGTGCTT<br>TATTTCTTCT<br>TTCAAGAATT   | CCAGTGGAGG<br>GGGGCTGTGG<br>CTCCTTGCTG<br>CCTCCTGGGA<br>GGAAGACGAT<br>TGCAGGTCTG<br>CTATGACCCT   | ATTTACTCCT<br>ATGTCCTGCG<br>AATCTGAGCA<br>GTGATAGCAA<br>GAGGTGCAGA<br>GCTATTTTAG<br>ATGACCCCAG  | ATGCCGGCGA<br>TGTCGCAGAG<br>GCACATTGCA<br>TCTTTGTGGC<br>AGATGAGGAT<br>TTGCCACAGC<br>TCAATGCCAG  | 360<br>420<br>480<br>540<br>600<br>660<br>720   |
| 45<br>50   | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT<br>CACCGTTGGC<br>GGCTGTCATT<br>ATGGTATGGC<br>GTACGAATTT   | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGCGCGA AATAGAATCG GGTCAGGCTC  | CTGCCCTGCC<br>CCATGTACGA<br>AAGTCTTTGA<br>TGGTTGGCAT<br>TGAAGTGCTT<br>TATTTCTTCT<br>TTCAAGAATT<br>TCTTCACTGG   | CCAGTGGAGG<br>GGGGCTGTGG<br>CTCCTGGGA<br>CCTCCTGGGA<br>GGAAGACGAT<br>TGCAGGTCTG<br>CTATGACCCT<br>CTGGGCTGCT  | ATTTACTCCT ATGTCCTGCG AATCTGAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCTCT   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG   | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780  |
|  | GATCGGCGCC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT<br>CACCGTTGGC<br>GGCTGTCATT<br>ATGGTATGGC<br>GTACGAATTT<br>AGGTGCCCTA   | ATCGTCAGCA<br>ACCGCCCAGG<br>ATCCAGTGCA<br>GCCTTGATGG<br>ATGAAGTGTA<br>GGGGGGCGCGA<br>AATAGAATCG<br>GGTCAGGCTC<br>CTTTGCTGTT  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TTCAAGAATT TCTTCACTGG CCTGTCCCCG  | CCAGTGGAGG GGGGCTGTGG CTCCTTGCTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC   | ATTTACTCCT ATGTCCTGCG AATCTGAGCA GTGATAGCAA GAGGTGCAGA GCTATTTAG ATGACCCCAG GCTTCTCTCT TCTTACCCAA   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840   |
|  | GATCGGCGCC CAACATOGTG CACCGGGCAG AGCAACCCGT CACCGTTGGC GGCTGTCATT ATGGTATGGC GTACCGAATGC CTATCCAAAA  | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA ATGAAGTGTA GGGGGCGCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT CCTGCACCTT   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGATGGCAT TGAAGTGCTT TATTTCTTCT TTCAAGAATT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA   | CCAGTGGAGG GGGCTGTGG CTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACGTG   | ATTTACTCCT ATGTCCTGCG AATCTCAGCA GAGGTGCAGA GAGGTGCAGA GCTATTTAG ATGACCCCAG GCTTCTCTCT TCTTACCCAA TGACACAGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCACAAGGCG GCCAAAAGGAG   | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780  |
|  | GATCGGCGCC CAACATOGTG CACCGGGCAG AGCAACCCGT CACCGTTGGC GGCTGTCATT ATGGTATGGC GTACCGAATGC CTATCCAAAA  | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA ATGAAGTGTA GGGGGCGCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT CCTGCACCTT   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TTCAAGAATT TCTTCACTGG CCTGTCCCCG  | CCAGTGGAGG GGGCTGTGG CTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACGTG   | ATTTACTCCT ATGTCCTGCG AATCTCAGCA GAGGTGCAGA GAGGTGCAGA GCTATTTAG ATGACCCCAG GCTTCTCTCT TCTTACCCAA TGACACAGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCACAAGGCG GCCAAAAGGAG   | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840   |
| 50   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT  | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGCGCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TGAAACAAAC  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TTCAAGAATT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA  | CCAGTGGAGG GGGCTGTGG CTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTAGGCTGCT AAAAACAACC AGACTACGTG CATTGAGATA  | ATTTACTCCT ATGTCCTGCG AATCTGAGCA GCTGATAGCAA GCTATTTTAG ATGACCCCAG GCTTCTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCAAAAGGAG CATTAGGACC  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-   |
| 50   | GATCGGCGCC CAACATCGTC CACCGGGCAG AGCAACCCGT CACCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA CTATCCCAAAA AAAATCATGT TTAGAATTTT   | ATCGTCAGCA<br>ACCGCCCAGG<br>ATCCAGTGCA<br>GCCTTGATGG<br>ATGAAGTGTA<br>GGGGGCGCGA<br>AATAGAATCG<br>GGTCAGGCTC<br>CTTTGCTGTT<br>CCTGCACCTT<br>TGAAACAAC<br>GGGTATTGTA  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TTCAAGAATT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA AGAAATGGA ATCTAAAGTA  | CCAGTGGAGG GGGGCTGTGG CTCCTTGCTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTAGGCTGCT AAAACAACC AGACTACGTG CATTGAGATA TGTTATTACA   | ATTTACTCCT ATGTCCTGCG ATGTCTGCG ATCTGAGCA GTGATAGCAA GAGGTGCAGA GCTATTTAG GCTCTCTCT TCTTACCCAA TGACACAGAG TGACACAGAG ATATCATTAA AAACAAACAA  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCAAAAGGAG CATTAGGAAC ACAAACAAAA   | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900  |
|  | GATCGGCGC<br>CAACATCGTG<br>CACCGGGCAG<br>AGCAACCCGT<br>CACCGTTGGC<br>GGCTGTCATT<br>ATGGTATGGC<br>GTACGAATTT<br>AGGTGCCCTA<br>CTATCCAAAA<br>AAAATCATGT<br>TTAGAATTTT<br>AACCCATGTG  | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGGCGGGA AATAGAATCG GGTCAGGCTC CTTTGCTGT CCTGCACCTT TGAAACAAAC GGGTATTGTA TTAAAATACT   | CTGCCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTCTCT TTCAAGAATT TCTTCACTGG CCCTGCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA CAGTGCTAAA   | CCAGTGGAGG GGGCCTGTGG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AAGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTTA   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCCCCCCCCC  | ATGCCGCGA TGTCGCAGAG GCACATGCA TCTTTGTGC AGATGAGAT TTGCCAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCACAAGGAC CATAGGAAC TCTTCTTCC   | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080   |
| 50   | GATCGGCGCC CAACATCGTC CACCAGGGCAG AGCAACCCGTT CACCGGTTGGC GGCTGTCATT ATGGTATTGGC GTACGAAATTT AGGTTGCCCATA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTGTA GGGGGCGCGA AATAGAATCG GGTCAGCCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA TGAAACAAAC AGGGAAAATAACT AGAGAAATAACT AGGGAAGATT  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TTCAAGAATT TCTTCACTGG CCAGCGGGAA CCAACAGGAAATGGA ATCTAAAGTAA TTTCCATTTG TTTCACTGG TCAGCGGGAA TCTAAAGTAA TGAGGATAA TTTCCATTTG  | CCAGTGGAGG GGGCTGTGG CTCCTTGGTG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA CATGGCTTAA CATGTCTTAA   | ATTTACTCCT ATGTCCTGCG ATGTCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900  |
| 50   | GATCGGCGCC CAACATCGTC CACCAGGGCAG AGCAACCCGTT CACCGGTTGGC GGCTGTCATT ATGGTATTGGC GTACGAAATTT AGGTTGCCCATA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTGTA GGGGGCGCGA AATAGAATCG GGTCAGCCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA TGAAACAAAC AGGGAAAATAACT AGAGAAATAACT AGGGAAGATT  | CTGCCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTCTCT TTCAAGAATT TCTTCACTGG CCCTGCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA CAGTGCTAAA   | CCAGTGGAGG GGGCTGTGG CTCCTTGGTG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA CATGGCTTAA CATGTCTTAA   | ATTTACTCCT ATGTCCTGCG ATGTCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080   |
| 50   | GATCGGCGCC CAACATCGTC CACCGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTT AACCCAATGT TCAATATAGG CAAATGGGGG   | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGCCCGA AATAGAATCG GGTCAGCCTC CTTTGCTGTT CCTGCACCTT TGAAACAAAC GGGTATGTA TTAAAATACT TAAAATACT AAGGGAGATT AAGGGGTCCT ACGGCAACATT AAGGGGTCCT   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTGC CCTTAAATAT CCTTAAATAT   | CCAGTGGAGG GGGCCTTGGG CTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTAGGACCCT CTGGGCTCCT AAAAACAACC AAGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT  | ATTTACTCCT ATGTCCTGCG ATGTCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50<br>55   | GATCGGCGCC CAACATCGTC CACCGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTT AACCCAATGT TCAATATAGG CAAATGGGGG   | ATCGTCAGCA ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGCCCGA AATAGAATCG GGTCAGCCTC CTTTGCTGTT CCTGCACCTT TGAAACAAAC GGGTATGTA TTAAAATACT TAAAATACT AAGGGAGATT AAGGGGTCCT ACGGCAACATT AAGGGGTCCT   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TTCAAGAATT TCTTCACTGG CCAGCGGGAA CCAACAGGAAATGGA ATCTAAAGTAA TTTCCATTTG TTTCACTGG TCAGCGGGAA TCTAAAGTAA TGAGGATAA TTTCCATTTG  | CCAGTGGAGG GGGCCTTGGG CTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTAGGACCCT CTGGGCTCCT AAAAACAACC AAGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT  | ATTTACTCCT ATGTCCTGCG ATGTCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140   |
| 50<br>55   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTTT TAGCACATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATCAAGTGTA GGGGGCGCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA GGGAACATT AAGGGGTCC GCCAGTAAAA  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTACACGG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA ATCTAAAGTA TTTCCATTTG CCTTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCCTTGGG CTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTAGGACCCT CTGGGCTCCT AAAAACAACC AAGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT  | ATTTACTCCT ATGTCCTGCG ATGTCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50   | GATCGGCGCC CAACATCGTC CACCAGGGCAG AGCAACCCGT CACCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA AAAATCATGT TTAGGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO:   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG GCCTGATGG ATGAAGTGTA GGGGGCGCGCA AATAGAAATCG GGTCAGGCTC CTTTGCTGTT TCGAACAAAC GGGTATTGTA TTAAAATACT TAAAATACT AAGGGAAGATT AAGGGTCCT GCCAGTAAAA C108 DNA S  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCAGCGGGAA CCAAAATGGA ATCTAAAGTA ATCTAAAGTA TTTCCATAG ATCTAAAGTA TTTCCATAG CCTTAAATAT AAAAAAAAAA   | CCAGTGGAGG GGGCCTTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAAC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50<br>55   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATT AGGTGCCCTA ATATCAAAA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA ACCGCCCCAGG ATGAAGTGTA GGGGGCCCGA AATAGAAATCG GGTCAGGCTC CTTTGCTGTT TCTAAACAAAC GGGTATTGTA TTAAAATACT AGGGAAGATT AAGGGGTCCT GCCAGTAAAA C108 DNA S Id Accessio  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA ATCTAAAGTA ATCTAAAGTA TTCCATTTC CCTTAAATTA AAAAAAAAA equence n #: AF5089   | CCAGTGGAGG GGGCCTTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAAC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50<br>55   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATT AGGTGCCCTA ATATCAAAA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG GCCTGATGG ATGAAGTGTA GGGGGCGCGCA AATAGAAATCG GGTCAGGCTC CTTTGCTGTT TCGAACAAAC GGGTATTGTA TTAAAATACT TAAAATACT AAGGGAAGATT AAGGGTCCT GCCAGTAAAA C108 DNA S  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA ATCTAAAGTA ATCTAAAGTA TTCCATTTC CCTTAAATTA AAAAAAAAA equence n #: AF5089   | CCAGTGGAGG GGGCCTTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAAC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50<br>55   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATT AGGTGCCCTA ATATCAAAA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA ACCGCCCCAGG ATGAAGTGTA GGGGGCCCGA AATAGAAATCG GGTCAGGCTC CTTTGCTGTT TCTAAACAAAC GGGTATTGTA TTAAAATACT AGGGAAGATT AAGGGGTCCT GCCAGTAAAA C108 DNA S Id Accessio  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA ATCTAAAGTA ATCTAAAGTA TTCCATTTC CCTTAAATTA AAAAAAAAA equence n #: AF5089   | CCAGTGGAGG GGGCCTTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAAC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50<br>55<br>60   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATT AGGTGCCCTA ATATCAAAA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTGTA GGGGGCGCGA AATAGAATCGT GGTCAGCCTC CTTGCTGTT TGAAACAAAC GGGTATTGTA TTAAAATACTT AAGGGAAGATT AAGGGATCCT GCCAGTAAAA C108 DNA S Id Accessio. Lence: 98   | CTGCCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTCTTCT TCTACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA ATTTCAATTA CAGTGCTAAA TTTCCATTTG CCTTAAATAT AAAAAAAAAA   | CCAGTGGAGG GGGCTCTTGG CCTCCTTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA  | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAAACA  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCAAAAGGAC CATTAGGAC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT   | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50<br>55<br>60   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATT AGGTGCCCTA ATATCAAAA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTGTA GGGGGCCCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TCTACACTT TGAAACAAAC GGGTATGTA TAAAATACT AAGGGAAGATT AAGGGTAGTCT GCCAGTAAAA C108 DNA S id Accession Lence: 98   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA ATCTAAAGTA ATCTAAAGTA TTCCATTTC CCTTAAATTA AAAAAAAAA equence n #: AF5089   | CCAGTGGAGG GGGCCTTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTCCT AAAAACAAC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCAGCA GTGATAGCAA GAGGTGCAGA GCTATTTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG TCAATGCCAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200  |
| 50<br>55   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTT TAACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Ac: Coding sequence  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTGTA GGGGGGCGCGA AATAGAATCT CCTTGCTGTT CCTGCACCTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGTAGTA AGGGAAGATT CCAGCAGTAAAA C108 DNA S id Accessio uence: 98   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTTG CCTTAAATAT TATTCCATTTG CCTTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCTCTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC CATGACCT CATTGAGATA TGTTATTACA TATTACTGCT ATATAGATA TATTACTGCT ATATAGATA AAAAAAA  64 . 1   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCAC GTGATAGCAA GAGGTGCAGA GCTATTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA AATCAACAAGAG GTATATTTA TCCCATTGAG GTATATATAC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCAAAAGGAG CATTAGGAC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTCT  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1080<br>1140<br>1200<br>1237   |
| 50<br>55<br>60   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATTGGC GTACGAAATTT AGGTGCCCTA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Acc Coding sequ  1   CAGAGCCGCA   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGGCGCGA AATAGAATCG GGTCAGCCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGGTCCT GCCAGTAAAA C108 DNA S id Accessio Lence: 98  11   AGGGCAGGGA  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTAAGAATT TCTTCACTGG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTG CCTTAAATAT AAAAAAAAA equence n #: AF5089 1.531 21 AGGCCTCCCC   | CCAGTGGAGG GGGCTCTTGG CCTCCTTGGTG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC CATGGCTACT CATTGAGATA TGTTATTACA CATGGCTTAA CATGAGATA TGTTATTACA ATATACTGCT ATATAGATAT AAAAAAA 64.1 31 GCACGGTGGG   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCAGCA GAGGTGCAGA GCTATTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAAACA  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG CCTTCTGGG CACCAAGGCC GCCATCTGGG CACAAGGAC CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGCG   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200<br>1237   |
| 50<br>55<br>60   | GATCGGCGCC CAACATCGTG CACCGGTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA AAAATCATGT TTAGGAATTT AACCCAAGG CAAATGGGG ATTAAAAATA Seq ID NO: Nucleic Ac: Coding sequence  CAGAGCCGCA CAGAGCCGCA CGGGGACAGG   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ACCGCCCAGG ACCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGCGCGGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TCAAACAAAC GGGTATTGTA TTAAAATACT AAGGGAAGATT AAGGGAGATT AAGGGTCCT GCCAGTAAAA  C108 DNA S id Accessic Lence: 98  11    AGGCAAGGAA AGGCACGGA AGCGCAGGGA CACTCGGGCT  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCAGCGGGAA CCAAAATGGA ATCTAAAGTA ATTTCATAGA ATCTAAAGTA ATCTAAATAT AAAAAAAAAA   | CCAGTGGAGG GGGCCTTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTCCT AAAAACAAC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA  64.1  .  31    GCACGGTGGG GCACGGTGGG GCACGGTGGG GCTAGGGATG   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCTGCA GTGATAGCAA GAGGTGCAGA GCTTCTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTAT TCCCATTTATTAT GTATATTAC  41  GGAAAGCGGC TCCTCCTGGA   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA GCACATTGCACAGC TCATTGCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1080<br>1140<br>1200<br>1237   |
| 50<br>55<br>60   | GATCGGCGCC CAACATCGTG CACCGGTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA AAAATCATGT TTAGGAATTT AACCCAAGG CAAATGGGG ATTAAAAATA Seq ID NO: Nucleic Ac: Coding sequence  CAGAGCCGCA CAGAGCCGCA CGGGGACAGG   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ACCGCCCAGG ACCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGCGCGGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TCAAACAAAC GGGTATTGTA TTAAAATACT AAGGGAAGATT AAGGGAGATT AAGGGTCCT GCCAGTAAAA  C108 DNA S id Accessic Lence: 98  11    AGGCAAGGAA AGGCACGGA AGCGCAGGGA CACTCGGGCT  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCAGCGGGAA CCAAAATGGA ATCTAAAGTA ATTTCATAGA ATCTAAAGTA ATCTAAATAT AAAAAAAAAA   | CCAGTGGAGG GGGCCTTTGG CCTCCTTGGTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGGCTCCT AAAAACAAC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA  64.1  .  31    GCACGGTGGG GCACGGTGGG GCACGGTGGG GCTAGGGATG   | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCTGCA GTGATAGCAA GAGGTGCAGA GCTTCTCTCT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTAT TCCCATTTATTAT GTATATTAC  41  GGAAAGCGGC TCCTCCTGGA   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA GCACATTGCACAGC TCATTGCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC GCAAAAGGAG CATTAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200<br>1237   |
| 50<br>55<br>60<br>65   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  1   CAGAGCCGGCA CGGGGACAGG TGGACCCGCC  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATCAAGTGTA GCCTTGATGG ATAGAATCG AATAGAATCG GGTCAGGCTC CTTTGCTGTT CCTGCACCTT TGAAACAAAC GGGAACAATT AAGGGTGCT GCCAGTAAAA Clob DNA S Lid Accessic Lence: 98  11    AGCGCAGGAGA AGCGCAGGGA AGCGCAGGGA AGCGCAGGGA ATGGGCCAGGGA AGCGCAGGGA ATGGGCCAGGGA ATGGGCCAGGGA ATGGGCCAGGGA ATGGGCCAGGGA ATGGGGCAGGGA ATGGGGCAGGGA ATGGGGCAGGGA ATGGGGCAGGGA   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TTCATGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTG CCTTAAATAT TTTCCATTG CCTTAAATAT AAAAAAAAA equence n #: AF5089 1531  21   AGGCCTCCCC GGCACTGCCT TCTGGGGCT   | CCAGTGGAGG GGGCTGTGG CCTCCTTGCTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTC TATGACCCT CTGGGCTGCT AAAAACAACC CATGGCTTATACCGTG CATTGAGATA TGTTATTACA ATATACTGCT ATATAGATA TATTACTGCT ATATAGATA  64 . 1  31    GCACGGTGGG GCACGGTGGG GCACGGTGGG GCACGGGTGGG CTGCTGGCTGCCTGCTGCCTGCCTGCCTGCC   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCA GTGATAGCAA GAGGTGCAGA ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAACAA AAACAACAA GTATATATAC  41    GGAAAGCGGC TCGTCCTGGA GTTCTCGGA GTTCTCGGCT  | ATGCCGGCGA TGTCGCAGAG GCACATGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACCAAGGCC GCACAAGGAC CATAGGACC ACAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGGG TAAGGAGG TAAGGTGGCA  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1080<br>1140<br>1200<br>1237   |
| 50<br>55<br>60<br>65   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATTGGC GTACGAAATTTT AGGTGCCCTA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Ac: Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCCGCC CGCTTTCGCC   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTGTA GGGGGGCGCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGGTCCT GCAGTATAGTA AGGGAAGATT AAGGGGTCCT GCAGTAAAA  11   AGGCAGGGA ATGAGAGA ATGAGAG   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA ATCTAAAGTA ATTTCAATTG CCTTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCTGTGG CCTCCTGGGA GGAGAGCGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAACAACC CAGGCTACT CATGAGATA TGTTATTACTAC ATTATACTAC ATTATAGATA TATTACTGCT ATATAGATA  31   GCACGGTGGG GCTAGGGATG CTGCTGGCTGC CAGTGCCTCC CAGTGCCTCC CAGTGCCTCC CAGTGCCTCC CAGTGCCTCC CAGTGCCTCC CAGTGCCTCC CACTCCCTCTC CTCTCTCCTCC CTCTCTCTCT  | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCACAG GCCTTCTGGG CACAAGGCC GCAAAGAGAG CATTAGGAC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGCG TAAGGTGGCA TAAGGTGGCA CAAGGCACCC GCAGCGACCC  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200<br>1237   |
| 50<br>55<br>60   | GATCGGCGCC CAACATCGTC CACCAGGGCAG AGCAACCCGTTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA AAAATCATGT TTAGGAATTTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCCGCC TTCTCCTGGC TTCTCCTGGC   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ACCGCCCAGG ACCAGCCCAGG ATGAAGTGTA GGGGGGGCGCGCA ATGAACAATC GGTCAGCCTC TGAAACAAAC GGGTATTGTA TTAAAATACT AGGGAAGATT AAGGGTCGC GCCAGTAAAA C108 DNA S id Accessic Lence: 98  11    AGGCAGGGA AGCCGGGCA CACTGGGCCAGCA TGGCAGGCA CACTGGGCCAGCA ATGGGGCAGGA ATCGTGGCCAGCA ATCGTGGCCAGCA ATCGTGGCCAA ATCGTGGCCAGCA  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTCTTCT TCTTCACTGG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA ATTCCATTG CCTTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCCTTGG CCTCCTGGGA GGAAGACGAT TGCAGGTCTG CTATGACCCT CTGGCTGCT CAAAAACAACC CATGAGATA TGTTATTACA CATGAGATA TATTACTGCT ATATAGATAT AAAAAAA  64.1  . 31   GCACCGTGGG GCACGGTGGG GCTAGGGATG CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC  | ATTTACTCCT ATGTCCTGCG ATGTCCTGCG ATGTCTGAGCA GAGGTGCAGA GAGGTGCCAG GCTTCTCTT TCTTACCCAA ATGACCACAGAG CTATCATTAA AAACAAACAA TCTTATTTA TCCCATTGAG GTATATATAC  41    GGAAAGCGC TCGTCTCGGA GTTCTCTGGA GTTCTGGGCT CGGATCTGGT AGTGTAGATC  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA AGATGAGAT TTTGCACAGC TCAATGCAG GCCTTCTGGG CACCAAGGCC CACAAGCAC ACAAACAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGCG TAAGGTGCA TCTGGAGGGC TAAGGTGCA CGAACAAA TCTTCTTTCC TTGTTTTCT  CGGTGCAGCG TAAGGTGCAA TCTGGAGGGC TCTGGAGGGCA CCTGAGGAACAT   | 360<br>420<br>480<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1140<br>1200<br>1237  |
| 50<br>55<br>60<br>65   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  L CAGAGCCGGCA CGGGGACAGG TGGACCCGCC CGCTTTCGCC CTCTCCTGGC CACCGAAATT  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATCAAGTGTA GCCTTGATGG ATAGAATCGT AATAGAATCGT CCTTGCTGTT CCTGCACCTT TGAAACAATA GGGAACAATT AAGGGTGCT GCCAGTAAAA Clob DNA S Lid Accessic Lence: 98  11    AGCGCAGGAGAT AAGGGTCCT ATGGCAGT ATGGCAGGT ATGGCAGT ATGGCAGT ATGGCGCT ATGGCGCT ATCGTCGCAT TTCATCGCAA   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TTCATGG CCTGTCCCCG CCAGCGGGAA ACGTAAAATGCA ATCTAAAGTA TTTCCATTG CCTTAAATAT AAAAAAAAA equence n #: AF5089 1531  21   AGGCCTCCCC GGCACTGCCT TCTGGGGCT TCTGGGGCT TCTGGGGCT TCTGGGGCT TCTGGAAATG TTCCGAAATG TTCCGAGAATAA   | CCAGTGGAGG GGGCTGTGG CCTCCTTGCTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTC TATGACCCT CTGGGCTGCT AAAAACAACC CATGGCTTATATACA CATGGCTTATATACA ATATACTGCT ATATAGATA TATTACTGCT ATATAGATA  64 . 1  31    GCACGGTGGG GCACGGTGGG GCACGGGAGG CTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTAC CGGACCCTAAC GTTAGAAATC   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCAC GTGATAGCAA GAGGTGCAGA ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG GTATATATAC  41    GGAAAGCGGC TCGTCCTGGA GTTCTGGGCT CCGGATCTGGT AGTGTAGATA   | ATGCCGGCGA TGTCGCAGAG GCACATGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGAC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGCG TAAGGAGCC CTGAGAGCAC CTGAGAGCAC CTGAGACACAT ATGATGTTGA   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900-<br>960<br>1020<br>1140<br>1200<br>1237   |
| 50<br>55<br>60<br>65   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  L CAGAGCCGGCA CGGGGACAGG TGGACCCGCC CGCTTTCGCC CTCTCCTGGC CACCGAAATT  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATCAAGTGTA GCCTTGATGG ATAGAATCGT AATAGAATCGT CCTTGCTGTT CCTGCACCTT TGAAACAATA GGGAACAATT AAGGGTGCT GCCAGTAAAA Clob DNA S Lid Accessic Lence: 98  11    AGCGCAGGAGAT AAGGGTCCT ATGGCAGT ATGGCAGGT ATGGCAGT ATGGCAGT ATGGCGCT ATGGCGCT ATCGTCGCAT TTCATCGCAA   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TTCATGG CCTGTCCCCG CCAGCGGGAA ACGTAAAATGCA ATCTAAAGTA TTTCCATTG CCTTAAATAT AAAAAAAAA equence n #: AF5089 1531  21   AGGCCTCCCC GGCACTGCCT TCTGGGGCT TCTGGGGCT TCTGGGGCT TCTGGGGCT TCTGGAAATG TTCCGAAATG TTCCGAGAATAA   | CCAGTGGAGG GGGCTGTGG CCTCCTTGCTG CCTCCTGGGA GGAAGACGAT TGCAGGTCTC TATGACCCT CTGGGCTGCT AAAAACAACC CATGGCTTATATACA CATGGCTTATATACA ATATACTGCT ATATAGATA TATTACTGCT ATATAGATA  64 . 1  31    GCACGGTGGG GCACGGTGGG GCACGGGAGG CTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTCT CAGTGCCTAC CGGACCCTAAC GTTAGAAATC   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCAC GTGATAGCAA GAGGTGCAGA ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTTA TCCCATTGAG GTATATATAC  41    GGAAAGCGGC TCGTCCTGGA GTTCTGGGCT CCGGATCTGGT AGTGTAGATA   | ATGCCGGCGA TGTCGCAGAG GCACATGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGAC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGCG TAAGGAGCC CTGAGAGCAC CTGAGAGCAC CTGAGACACAT ATGATGTTGA   | 360<br>420<br>480<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1140<br>1200<br>1237  |
| 50<br>55<br>60<br>65   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTGGC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Acc Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCGCC CGCTTTCGCC TTTCCCTAGCT TCACCGAAGTT AGCTTATGTG  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTGTA GGGGGGCGCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGGTCCT GCAGTAATAA C108 DNA Si LI AGGGCAGGGA LI AGGGCAGGGA CACTGGGCT TGAACAAC GGTATAGTA AGGGGAGGA TCGGGCT TGCCCACGT ATCGGGCT TGTCCCACGT TTCATCGCAA ATCGTGGCAT ATCGTGGCAT TCATCGCAA GGACTAGCAA GGACTAGCAA GGACTAGAGA  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA ATCTAAAGTA ATTTCAATTG CCTTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCTGTGG CCTCCTTGGTG CCTCCTGGGA GGAGACGATT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAACAACC CAGGCTACT CATGAGATA TGTTATTACTACA TATTACTGCT ATATAGATA  31   GCACGGTGGG GCTAGGGATG CTGCTGCT CAGGCTTCC CAGGCTCCT CAGGCTTCC CAGGCTTCC CAGGCTTCC CAGGCTTCC CAGGCTTCC CAGTCCCTCT CAGTACCATC CTGGAATC CTGGAATC CTGTGGAATC CTGTGGAATC CTTGGAATTC   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACAAGGCC GCAAAGCAAA  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1080<br>1140<br>1200<br>1237   |
| 50<br>55<br>60<br>65   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTTGGC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCGCC CGCTTTCGCC TTCTCCTGGC CACCGAAATT AGCTTTATGTG TAAAGCATTT  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGGCGCGA AATAGAATCGT GGTCAGCCTC TTGAACAAAC GGGTATTGTA TTAAAATACTT AGGGAAGATT AAGGGGTCCT GCCAGTAAAA C108 DNA S id Accessio Lence: 98  11   AGGCCAGGGA ATCGGGCT ATCGTGGCT ATGGCCAGGA ATCGGGCT ATCGTGGCAT ATCGTGAAAACC   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTACTGG CCTGTCCCCG CCAGCGGGAA ACGTACAAAAAAAAAA   | CCAGTGGAGG GGGCTTTGG CCTCCTTGGGA GGAGAGCCAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACGTG CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA  64.1  . 31   GCACGGTGGG GCTAGGGATG CTGCTGGGTTGG CTGCTGGCTGG CTGCTGGCTGG CTGCTGGCTG  | ATTTACTCCT ATGTCCTCCCT ATGTCCTCCCCCCCCCC  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGAT TTGCCACAG GCCTTCTGGG CACCAAGGCC GCACAAGGAC CATAGGAC ACAAACAAA TCTTCTTTCT TAATCATACT ATGTTTTTCT  51   COGTGCAGCG TAAGGTGGCA TCTGGAGGGC GCAGCAACCC CTGAGAACAT ATGATGTTGA  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1080<br>1140<br>1200<br>1237   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | GATCGGCGCC CAACATCGTC CACCGTTGGC GGCTGTCATT AGGTTATGGC GTACGAATTT AGGAATTT AACACCATGT TTAGGAATTT AACACCATGT TCAATAAAATA Seq ID NO: Nucleic Aci Coding sequ  CAGAGCCGCA CGGGGACAGG TGGACCCGCC TCTCCTGGC TTCTCCTGGC CACCGAATT AGCTTATGTG TAAAGATT AGCTTATGTG TTTTCTTGGC TAGCTTTTGTCT TAGCTTTTTTTT GAGTTTGTCT   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ACCGCCCAGG GCCTTGATGG GCCTTGATGG ATGAAGTGTA GGGGGCGCCGA AATAGAATCG GGTCAGGCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA AAGGGAAGATT AAGGGAAGATT AAGGGAAGATT AAGGGATATAAA LCT CCAGCAGTAAAA  C108 DNA S LI ACCGGGCAGGAA CACTGGGCT ATCGGCGCT ATCGGGCT ATCGGGCT ATCGGGCT ATCGGGCT ATCGTCACGT ATCGTCACAGT TTCATCGCAA AGGGAAACAT TTCATCGCAA AGGGAAACAT   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTCTTCT TCTTCACTGG CCAGCGGGAA CGAAAATGA ATCTAAAGTA ATCTAAAGTA ATCTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCTGTGG GGGGCTGTGG CTCCTTGGTGA CCTCCTGGGAA GGAAGACCAT TGCAGGTCTG CTAGGACCCT CTGGGCTGCT AAAAACAACC CAGTCTGG CATTAGATA TGTTATTACA CATGGCTTAA AAAAAAA  64.1  31  GCACGGTGGG GCACGGTGGG GCACGGTGGG GCACGGTGGG GCACGGTGGG GCTAGGGATC CTGGGCTTACTAGAAATC TGTTAGAAATC TTAGAATCT TGTGATTCT TGTGCATTCT TGCACTCGTT TGACTTGTCT   | ATTTACTCCT ATGTCCTGCT ATGTCCTGCG ATGTCTGAGCA GAGGTGCAGA GCTATTTTAG ATGACCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTA TCCCATTGAG GTATATATAC  41    GGAAAGCGC TCGTCCTGGA GTTGTGGGCT CGGATCTGGT CGGATCTGGT AGTGTAGATC ATCAACGAAG GAATTAAAAT ATCAACGAAG GAATTAAAAT AAACTAACCGAA GAACTGATCC  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC CCAAAAGGAC ACAAACAAA TCTTCTTTCC  S1   CGGTGCAGCG TAAGGTGCA TCTGGAGGGC TAAGGTGCA TCTGGAGGGC CCTGAGGAACAT ATGATTTA ATGTTTTA ATGTTTTA TTGTGGCCA CTGGGGAACAT ATGATGTTGA TGGTGGCCAA CTGGTGGCCAA CTGGTGGCCAA  | 360<br>420<br>480<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1120<br>1237  |
| 50<br>55<br>60<br>65   | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGGCAG AGCAACCCGT ATGGTATGGC GGTATCATT AGGTGCCCTA CTATCCAAAA AAAATCATGT TAAAATCATGT TAAAATCATGT TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Ac: COding sequilibrian  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCTTGATGG ATCAGAGTATA GCGCTGATGA AATAGAATCTA GGGCAGCCTC CTTTGCTGTT TCAAACAAAC GGGTATTGATA AGGGAAGATT AAGGGGTCC CTAAACAAAC CIOR DNA SI AGGCAGGGC LI AGCGCAGGGA ACCTGGGCT TTAAACAAC CACTGGGCT TTAACAAC AGGAAGAAT AGGGGAGGA CACTGGGCT TTCCACGGCT TTCATCGGCTA TTCATCGGCAA CGGCTGAGAA CTGAAAAACAT TGCTCCTGTG   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTTG CCTTAAATAT AAAAAAAAA  EQUENCE #: AF5089 1531  21    AGGCCTCCCC GGCACTGCCT TCTGGGGCTT CCTGCAAATG TCCGAGAATA ACAGTACAAA ATCTGACAAT ACCAGAAAAA ATCTGACAAT TCCGTCACCT ACATTATGTG  | CCAGTGGAGG GGGCTGTGG CCTCCTTGCTG CCTCCTGGGA GGAGAGCGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC CATGGCTTATACGTG CATTGAGATA TGTTATTACA TATTACTGCT ATATAGATA  64.1  . 31   GCACCGTGGG GCTAGGGATGG CTGCTGGCTGC CAGTGCCTCT CAGTGCCTCT CAGTGCTTA TGTGAAATC CTGCTGCTGCTGC CAGTGCCTAC CAGTGCCTAC CAGTGCCTAC CAGTACAAT TGCACTTGACT TGACTACAAT TGACTTGTCT GATCAAGACT GATCAAGACT GATCAAGACT GATCAAGACT GATCAAGACT GATCAAGACT GATCAAGACT CTTTGCTT  | ATTTACTCCT ATGTCCTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCA GCTGATAGCAA GAGGTGCAGA GCTATTTAG GCTATTTAG TCATCACT TCTTACCCAA AAACAACAA AAACAACAA TCATATTTA TCCCATTGAG GTATATATA TCCCATTGAG GTATATATAC  41    GGAAAGCGGC TCGTCCTGGA GTTCTGGGCT CGGATCTGGT AGTTATAGATC ATCAACGAAG GGATTAAAAT TTTACCCGAA GAACTGATCC CTCCAAGAGG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACAAGGCC GCAAAAGGAG CATTAGGAC ACAAACAAAA TCTTGTTTCT  51   CGGTGCAGG TAAGGAGC GCAGGGACCC CTGAGAACAT ATGTTTTGT ATGTTTTGAGACGA TCTGGAGACAT ATGTGTGAGACAT ATGTGTGCAC TCTGGAGACAT ATGTGGCCAA CCAAACTGAC TGGTGGCAA CTGAAACTGAC TGGTGGGCAA CTGAAACTGAC  | 360<br>420<br>480<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1120<br>1237  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGGCAG AGCAACCCGT ATGGTATGGC GGTATCATT AGGTGCCCTA CTATCCAAAA AAAATCATGT TAAAATCATGT TAAAATCATGT TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Ac: COding sequilibrian  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCTTGATGG ATCAGAGTATA GCGCTGATGA AATAGAATCTA GGGCAGCCTC CTTTGCTGTT TCAAACAAAC GGGTATTGATA AGGGAAGATT AAGGGGTCC CTAAACAAAC CIOR DNA SI AGGCAGGGC LII AGCGCAGGGA ACCTGGGCT TTGAAACAAC CGGTTATGTA AGGGGAGGAC TTCATCGGCT TTTAAATACT AGGGAGGAGACATT TTCATCGGCT TTCATCGGCT TTCATCGGCT TTCATCGCAA CGACTGAGAA CCTGAAAAACAT TGCTCCTGTG   | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTTG CCTTAAATAT AAAAAAAAA  EQUENCE #: AF5089 1531  21    AGGCCTCCCC GGCACTGCCT TCTGGGGCTT CCTGCAAATG TCCGAGAATA ACAGTACAAA ATCTGACAAT ACCAGAAAAA ATCTGACAAT TCCGTCACCT ACATTATGTG  | CCAGTGGAGG GGGCTGTGG CCTCCTTGCTG CCTCCTGGGA GGAGAGCGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC CATGGCTTATACGTG CATTGAGATA TGTTATTACA TATTACTGCT ATATAGATA  64.1  . 31   GCACCGTGGG GCTAGGGATGG CTGCTGGCTGC CAGTGCCTCT CAGTGCCTCT CAGTGCTTA TGTGAAATC CTGCTGCTGCTGC CAGTGCCTAC CTGCTGCTTC CAGTACAAT TGTGAATTTCTCT TGCAATCAAT TGACTTGTCT GATCAAGACT CTTTGCTT  | ATTTACTCCT ATGTCCTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCA GCTGATAGCAA GAGGTGCAGA GCTATTTAG GCTATTTAG TCATCACT TCTTACCCAA AAACAACAA AAACAACAA TCATATTTA TCCCATTGAG GTATATATA TCCCATTGAG GTATATATAC  41    GGAAAGCGGC TCGTCCTGGA GTTCTGGGCT CGGATCTGGT AGTTATAGATC ATCAACGAAG GGATTAAAAT TTTACCCGAA GAACTGATCC CTCCAAGAGG  | ATGCCGGCGA TGTCGCAGAG GCACATTGCA AGATGAGGAT TTGCCACAGC TCAATGCCAG GCCTTCTGGG CACCAAGGCC CCAAAAGGAC ACAAACAAA TCTTCTTTCC  S1   CGGTGCAGCG TAAGGTGCA TCTGGAGGGC TAAGGTGCA TCTGGAGGGC CCTGAGGAACAT ATGATTTA ATGTTTTA ATGTTTTA TTGTGGCCA CTGGGGAACAT ATGATGTTGA TGGTGGCCAA CTGGTGGCCAA CTGGTGGCCAA  | 360<br>420<br>480<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1120<br>1237  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTGGCC GGCTGTCATT ATGGTATGGC GTACGAAATTT AGGTGCCCTA AAAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Acc Coding sequ CAGAGCCGCA CGGGGACAGG TGGACCGCC TCCCTGGCC TTCTCCTGGCC TTCTCCTGGCC TTCTCCTGGCC TTCACTTATTG TAAAGCATTT GAGTTTGTCT TCACATTACT TCCATTTACT TCACATACT TCCACTACT TCCACTACAC TCCACACACT TCACCGCACACT TCACCGGCACACT TCCACCACACACT TCACCACACACT TCACCACACACT TCACCACACACT TCCACCACACACT TCACCACACACT TCCACCACACACT TCCACCACACACT TCACCACACACT TCCACCACACACT TCACCACACACT TCACCACACACA  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTTA GGGGGGCGCGA AATAGAATCT CCTGCACCTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGGTCCT GCCAGTAAAAA  LI AGGCAGCGC ATCGGGCT TTCAACCACT TTAAATATAT TTAAATATAT AGGGGAAGATT AAGGGGTCCT ACCGGCT ATCGCGCT ATCGGCCT TCATCGCAGT ATCGTGGCAT ATCGTGGCAT ATCGTGGCAT ATCGTGGCAT ATCGTGGCAT ATCGTGGCAT ATCGTGGCAT ATCGTGGCAT ATCGTGAGAA CTGAAAAACA AGGACTAGAAAACA AGGACTTTGT CCAGGATTTGT CCAGGATTTTGT CCAGGATTTGT CCAGGATTTTT CCAGGATTTTT CCAGGATTTTT CCAGGATTTTT CCAGGATTTTT CCAGGATTTTT CCAGGATTTTT CCAGGATTTTT CCAGGA | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGA ATCTAAAGTA TTTCCATTG CCTTAAATAT AAAAAAAAA CQUENCE n #: AF5089 1.531 21   AGGCCTCCCC GGCACTGGCT TCTGGGGGTT TCTGGGGGTT CCTGCAAATG TTCCGAAATG ATCTGCAAATG ATCTGCAAATG ATCTGCAAATG ATCTGCAAATG ATCTGCAAATG ATCTGCAAATG ACTCTCCCAAATG TCCAGCACTCCA ACATTATCTG ACTCTCAAATGT ACACTTACCTG ACTTACCTG ACTTCCCAAA   | CCAGTGGAGG GGGCTGTGG CCTCCTTGGGA GGAGAGCCAT CCTGGGAGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACCGT CATTGAGATA TGTTATTACA CATGGCTTAA AAAAAA  64.1   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCACAGG CCTTCTGGG CACCAAGGCC GCACAAGGAC CATAGGAC ACAAACAAAA TCTTCTTTCT ATGTTTTCT  51   CGGTGCAGCG TAAGGACCA TCTGGAGGGC CCAGGACACA ATGATGTTGA TCTGGAGGGC CTGAGAACAT ATGATGTTGA TGTGGTCAA ACAAACTGAC CGTGGGCAAA CCAAACTGAA CCCTGGGCAAA   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>9900-<br>1080<br>1140<br>1200<br>1237   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGTT CACCGGTCAGT ATGGTATGGC GGTAGTCATT ATGGTATGGC GTACCAAAA AAAATCATGT TTAGAATTTT AACCCATGTG CCAATAAAAAT Seq ID NO: Nucleic Aci Coding sequ  L CAGAGCCGCA CGGGACAGG TGGACCGCC CGCTTTCGCC TCCTCGGC CACCGAAATT AGCTTATGTG TAAACATT TCGATTTAGTG TAAACATT TCCATTTACT TCCATTTACT TCCATTTACT TCCATTACAA TCCAGACACT CCTGCAGATA  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATCAAGTGTA GCCTTGATGG ATAAGATCG GGTCAGGCTC CTTTGCTGTT TGAAACAAC CTGACCTT TGAAACAAC TTAAAATACT AGGGAACATT AAGGGTCC CTGCACGTAAAACAC C108 DNA S LI AGCCCAGTAAAA C108 DNA S LI AGCCCAGGCA CACTAGGGCT ATGCGCGCT ATGCGCGCT ATGCGCGCT ATGCGCGCT ATGCGCGCT TTCATCGCAA GGACTGAGAA CTGAAAACAC TGAAAAACAT TGCTCCTGGC CAGGATTTGT CACGATTGTC CAGGATTTGT CACGATTGTC CACGATTTGT CACGATTTGTC CCCCAATTTGTC CCCAATTTGTC CCCAATTTCTC CCCAATTTGTC CCCAATTTGTC CCCAATTTGTC CCCAATTTGTC CCCAATTTGTC CCCAATTTGTC CCCAATTTCTC CCCAATTCTC CCCAATTTCTC CCCAA | CTGCCTGCC CCATGTACGA AAGTCTTGA TGGTTGGCAT TGAAGTGCTT TTATTCTTCT TTCAAGAATT TCTTCACTGG CCCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTG CCTTAAATAT AAAAAAAAA equence n #: AF5089 1531  21   AGGCCTCCCC GGCACTGGCT TCTGGGGCT TCTGGGGCT TCTGGGGCT TCTGGAATG TCCTGCAAATG TCCTGCAAATG TTCCAGAAAAG ATCTGACAAT TCCAGAAAAG ATCTGCACACT ACATTATGTG ACTGCCTCA ACTGCATTA   | CCAGTGGAGG GGGCTGTGG GGGAGCTGTGG CCTCCTGGGA GGAAGACGAT TGCAGGTCTC TATGACCCT CTGGGCTGCT AAAAACAACC ATGTATATACA ATGTATATACA ATATTACTGCT ATATACTGCT ATATACTGCT ATATACTGCT ATATACTGCT ATATACTGCT GCACGGGGGGGGGG  | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACCAAGGCC GCACAAGGAC CATAGGAC ACAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGCG GCAGGACCC CTGGAGACAT ATGATGTTGA TCTGGACCA TCTGGAGCGC GCAGCACCC CTGGAACAT ATGATGTTGA TTGTGGCTCA ACAACTGAC TGGTGGCCAA CTAATCCAG CCTGGCAAA CTAATCCAG CCTGCCAAA ACAACTGAC TGGTGGCCAA CTAATCCAG   | 360<br>420<br>480<br>540<br>660<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1237  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | GATCGGGGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGGCAG AGCAACCCGT ATGGTATGGC GGTATCATT AGGTGCCCTA CTATCCAAAA AAAATCATGT TTAGAATTT TAGAATTTT AACCCATGTG TCAATAAAAAT Seq ID NO: Nucleic Ac: COding sequilibrian Sequili | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG GCTTGATGG ATCAGAGTATA GCGCTGATGA AATAGAATCTA GGGCAGCCTC CTTTGCTGTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGTCC TTAAAATACT AGGGAAGATT AAGGGTCCT GCAGTAAAA  C108 DNA S: Li AGCGGAGGA AGCAGGGA TGTCAGGCT TTCATCGGCT TTCATCGGCT TTCATCGGCT TTCATCGGCT TTCATCGCAA CGGCTGAGAA CTGAAAAACA TGGACTGAGAA TGGTCCTCTG CAGGATTTGT CAGGATTGTC CAGGATTTGT CAGGATTTGT CAGGATTTGT CAGGATTGTT CAGATTGTT CAGGATTGTT CAGGATTGT CAGATTGT CAGGATTGT CAGGATT CAGGATT CAGGATT CAG | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTCAAAGT TTTCATTG CCTTAAATAT AAAAAAAAA  EQUENCE #: AF5089 1531  21    AGGCCTCCCC GGCACTGCCT TCTGGGGCTT CCTGCAAATG TTCCGAGATT TCCGAGATA ACTGCACAA ATCTGACAAT ACCAGAAAAG ATCTGACAAT CCTGCACAAT CCTGCACAAT CCTGCACACT ACATTATGCTG ACTTGCCAT CCTTTACCTGCA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACA CCTTTACCCTCCACAC CCTTTACCCTCCACC CCTTTACCCTCACC CCTTTACCCTCCACC CCTTTACCCTCCACC CCTTTACCCTCCACC CCTTTACCCTCCACC CCTTTTACCCTCCACC CCTTTTACCCTCCACC CCTTTTACCCTCCACC CCTTTTACCTCCACC CCTTTTTCCCTCCC | CCAGTGGAGG GGGCTGTGG CCTCCTTGCTG CCTCCTGGGA GGAGAGCGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAACAACC CATGGCTTCT CATTGAGATA TGTTATTACA TATTACTGCT ATATAGATA TATTACTGCT ATATAGATA  64.1   | ATTTACTCCT ATGTCCTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCA GCTGATAGCAA GAGGTGCAGA GCTATTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TCACACAGAG CTATCATTAA AAACAACAA TCTTATTTA TCCCATTGAG GTATATATAA GTATATATAC  41    GGAAAGCGGC TCGGTCTGGA GTTCTGGGT CGGATCTGGT AGTTTAGATC ATCAACAAA GGATTAAAAT TTTACCCGAA GAACTGATCC GCCCCCTA GGTCGCACCTA GGTCATCCGG AGAATATTC GCCCACCTA  | ATGCCGGCGA TGTCGCAGAG GCACATGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACCAAGGCC GCACAAGGCC GCAAAAGGAG CATTAGGAC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTCT  51   CGGTGCAGGC GCAGGGACCC CTGAGAACAT ATGTGTGGAC ACAAACTGAC TGGTGGCCAA ACAACTGAC CCTGGCAAA ACCTCACTGT TTCCTAATAT  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1237  |
| 50<br>55<br>60<br>65<br>70                                       | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTGGCC GGCTGTCATT ATGGTATTGGC GTACGAAATTTT AGGTGCCCTA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Acc Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCCGCC CGCTTTCGCC TTCTCCTGGC CACCGAAATT AGCTTATGTG TAAAGCATTT GAGTTTGTC TCCATTTACA TCCAGACACT CCTGCAGATA TCCAGACACT CCTGCAGATA TCCAGACACT CCTGCAGATA GGAGGAAGGA GGAGGAAGGA GGAGGAAGGA GGAGGA  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTATA GGGGGGCGCGA AATAGAATCT CCTGCACCTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGGTCCT CAGGACT LENCAGACA LENCAGACAC LI AGGGAAGATT AGGGAAGAT AGGGCAGGGA CACTCGGGCT TGTCCCACGT ATCGCGCT TTCATCGCAA ATCGGGCT TTCATCGCAA ATCGGGCT TTCATCGAAAAC AGGAAAAACT AGGAAAAACT ATCGGACT TCCCACGT TTCATCGAAA AGGAAACATT TCATCGCAA AGGAAACATT TCATCTGTAACC CCCAATTGTC CAGGATTTGT CATTGTTAACC GTTGGTAACC   | CTGCCTGCC CCATGTACGA AAGTCTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTAAGAATT TCTTCACTGG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA AAAAAAAAAA  | CCAGTGGAGG GGGCTGTGG CCTCCTTGGTG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CAAAACAACC CAGGCTACT CAGGCTACT CAGGCTAC CATGCATA TATTACTGCT ATATACTGCT ATATACTGCT ATATAGATA TATTACTGCT ATATAGATA  31   GCACGGTGGG GCTAGGGATG CTGCTGGCTG CAGTGCCTCT GGAGCTAAC TGTTAGAATC TGTGAATCT TGACAATCTGTCAACACT TGACAATCTGTCAAACACT TGACAATCTGTCAAACACT TGAAAACACT TGAAAACCT TGAAAACACT TGAAAACACT TGAAAACCT TGAAAACCT TGAAAACCT TGAAAACACT TGAAAACACT TGAAAACACT TGAAAACACT TGAAAACACT TGAAAACACT TGAAAACATATGAAT | ATTTACTCCT ATGTCCTCCCT ATGTCCTCCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACAAGGCC GCAAAGCAGA CATAGGAC ACAAACAAAA TCTTCTTTCT TAATCATACT ATGTTTTCT  51   CGGTGCAGCG GCAGCGC GCAGCGCC CTGAGAACAT ATGTCTTCATTAC TTGTGGGCCA ACAACTGAC TGGTGGCCAC CCTGGAGACAT ATGTGTTTAC ATGTTTCA ATGTTCCAACACGG CCCTGCCAAA ACCTCACTGT TTCCTAATAT TCCTCAATAT TCCTCAATAT TCCTCAATAT TCCTCAACGGG  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1237  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA AAAATCATGT TTAGAATTTT AACCCATGGG CAAATGGGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCGCC TCTCTCGCC CGCTTTGGCC TCTCTCGCC CACCGAATT AGCTTATGTG TAAACCATTT GAGTTGTCT TCCATTTACA TCCAGAGCACT CCTGCAGATA GGAGGACACT CCTGCAGATA GGAGGACACT CCTGCAGATA GGAGGACGGAT CCTGCAGATA GGAGGAAGGA GTATTGGGAT CCTCTTAACG CTCCTTAACG CTCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG TCCTTAACG TCCCTTAACG CTCCTTAACG TCCTTAACG TCCTTAACG TCCCTTAACG TCCCTTAACG TCCTTAACG TCCCTTAACG TCCTTTAACG TCCTTTACCT TCCCTTAACG TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCCTTTAACG TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTTTTTT   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTTA GGGGGGCGCGA AATAGAATCT TGAAACAAAC GGGTATTGTA TTAAAATACT AGGGAAGATT AAGGGTGCT GCCAGTAAAA C108 DNA S id Accessic Lence: 98  11    AGGGCAGGGA AGGCCAGGGA CACTCGGGCT ATCGTGGCAT ATGTGCAA CGATTACAAAAAC CGATTACAAAAAC CGATTACAAAAAC AGGAAACATT TCATCGCAA CGATTACATACAA AGGAAACATT TGCTCCTCTGG CAGGTTTTCA CAGGATTTGT AAGTCTAACA ATGATGAACA ATGATGAACA ATGATGAACA ATGATGAACA ATGATGAACA ATGATTACA ATGATGAACA ATGATTGTAACC ATAACTAACA   | CTGCCTGCC CCATGTACGA AGGTTTGGCAT TGAAGTGCTT TATTCTTCT TCTTCACTGG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA ATTCCATTG CCTTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCTGTGG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGCTGCT CTGGCTGCT CTGGCTGCT ANAAACAACC CATGAGATA TGTTATTACA CATGAGATA TGTTATTACA CATGAGATA  31    GCACCGTGGG GCTAGGGATG GCAGGGATG TGGAGCCTCT GGAGCCTAC GGAGCCTAC TGTGGATCT TGTAGAATC TGTAGAATC TGACATCAT TGACATCAT TGACATCAT TGACATCAT TGACATCT TAAAACAC TTAAAACAC TTAAAACAC TTAAAAACAC TTAAAAACAC TTAAAAACAC TGACAACACT TGACATCT TGAAAACAC TGCAAAACAC TGCAAACACT TGCAAACACT TAGAAACAC TAGAAACAC TAGAAGACT TAGAAGTGGG  | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA AGATGAGAT TTTGCACAGC TCAATGCAGG GCCTTCTGGG CACCAAGGCC CACAAGGAC CATAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGGG TAAGGTGCA CGAGAGCAC CTAGGACCA CTAGAACAAA ATGTTTTT TTTGGCTCA TTGTGGCTCA TGGTGGCAA ACTAATCTAA ACCACAGGG CCTTGCAACAT TTCCTAATAT ACACACAGGG CTTGTGGGCC CTTGGACAGC CCTGGCAAA ACCTCACTGT TTCCTAATAT ACACACAGGG CTTGTGTGGC CTTGTTGTGCC CTTGTTGGC CTTGTTGGC CTTGTTGGCC CTTGTTGGC CTTGTTGGCC CTTGTTGGCC CTTGTTGGCC CTTGTTGGCC CTTGTTGGCC CTTGTTGTGGC CTTGTTGGCC CTTGTTGCC CTTGTTGC CTTGTTGCC CTTGCC CTTGTTGCC CTTTTTTTT | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1237  |
| 50<br>55<br>60<br>65<br>70                                       | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA AAAATCATGT TTAGAATTTT AACCCATGGG CAAATGGGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCGCC TCTCTCGCC CGCTTTGGCC TCTCTCGCC CACCGAATT AGCTTATGTG TAAACCATTT GAGTTGTCT TCCATTTACA TCCAGAGCACT CCTGCAGATA GGAGGACACT CCTGCAGATA GGAGGACACT CCTGCAGATA GGAGGACGGAT CCTGCAGATA GGAGGAAGGA GTATTGGGAT CCTCTTAACG CTCCTTAACG CTCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG CTCCTTAACG TCCTTAACG TCCCTTAACG CTCCTTAACG TCCTTAACG TCCTTAACG TCCCTTAACG TCCCTTAACG TCCTTAACG TCCCTTAACG TCCTTTAACG TCCTTTACCT TCCCTTAACG TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCCTTTAACG TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTACCT TCCTTTTTTTT   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ACCGCCCAGG GCCTTGATGG ATGAAGTTA GGGGGGCGCGA AATAGAATCT TGAAACAAAC GGGTATTGTA TTAAAATACT AGGGAAGATT AAGGGTGCT GCCAGTAAAA C108 DNA S id Accessic Lence: 98  11    AGGGCAGGGA AGGCCAGGGA CACTCGGGCT ATCGTGGCAT ATGTGCAA CGATTACAAAAAC CGATTACAAAAAC CGATTACAAAAAC AGGAAACATT TCATCGCAA CGATTACATACAA AGGAAACATT TGCTCCTCTGG CAGGTTTTCA CAGGATTTGT AAGTCTAACA ATGATGAACA ATGATGAACA ATGATGAACA ATGATGAACA ATGATGAACA ATGATTACA ATGATGAACA ATGATTGTAACC ATAACTAACA   | CTGCCTGCC CCATGTACGA AGGTTTGGCAT TGAAGTGCTT TATTCTTCT TCTTCACTGG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA ATTCCATTG CCTTAAATAT AAAAAAAAAA  | CCAGTGGAGG GGGCTGTGG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGCTGCT CTGGCTGCT CTGGCTGCT ANAAACAACC CATGAGATA TGTTATTACA CATGAGATA TGTTATTACA CATGAGATA  31    GCACCGTGGG GCTAGGGATG GCAGGGATG TGGAGCCTCT GGAGCCTAC GGAGCCTAC TGTGGATCT TGTAGAATC TGTAGAATC TGACATCAT TGACATCAT TGACATCAT TGACATCAT TGACATCT TAAAACAC TTAAAACAC TTAAAACAC TTAAAAACAC TTAAAAACAC TTAAAAACAC TGACAACACT TGACATCT TGAAAACAC TGCAAAACAC TGCAAACACT TGCAAACACT TAGAAACAC TAGAAACAC TAGAAGACT TAGAAGTGGG  | ATTTACTCCT ATGTCCTCCT ATGTCCTCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA AGATGAGAT TTTGCACAGC TCAATGCAGG GCCTTCTGGG CACCAAGGCC CACAAGGAC CATAGGACC ACAAACAAAA TCTTCTTTCC TAATCATACT ATGTTTTTCT  51   CGGTGCAGGG TAAGGTGCA CGAGAGCAC CTAGGACCA CTAGAACAAA ATGTTTTT TTTGGCTCA TTGTGGCTCA TGGTGGCAA ACTAATCTAA ACCACAGGG CCTTGCAACAT TTCCTAATAT ACACACAGGG CTTGTGGGCC CTTGGACAGC CCTGGCAAA ACCTCACTGT TTCCTAATAT ACACACAGGG CTTGTGTGGC CTTGTTGTGCC CTTGTTGGC CTTGTTGGC CTTGTTGGCC CTTGTTGGC CTTGTTGGCC CTTGTTGGCC CTTGTTGGCC CTTGTTGGCC CTTGTTGGCC CTTGTTGTGGC CTTGTTGGCC CTTGTTGCC CTTGTTGC CTTGTTGCC CTTGCC CTTGTTGCC CTTTTTTTT | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1020<br>1140<br>1200<br>1237   |
| 50<br>55<br>60<br>65<br>70                                       | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTGGC GGCTGTCATT ATGGTATGGC GTACGAATTT AGGTGCCCTA TTAGAATTT TAGAATTT TAGAATTT TAGAATTT AACCCATGTG TCAATATAGG CAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Ac: Coding sequilibrian  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTGTA GGGGGGCGCGA AATAGAATCT CCTGCACCTT CCTGCACCTT TGAAACAAAC GGGTATTGTA AGGGAAGATT AAGGGTCC CTAGACGAT AAGGGTAGAA  C108 DNA S: did Accessio Lence: 98  11  | CTGCCTGCC CCATGTACGA AAGTCTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTTCACTGG CCTGTCCCCG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA TTTCCATTG CCTTAAATAT AAAAAAAAA  equence   #: AF5089 1531  21   AGGCCTCCCC GGCACTGCCT TCTGGGGCTT CCTGCAAATG TTCCGAGATT TCCGAGATA ATCAACATCGCA ACTTACCTGCA ACTTACCTGCA ACTTACCTGCA CTTTCCCACT CCTTTACCTGCA TTTCCACT CCTTTACCTGCA TTTCCACT CCTTTACCTGCA TTTCCACT CCTTTACCTGCA TTTCCACT TTTCATCCGA TTTCATCCGA TTTCATCCGA TTTCATCCGA TTTCATCCGA TTTCATCCGA   | CCAGTGGAGG GGGCTGTGG CCTCCTTGCTG CCTCCTGGGA GGAGAGCGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAACAACC CATGGCTTATACCTG CATTGAGATA TGTTATTACA TATTACTGCT ATATAGATA TATTACTGCT ATATAGATA  64.1  | ATTTACTCCT ATGTCCTCCT ATGTCCTCCT ATGTCCTCCCA GTGATAGCAA GAGGTGCAGA GCTATTTAG ATGACCCCAG GCTTCTCTT TCTTACCCAA TGACACAGAG CTATCATTAA AAACAAACAA TCTTATTTA TCCCATTGAG GTATATATAC  41    GGAAAGCGGC TCGTCCTGGA GTTGTGGGCT CGGATCTGGT AGTATAAAAT TTTACCCGAA GAACTAACAA GAACTAACAG GAACTAACAG CACCCTA GGTGATCTCG GAACCAACC AAGCACATAT CCCCACCTA GGTGATCCCG GAACAAGCC AAGCACAACC AACGACAACC AACGACAACC AACGACAATC ACTGTGCATT | ATGCCGGCGA TGTCGCAGAG GCACATGCA TCTTTGTGGC AGATGAGGAT TTGCCACAG GCCTTCTGGG CACCAAGGCC GCACAAGGCC GCAAAGGAG CATTAGGAC ACAAACAAA TCTTCTTTCC TAATCATACT ATGTTTTCT  51   CGGTGCAGGG TAAGGTGGC GCAGGACAC TCTGGAGAACAT ATGTTTTGA TTGTGGCTCA ACAAACTGAC TGGTGGGCAA ACCTCACTGT TTCCTAATAT ACACACAGG CTTGGTGGCAA CCTCACTGT TTCCTAATAT ACACACAGG CTTGGTGGCCAC CTTGGTGGCCAC CTTGGTGGCCAC TTCTGTGTGGC TTGCACAC  | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1237  |
| 50<br>55<br>60<br>65<br>70                                       | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT CACCGGTGGCC GGCTGTCATT ATGGTATTGGC GTACGAAATTTT AGGTGCCCTA AAAATCATGT TTAGAATTTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Acic Coding sequ  1   CAGGACCGCA CGGGGACAGG TGGACCGCC CCCTTTCGCC TTCTCCTGGC CACCGAAATT AGCTTATGTG TAAAGCATTT GAGTTTTGTC TCCATTTACA TCCAGACAC CCTGCAGATA TCCAGACAC TCCTTCAGGG GTATTGGGAT TCCATTAGGG GGAAAATTT TCCAGACACT TCCTTAAGG GTATTGGGAT CTCCTTAAGG GGAAAATTT TATCACATTT   | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTTA GGGGGGCGCGA AATAGAATCT CCTGCACCTT TGAAACAAC GGGTATTGTA AGGGAAGATT AAGGGGTCC CTAGACAAC CLOB DNA S LL ACCESSIO LENCE: 98  11    AGGCAGGGA ATCGAGCT TCAACAGC TCCAACGT TCATGGCAT ATCGGCT TCCACGGT TCCACG    | CTGCCTGCC CCATGTACGA AAGTCTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTAAGAATT TCTTCACTGG CCAGCGGGAA CGAAAATGGA ATCTAAAGTA AAAAAAAAAA  | CCAGTGGAGG GGGCTGTGG GGGGCTGTGG CCTCCTGGGA GGAGAGCGAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAACAACC CATGGCTTATATACCGT CATTGAGATA TGTTATTACAC ATATAGGTTA AAAAAA  64.1  31   GCACGGTGGG GCTAGGGATG CTGCTGGCTG CAGTGCCTTG GAAGCCTAAC TGTTAGAATC TGTGAAATC TGTGAAATC TGACAATCTG TAAGAATC TGACAAGCGT TGACAATCTG TAAGAATCT TGACAATCTG TAAGAATCTG TAACATCTG TGCCACCCACCGC CCCACCACCTGC CCCACCACCTGC CCCACCACCTGC CTCACCACCACCTGC CCACCACCACCACCACCACCACCACCACCACCACCACC  | ATTTACTCCT ATGTCCTCCCT ATGTCCTCCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCG AGATGAGAT TCTTTGTGGC AGATGAGAT TTGCCACAG GCCTTCTGGG CACAAGGCC GCAAAGCAAA   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1237<br>60<br>120<br>1237<br>60<br>420<br>480<br>540<br>660<br>660<br>720<br>780<br>840<br>960<br>1020  |
| 50<br>55<br>60<br>65<br>70                                       | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT GACCGGTGGCC GGCTGTCATT AGGTGCCCTTA AGAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCGCC CGCTTTCGCC TTCTCCTGGC CACCGAATT TAGCTTTTTT GAGTTTGTCT TCCATTTACT TCCATTTACT CCTGCAGATA GGAGGAAGAC GGAAATCTT TCCTGGATA GGAGGAAGCG GGAAAATCTT TCCTGCAGATA TCCCAGACACT CCTGCAGATA GGAGGAAGGG GGAAAATCTT TATCACATTT AGCCAACCCC TTCTCCTTAGG GGAAAATCTT TATCACATTT AGCCAACCCC  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTTA GGGGGGCGCGA AATAGAATCT TGAAACAAAC GGGTATTGTA TTAAAATACTT AGGGAACAT 11 AGGGACAGCGC ATGGCGCG ATGGCGCGCA ATGGCGCAGCA TTCATCGCGTA ATGGCGCAGCA TTCATCGCAGT ATCGTGGCT TTCATCGCAA ATGGCGCAGT ATCGTGCCAT TCATCGCAGT ATCGTGGCAT TCATCGCAGT ATCGTGGCAT TCATCGCAGT ATGTCCAGGT ATGTCCAGGT ATGTGTGCAACA CTGAAAACAC CTGAGATTTGT CCCAATTGTG AAGTCTATCA ATACTAACA ATACTAACA CTCGAATCTC AAACCAGCGCC  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTACTGG CCTGCCCGG CCAGCGGGAA ACGTGCTAAA ATTTCATTG CCTTAAATAT AAAAAAAAA equence n #: AF5089: 1531  21    AGGCCTCCCC GGCACTGGCT TCTGGGGCT TCTGGGGCT TCTGGAATG TCCGAAAAG ATCCAAAAAG ATCCAAAAAG ATCCACAAAAG GCAACTGCAA ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCAA TTCACCAAA TTCACCAAA TTCACCAAA TTCACAAT TCTGCAAATG TCTGCAAATG TCTGCAAATG TCCGTCACCT ACATTATCTG ACTTACCTG ACTTACCTG ATTACCTG ATCAAGATTC CCAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CAACCTCAGA TTCAAGATTC  | CCAGTGGAGG GGGCTGTGG GGGGCTGTGG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACCGT CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA  64.1  . 31   GCACCGTGGG GCTAGGGATG GCTAGGGATG CTGCTGGCTG GCACTACGGATG TGAGGATC TGGAGCTAAC GTTAGAAATC TGACTAGAT TGACTAGAT TGACTGTCT CACACTCG TGAAACCTC TAGAAATCT TGAAAGCAC TGCAAATCTG TAGAAATCT TGAAAGCAC TGCAAATCTG TAGAAGCAC TGCAAATCTG TAGAAGCAC TGCACACTGG TGTCAACCCC CCACCACTGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC  | ATTTACTCCT ATGTCCTCCCT ATGTCCTCCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCA AGATGAGAT TTTGCACAGC TCAATGCAG GCCTTCTGGG CACCAAGGCC GCACAAGGAC CATAGGACC ACAAACAAA TCTTCTTTCT ATGTTTTCT  51   CGGTGCAGCG TAAGGTGCA CTAAGGACCA CTAAGGACCA TCTGGAGGGC CCTGAGAACAT ATGATGTTGA TTGTGCTCA ACAAACAGG CCTTGGCAAA CCTAATAT ACACACAGG CTTGTGTGCC TTGCACAGC TTCCTAATAT ACACACAGG CTTGTGTGCC TTGCACAGC TTGTGTGCC TTGCACAGC TTTCCTAATAT ACACACAGG CTTGTGTGCC TTGCACCAAC TCACTGTGAA ATGAGTCCAA   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1237<br>60<br>120<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1020<br>1020<br>1020<br>1020<br>1020<br>1020<br>10              |
| 50<br>55<br>60<br>65<br>70                                       | GATCGGCGCC CAACATCGTG CACCGGGCAG AGCAACCCGT GACCGGTGGCC GGCTGTCATT AGGTGCCCTTA AGAATCATGT TTAGAATTT AACCCATGTG TCAATATAGG CAAATGGGGG ATTAAAAATA Seq ID NO: Nucleic Aci Coding sequ  1   CAGAGCCGCA CGGGGACAGG TGGACCGCC CGCTTTCGCC TTCTCCTGGC CACCGAATT TAGCTTTTTT GAGTTTGTCT TCCATTTACT TCCATTTACT CCTGCAGATA GGAGGAAGAC GGAAATCTT TCCTGGATA GGAGGAAGCG GGAAAATCTT TCCTGCAGATA TCCCAGACACT CCTGCAGATA GGAGGAAGGG GGAAAATCTT TATCACATTT AGCCAACCCC TTCTCCTTAGG GGAAAATCTT TATCACATTT AGCCAACCCC  | ATCGTCAGCA ACCGCCCAGG ACCGCCCAGG ATCCAGTGCA GCCTTGATGG ATGAAGTTA GGGGGGCGCGA AATAGAATCT TGAAACAAAC GGGTATTGTA TTAAAATACTT AGGGAACAT 11 AGGGACAGCGC ATGGCGCG ATGGCGCGCA ATGGCGCAGCA TTCATCGCGTA ATGGCGCAGCA TTCATCGCAGT ATCGTGGCT TTCATCGCAA ATGGCGCAGT ATCGTGCCAT TCATCGCAGT ATCGTGGCAT TCATCGCAGT ATCGTGGCAT TCATCGCAGT ATGTCCAGGT ATGTCCAGGT ATGTGTGCAACA CTGAAAACAC CTGAGATTTGT CCCAATTGTG AAGTCTATCA ATACTAACA ATACTAACA CTCGAATCTC AAACCAGCGCC  | CTGCCTGCC CCATGTACGA AAGTCTTTGA TGGTTGGCAT TGAAGTGCTT TATTTCTTCT TCTACTGG CCTGCCCGG CCAGCGGGAA ACGTGCTAAA ATTTCATTG CCTTAAATAT AAAAAAAAA equence n #: AF5089: 1531  21    AGGCCTCCCC GGCACTGGCT TCTGGGGCT TCTGGGGCT TCTGGAATG TCCGAAAAG ATCCAAAAAG ATCCAAAAAG ATCCACAAAAG GCAACTGCAA ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCTG ACTTACCAA TTCACCAAA TTCACCAAA TTCACCAAA TTCACAAT TCTGCAAATG TCTGCAAATG TCTGCAAATG TCCGTCACCT ACATTATCTG ACTTACCTG ACTTACCTG ATTACCTG ATCAAGATTC CCAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CAACCTCAGA TTCAAGATTC CCAACCTCAGA TTCAAGATTC CAACCTCAGA TTCAAGATTC  | CCAGTGGAGG GGGCTGTGG GGGGCTGTGG CCTCCTGGGA GGAGACCAT TGCAGGTCTG CTATGACCCT CTGGGCTGCT AAAAACAACC AGACTACCGT CATTGAGATA TGTTATTACA CATGGCTTAA TATTACTGCT ATATAGATAT AAAAAAA  64.1  . 31   GCACCGTGGG GCTAGGGATG GCTAGGGATG CTGCTGGCTG GCACTACGGATG TGAGGATC TGGAGCTAAC GTTAGAAATC TGACTAGAT TGACTAGAT TGACTGTCT CACACTCG TGAAACCTC TAGAAATCT TGAAAGCAC TGCAAATCTG TAGAAATCT TGAAAGCAC TGCAAATCTG TAGAAGCAC TGCAAATCTG TAGAAGCAC TGCACACTGG TGTCAACCCC CCACCACTGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC TCTATAACGGG TGTAAACGCC  | ATTTACTCCT ATGTCCTCCCT ATGTCCTCCCCT ATGTCCTCCCCCCCCCC   | ATGCCGGCGA TGTCGCAGAG GCACATTGCG AGATGAGAT TCTTTGTGGC AGATGAGAT TTGCCACAG GCCTTCTGGG CACAAGGCC GCAAAGCAAA   | 360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1237<br>60<br>120<br>1237<br>60<br>120<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>900<br>900<br>900<br>900<br>900<br>900<br>900<br>900<br>9 |

|     |            |              |            | Om) C) Omom.      |              | 1 MC 1 OF 1 MCC          | 1200 |
|-----|------------|--------------|------------|-------------------|--------------|--------------------------|------|
|     |            | ACTCACATGA   |            |                   |              |                          | 1200 |
|     |            | AAACAGATTT   |            |                   |              |                          | 1260 |
|     |            | TATCCTGATG   |            |                   |              |                          | 1320 |
| 5   |            | AACAGAAGTA   |            |                   |              |                          | 1380 |
| 3   |            | TCGGTCTATG   |            |                   |              |                          | 1440 |
|     |            | TTTCTGCTTA   |            |                   |              |                          | 1500 |
|     |            | AAGATCCCAC   |            |                   |              |                          | 1560 |
|     |            | TTGTTGGTTG   |            |                   |              |                          | 1620 |
| 10  | TTATCCCGGG | AAGTGCTGCT   | TATCTGGGGT | TTTCTGGTAG        | ATGTGGGCGG   | TGTTTGGAGG               | 1680 |
| 10  | CTGTACTATA | TGAAGCCTGC   | ATATACTGTG | <b>AGCTGTGATT</b> | GGGGAACACC   | AATGCAGAGG               | 1740 |
|     | TAACTCTCAG | GCAGCTAAGC   | AGCACCTCAA | GAAAACATGT        | TAAATTAATG   | CTTCTCTTCT               | 1800 |
|     |            | CAAATACAAA   |            |                   |              |                          | 1860 |
|     |            | TTTGACCCTA   |            |                   |              |                          | 1920 |
|     |            | AGTTAAAAAA   |            |                   |              |                          | 1980 |
| 15  |            | ATGTAACACA   |            |                   |              |                          | 2040 |
|     |            | TGACTTTTTC   |            |                   |              |                          | 2100 |
|     |            | GGGACTTGGT   |            |                   |              |                          | 2160 |
|     |            | TAGCTTAGGT   |            |                   |              |                          | 2220 |
|     |            |              |            |                   |              |                          | 2280 |
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| 5   | AIGITCAATI               | · AATGGCATGA | AATACCAAGA               | AATTAATCCT                 | ACACTTETAC   |  | 60<br>120    |
| )   | AACACCAGAC               | TCTTCAGAAG   | GAAACTTATC               | TTATCTTAGT                 | ACTITATION   | A TOTAL A CAR                          | 180          |
|     | CITATCCCAT               | CITACAACCA   | GTTCCTCTTT               | CAGAACCAGT                 | ררית את אבורים יי  | * ***                                  | 240          |
|     | CAATCTTCAA               | CATGATCTCT   | TCTTTAAAGC               | AGTCAGTCTC                 | TGTCACACTG   | TACAGATTAG                             | 300          |
|     | GTTGGAGTAC               | TATGCATTGCA  | CIGGIGATGG               | TCCCTGGCAA                 | TCCAACCTGG   | CACCATCGCA<br>CTGCAAGGAT               | 360          |
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|     | GGAACGGTAC               | AAACTGCTTC   | ' ATATTCTGGA             | ATTTGATTCA                 | GATOGTACCA   | CARTCACTOR                             | 480          |
|     | AMITGITUAG               | GCACCTTCAG   | GTGAGAAGTT               | תרוב אורוב היווע מיווע מי  | ሽ ሽ ሽ ሽ ር ር ሽ ር ር ጥጥር  | 2000200220                             | 540<br>600   |
|     | TUTUUUTAAA               | TGTATAGGTG   | GAGAAATAGA               | AAAAACCACA                 | ATTCATCTAC   | DOMESTIC ACTURE                        | 660          |
| 15  | TTTGAAAGGG               | CTAAGAACTC   | TGTGTATAGC               | ΑΤΑΤΑΘΑΑΑΑ                 | <b>ምምጥ እር አጥር እ እ</b>  | 33030mamos                             | 720          |
| 10  | GGCAGCTCTT               | AAACGCATAT   | TIGAAGCCAG               | GACTGCCTTG                 | CAGCAGCGGG   | AAGAGAAATT<br>CAGCAGTAGA               | 780          |
|     | AGACAGACTA               | CAAGATAAAG   | TTCGAGAAAGA              | TATTERACE                  | CTTGGAGCCA   | CAGCAGTAGA                             | 840          |
|     | AGIAIGGGIA               | CITACTGGGG   | ATAAACATGA               | لسنتكليات لان لا لا لا     | A CTYCTYC A CYTY   | TATCAMORGO                             | 900<br>960   |
| 20  | CCATTTTCAT               | AGAACCATGA   | ACATCCTTGA               | ACTTATABAC                 | CACAAATCAC   | A CACOCA ORG                           | 1020         |
| 20  | TGCTGAACAA               | TIGAGGCAGC   | TTGCCAGAAG               | AATTACAGAG                 | CATCATCTCA   | TTCTCTTTCT                             | 1080         |
|     | GCTGGTAGTG               | GATGGGACCA   | GCCTATCTCT               | TGCACTCAGG                 | GAGCATCAAA   | ስ እ ርማ እ መምጠ እ ጠ                       | 1140         |
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| 25  | AGAAGGAAGA               | CAGGCTGCAA   | GAAACAGTGA               | מידמדערים                  | CCCACAMMA  | N/WWW.Com.com.com                      | 1320<br>1380 |
|     | CAAATIGCTT               | TITGTTCATG   | GTCATTTTTA               | TTATATTACA                 | ATACCTACCC   | משכע מיויבעוייו                        | 1440         |
|     | IIIIIIIIAT               | AAGAATGTGT   | GCTTTATCAC               | ACCCCAGTTT                 | תיים מיים מיים מיים  | TOTA CONCERNS                          | 1500         |
|     | TTCCCTACCT               | CAAACATTGT   | ATGACAGCGT               | GTACCTGACT                 | TTATACAATA   | TTTGTTTTAC                             | 1560         |
| 30  | AAATAAGCCC               | ACCCTTTATC   | ATAGTCTTTT<br>GAGACATTAG | GGAACAGCAT                 | GTAGACCCTC   | ATGTGTTACA                             | 1620         |
|     | ICITIATIGG               | ACCATCCTGG   | GCTTCAGTCA               | TOTAL                      | فالملماماماماماماماما  | CD TOOMS Owner                         | 1680         |
|     | ACTAATAGGG               | AAAGATACAT   | CTCTGCTTGG               | AAATGGCCAG                 | ATCTTTCC AA  | A COCC A CIA MAN                       | 1740<br>1800 |
|     | IGGCACTITG               | GTCTTCACAG   | TCATGGTTAT               | TACACTCACA                 | CTABACATOO   | CECTOCO N N N O                        | 1860         |
| 35  | TCATTTTTGG               | ACTTGGATCA   | ACCATCTCGT               | TACCTCCCA                  | ጥርጥስጥጥስጥስጥ   | TITLE & COMMISSION                     | 1920         |
| 20  | TOTOTOTO                 | CACCECCEC    | GGATTCTCTG<br>CAAGTGGTTC | GCCATTTTTG                 | GGCTCCCAGA   | ATATGTATTT                             | 1980         |
|     | TACATGTCTA               | TTTCTTGATA   | TCATAAAGAA               | TGCTTGGTTT                 | GCCATAATCC   | TCATGGTTGT                             | 2040         |
|     | IACIGAAAAG               | GCACAGCTTA   | CTCLABACABA              | TOPACCITATO                | AACTCCCTCCC  | 1 CTT C C 1 C C C C                    | 2100         |
| 40  | CIGITICCCC               | GAAGGAGAAG   | CAGCGTGTGC               | ATCTCTTCA                  | ACABTOCTO  | A A COC A COMMA DO                     | 2160<br>2220 |
| 40  | AGGAAGATGT               | AGTCCAACCC   | ACATCAGCAG               | ATCATGGAGT                 | CCATCCCATC   | CONTRACTOR IN A                        | 2280         |
|     | CANCUACAGG               | AGCATCTTGA   | CTCTCTCCAC               | AATGGACTCA                 | The State of the Public of the | NA ACCCCCA C                           | 2340         |
|     | ATGGCCACAC               | TAGCTCTCAA   | TTCACCTCCT<br>ATTAATTTCC | TTCCTAAAAT                 | TCAGTGTGAT   | CACCCTGTTA                             | 2400         |
|     | GAGTTATAAT               | GGCAAACAAA   | CAGAAAGCAT               | TAGTACANCO                 | TAGTAGTTCA   | TACCCACTCA                             | 2460         |
| 45  | IGAATCIGAA               | CATGTTAAAA   | TTTGAGAATA               | AACACACATT                 | AND THE PARTY OF T | MINOUS COMM                            | 2520         |
|     | IGICCCTIGI               | GCTTATGGGA   | CTCCTAATGG               | CATTTCACTC                 | TOTAL CONTRACT   | CCCsmmsmsm                             | 2580<br>2640 |
|     | TITIAATATAA              | ATGTAGAAAA   | AAGAGAGAAA               | מממייבומיידייוי            | CD Cate Valuations   | TROTTE TO CO                           | 2700         |
|     | LIGATIATIG               | ACTUTTUTAT   | TTAAATCTGC               | יים ממידבודי וידיד         | TATIONSAN  | CHIRDRO COMPO                          | 2760         |
| 50  | ATACTGAGGA               | ATTTTTTATTA  | GAGTTATATT<br>CTCAGTGACC | TAAAGCTTTT                 | CATGGGAAAA   | GTTAATGTGA                             | 2820         |
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|     | CAAGGGTATA               | TCATATATAC   | AAATCAGGAA               | <b>ずじなびながらなか</b>           | TONOTONACT   | TOTAL S. S. CORROLL CO.                | 3000<br>3060 |
| 55  | GITTACTAAT               | ATTTTTGTGA   | CAGAGTATAA               | ልሮልርሃርንግስ ተል               | CONCIONA A BOT   | M3 C3 M3 CM3 C                         | 3120         |
| ,55 | IAGCATATTA               | TTAATTTAAT   | GTCTTTATCA               | ALLAND A CALALLA           | ALC: UNIT COLORISM   | 7 2 management                         | 3180         |
|     | CATOGTTGTA               | CACTUTALOT   | TTTCTCTTTA<br>ATATCAATAA | CCTGAAGGCT                 | CTGTGTATAG   | TATTTCATGA                             | 3240         |
|     | TAIGITTAAT               | TATACAAATC   | AGAATAGTAT               | A STEPS ATTEND             | ATC ABEACAN  | *****                                  | 3300         |
| 60  | CICITICIGE               | AGCCGACTTA   | GACATGCTCT               | TCCCTTTCTA                 | TARCCTRGRT   | THE REAL PROPERTY.                     | 3360<br>3420 |
| 60  | MUGGITTCAG               | TTAATAATCT   | TATTTTCAGG               | TTATCTCATC                 | TABOTTATAC   | C3 2 2 Cm2 CC2                         | 3480         |
|     | CHAIACAGIG               | AGTTCTGCCA   | GTGTCCCAGT               | ACABGGGATA                 | THE PROPERTY OF THE PROPERTY O | COOMORGON                              | 3540         |
|     | IGIAAAAAIG               | CICAACITGI   | ATCAGGTAAT               | GTTAGCA ATA                | DOWN & ATTO A  | T110110010                             |              |
|     | AATTTATCAA               | GTAGTTCAGT   | ATTGTCATTT               | CTTTTTTCTTT                | AAAACCTAAC   | TTCCATCCTG                             |              |
| 65  | IIAAGATTTA               | GAAGTGATTA   | TALE CALMANT VALLE       | እ እ ርጥክ ጥጥክ ርም             | CACCOCCANAC  | G111                                   | 3720         |
|     | TIGINIACAT               | ATTAAGATAA   | TEGTTAAATG               | CALCALACTED TO A           | B B COMMUNICACIO   | MMC2 2 2 2 2000                        | 3780<br>3840 |
|     | WILLCCITIA               | TGGAGATTTA   | TIGITGCAGCC              | الماليطينات والإبلاث       | THE RESTORAGE  | 200220000                              | 3900         |
|     | GGCTTCTAGA               | ATTGGACTGG   | CAGGGGAAAC               | <b>ΔΑΤΟΟΤΑΛΛΙ</b>          | ACACA A ARMA   | 1010000                                | 3960         |
| 70  | TARGERTATT               | AACTAT       | TATTTTCTTG               | CTAATGTAAC                 | ATTTGTCTGT   | TCCAGTGATG                             | 4020         |
|     | GATATTTCAT               | AGCTGGATTT   | GCTAAATATT               | AATITICAAA                 | AATAGTCCTT   | CTTTAACTTA<br>AAGAATAATA               | 4080         |
|     | CONCOLNCAN               | TGTCTGCATT   | CACTAATTCA               | ממבותיים היודים א          | クカヘイスススカルス   |  | 4140         |
|     | CICHGIAGAG               | TACTAGGTGG   | GAGGATATGG               | እ እ እ ጥጥጥር ርጥቦ .           | ልሞሽ ሽ ሽ ሽ መ <b>ር</b> መር  | MM2 M2 2 2 2 00                        | 4200<br>4260 |
| 75  | IGCATATAAC               | AAAATGACAC   | CCAGTAGGCC               | <b>ጥርሮልሞሞልሮልሞ</b>          | ተሞል ርክ ሞርክ ርጥ  | COCCOOK & DOWN                         | 4320         |
| , , | CCCVI CWWYI              | AAACIGAGTA   | CIGACACCAG               | ACD A ACACTC               | ርል እ አርምር አ ጥ አ  | ******                                 | 4380         |
|     | IGACCAACIG               | CAGCAAGACA   | GGAGGTCAGC               | <b>ጥርርርርቸልቸልል</b>          | TO A SHORT STATE OF THE PARTY O | 1 COCCOO COCC                          | 4440         |
|     | ATGTAATTTT<br>AAGTAAATGG | CAACCACTAG   | TGTCCTCATC               | יייידיציים או אביציים      | ስርጥርርር እ እ mo  |  | 4500         |
| 90  | IIMMOCAAA                | ATTAICTIGT   | GATHITHAACA              | <u> አያያርያርተተተተ</u>         | مستحدث لا بتنجيش لا يلي  |  | 4560         |
| 80  | CHAIGCAGIC               | 1GCAAGCTTT   | CAGTACTTT                | татырты                    | A TT (") アノーマー   | M111100000                             |              |
|     | MCINCGINAC               | CAGTAATCAC . | AAGGAAAGTG               | արիարարիինի և              | Publication and a  | * * * * * ***                          |              |
|     | CITICGAAAG               | TARGARIT     | חיי⊃ א אידיי מעדע        | יייטידע אידער אייטין איזיי | TV-7-1   |  |              |
|     | GAGGGCTGTA               | AGCCTGAAGA   | TAGTGGCCNAC              | CAAATCGATT                 | CTTTCCTT   | AGAGCAAAAT<br>TGCCTCGTCT<br>TTGCCCCTCA | 4860         |
|     |                          |              |                          |                            | GIIICCAAAA   | TIGCCCCTCA                             | 4920         |

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        ATGATTGCCA ACTCCGTGGT GGTCTGGGTG AATATCCAGG CCAAGACCAC AGGCTATGAC
                                                                                    360
        ACGCACTGCT ACATCTTGAA CCTGGCCATT GCCGACCTGT GGGTTGTCCT CACCATCCCA
                                                                                    420
        GTCTGGGTGG TCAGTCTCGT GCAGCACAAC CAGTGGCCCA TGGGCGAGCT CACGTGCAAA
        GTCACACAC TCATCTTCTC CATCAACCTC TTCGGCAGCA TTTTCTTCCT CACGTGCATG AGCGTGGACC GCTACCTCTC CATCACCTAC TTCACCAACA CCCCCAGCAG CAGGAAGAAG
                                                                                    540
70
                                                                                    600
        ATGGTACGCC GTGTCGTCTG CATCCTGGTG TGGCTGCTGG CCTTCTGCGT GTCTCTGCCT
                                                                                    660
        GACACCTACT ACCTGAAGAC CGTCACGTCT GCGTCCAACA ATGAGACCTA CTGCCGGTCC
TTCTACCCCG AGCACAGCAT CAAGGAGTGG CTGATCGGCA TGGAGCTGGT CTCCGTTGTC
                                                                                    780
        TTGGGCTTTG CCGTTCCCTT CTCCATTATC GCTGTCTTCT ACTTCCTGCT GGCCAGAGCC
                                                                                    840
75
        ATCTCGGCGT CCAGTGACCA GGAGAAGCAC AGCAGCCGGA AGATCATCTT CTCCTACGTG
                                                                                    900
        GTGGTCTTCC TTGTCTGCTG GCTGCCCTAC CACGTGGCGG TGCTGCTGGA CATCTTCTCC
        ATCCTGCACT ACATCCCTTT CACCTGCCGG CTGGAGCACG CCCTCTTCAC GGCCCTGCAT
                                                                                    1020
        GTCACACAGT GCCTGTCGCT GGTGCACTGC TGCGTCAACC CTGTCCTCTA CAGCTTCATC
                                                                                    1080
        AATCGCAACT ACAGGTACGA GCTGATGAAG GCCTTCATCT TCAAGTACTC GGCCAAAACA
                                                                                    1140
80
        GGGCTCACCA AGCTCATCGA TGCCTCCAGA GTCTCAGAGA CGGAGTACTC TGCCTTGGAG
                                                                                    1200
        CAGAGCACCA AATGATCTGC CCTGGAGAGG CTCTGGGACG GGTTTACTTG TTTTTGAACA
                                                                                    1260
        GGGTGATGGG CCCTATGGTT TTCTAGAGCA AAGCAAAGTA GCTTCGGGTC TTGATGCTTG
                                                                                    1320
        AGTAGAGTGA AGAGGGGAGC ACGTGCCCCC TGCATCCATT CTCTCTTTCT CTTGATGACG
CAGCTGTCAT TTGGCTGTGC GTGCTGACAG TTTTGCAACA GGCAGAGCTG TGTCGCACAG
                                                                                    1440
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|          | CAGTGCTGTG  | CGTCAGAGCC  | AGCTGAGGAC               | AGGCTTGCCT | GGACTTCTGT | AAGATAGGAT               | 1500         |
|----------|-------------|-------------|--------------------------|------------|------------|--------------------------|--------------|
|          |             |             | TTTATATGGT               |            |            |                          | 1560         |
|          |             |             | ATAAATGTAT<br>TATATTCAGA |            |            |                          | 1620<br>1680 |
| 5        |             |             | CTAATTGTTA               |            |            |                          | 1740         |
|          |             |             | GCCAGTCTTG               |            |            |                          | 1800         |
|          |             |             | CGGCACGGGA               |            |            |                          | 1860         |
|          |             |             | TAAAGTTACA<br>GAACAGTTGC |            |            |                          | 1920<br>1980 |
| 10       |             | AATAAAGATT  |                          |            |            |                          | 2010         |
|          | Seq ID NO:  | C116 DNA Se | quence                   |            |            |                          |              |
|          |             |             | #: NM_0003               | 50.1       |            |                          |              |
| 15       | coarng sequ | ence: 826   | 1903                     |            |            |                          |              |
|          | 1           | 11          | 21                       | 31         | 41         | 51                       |              |
|          |             | )           |                          | 1          |            | TO A COOR A STORM        | <b>co</b>    |
|          |             |             | TGTCCTTTGC<br>CATGGGCTTC |            |            |                          | 60<br>120    |
| 20       | AACTGGACCC  | TGCGGAAAAG  | GCAAAAGATT               | CGCTTTGTGG | TGGAACTCGT | GTGGCCTTTA               | 180          |
|          |             |             | CTGGTTAAGG               |            |            |                          | 240          |
|          |             |             | GATGCCCTCA<br>CTGTTTTCAA |            |            |                          | 300<br>360   |
| ~-       |             |             | CATCTTGGCA               |            |            |                          | 420          |
| 25       |             |             | GCACCTTGGC               |            |            |                          | 480          |
|          |             |             | GACTCACCCG<br>AGAAACACTG |            |            |                          | 540<br>600   |
|          |             |             | TCTGATCAAC               |            |            |                          | 660          |
| 20       | GGAGTCCCGG  | ACCTGGCGCT  | GAAGGACATC               | GCCTGCAGCG | AGGCCCTCCT | GGAGCGCTTC               | 720          |
| 30       |             |             | CGGGGCAAAG               |            |            |                          | 780          |
|          |             |             | AGAAGACACT<br>CCTAGACAGC |            |            |                          | 840<br>900   |
|          |             |             | GTCACCAAGA               |            |            |                          | 960          |
| 35       |             |             | CAGGCCCCTC               |            |            |                          | 1020         |
| 33       |             |             | TGACCTCCTG               |            |            | TGGCTCTCGG               | 1080<br>1140 |
|          |             |             | TTCTTATGAC               |            |            |                          | 1200         |
|          |             |             |                          |            |            | AAAGCCTTTG               | 1260         |
| 40       |             |             | CACTCCTGAT               |            |            | ACTGAAGAAT<br>CTGGGAAGAA | 1320<br>1380 |
| 10       |             |             | CTTCTTTGAC               |            |            |                          | 1440         |
|          | ACCCTGGGGA  | ACCCAACAGT  | AAAAGACTTT               | TTGAATAGGC | AGCTTGGTGA | AGAAGGTATT               | 1500         |
|          |             |             |                          |            |            | GGCTGACGAC<br>CCGCCTGGTC | 1560         |
| 45       |             |             |                          |            |            | TGAAACTCAG               | 1620<br>1680 |
|          | CTCACCCAAC  | GTGCCCTCTC  | TCTACTGGAG               | GAAAACATGT | TCTGGGCCGG | AGTGGTATTC               | 1740         |
|          |             |             |                          |            |            | GATCCGAATG               | 1800         |
| <u> </u> |             |             |                          |            |            | TTCTGGTCCC<br>TCTGCAGGAC | 1860<br>1920 |
| 50       | ATGGTTGAAC  | AGGGGATCAC  | AAGGAGCCAG               | GTGCAGGCGG | AGGCTCCAGT | TGGAATCTAC               | 1980         |
|          |             |             |                          |            |            | CCTGAACCGC               | 2040         |
|          |             |             |                          |            |            | TGTGAAGAGC<br>TGTCTCCAAT | 2100<br>2160 |
|          |             |             |                          |            |            | GAGCATCTTC               | 2220         |
| 55       |             |             |                          |            |            | ATTCATCCTC               | 2280         |
|          |             |             |                          |            |            | GCTCAGCACC               | 2340<br>2400 |
|          | CTGCCACACA  | TCCTGTGCTT  | CGCCTGGCAG               | GACCGCATGA | CCGCTGAGCT | GAAGAAGGCT               | 2460         |
| 60       |             |             |                          |            |            | TCGCTTTGAA               | 2520         |
| 00       |             |             |                          |            |            | AGGGGACGAA               | 2580<br>2640 |
|          | GCTTGGTACC  | TTGATCAGGT  | GTTTCCAGGA               | GACTATGGAA | CCCCACTTCC | TTGGTACTTT               | 2700         |
|          |             |             |                          |            |            | AGAAAGAGCC               | 2760         |
| 65       |             |             |                          |            |            | AGAAGGAATA<br>CGTGAAGAAT | 2820<br>2880 |
|          | CTGGTAAAGA  | TTTTTGAGCC  | CTGTGGCCGG               | CCAGCTGTGG | ACCGTCTGAA | CATCACCITC               | 2940         |
|          |             |             |                          |            |            | CACCACCTTG               | 3000         |
|          |             |             |                          |            |            | GGGAAGGGAC<br>GCACAACATC | 3060<br>3120 |
| 70       |             |             |                          |            |            | GAAAGGAAAG               | 3180         |
|          |             |             |                          |            |            | CCTCCACCAC               | 3240         |
|          |             |             |                          |            |            | GTCGGTTGCC               | 3300         |
|          |             |             |                          |            |            | TGGGGTGGAC CAGAACCATC    | 3360<br>3420 |
| 75       | ATCATGCCCA  | CTCACCACAT  | GGACGAGGCC               | GACCACCAA  | GGGACCGCAT | TGCCATCATT               | 3480         |
|          |             |             |                          |            |            | CTTTGGCACA               | 3540<br>3600 |
|          |             |             |                          |            |            | GAAAGGCAGT<br>CCACGTCGAT | 3660         |
| 00       | GACCTAACTO  | CAGAACAAGI  | CCTGGATGG                | GATGTAAAT  | AGCTGATGGA | TGTAGTTCTC               | 3720         |
| 80       | CACCATGITO  | CAGAGGCAA   | GCTGGTGGAG               | TGCATTGGT  | AAGAACTTAT | CTTCCTTCTT               | 3780         |
|          |             |             |                          |            |            | GGAGGAGACG<br>AGAGATTTTT |              |
|          | CTGAAGGTC   | CGGAGGATTO  | TGATTCAGG                | CCTCTGTTTC | CGGGTGGCGC | TCAGCAGAAA               | 3960         |
|          | AGAGAAAACG  | TCAACCCCCC  | ACACCCCTG                | TTGGGTCCC  | GAGAGAAGGC | TGGACAGACA               | 4020         |

```
CCCCAGGACT CCAATGTCTG CTCCCCAGGG GCGCCGGCTG CTCACCCAGA GGGCCAGCCT
                                                                                                  4080
           CCCCCAGAGC CAGAGTGCCC AGGCCCGCAG CTCAACACGG GGACACAGCT GGTCCTCCAG
           CATGTGCAGG CGCTGCTGGT CAAGAGATTC CAACACACCA TCCGCAGCCA CAAGGACTTC
                                                                                                  4140
                                                                                                  4200
          CTGGCGCAGA TCGTGCTCCC GGCTACCTTT GTGTTTTTGG CTCTGATGCT TTCTATTGTT
   5
          ATCCTTCCTT TTGGCGAATA CCCCGCTTTG ACCCTTCACC CCTGGATATA TGGGCAGCAG TACACCTTCT TCAGCATGGA TGAACCAGGC AGTGAGCAGT TCACGGTACT TGCAGACGTC
                                                                                                  4260
                                                                                                  4320
                                                                                                  4380
          CTCCTGAATA AGCCAGGCTT TGGCAACCGC TGCCTGAAGG AAGGGTGGCT TCCGGAGTAC
          CCCTGTGGCA ACTCAACACC CTGGAAGACT CCTTCTGTGT CCCCAAACAT CACCCAGCTG
TTCCAGAAGC AGAAATGGAC ACAGGTCAAC CCTTCACCAT CCTGCAGGTG CAGCACCAGG
                                                                                                  4440
                                                                                                  4500
  10
          GAGAAGCTCA CCATGCTGCC AGAGTGCCCC GAGGGTGCCG GGGGCCTCCC GCCCCCCAG
                                                                                                  4560
                                                                                                  4620
          AGAACACAGC GCAGCACGGA AATTCTACAA GACCTGACGG ACAGGAACAT CTCCGACTTC
           TTGGTAAAAA CGTATCCTGC TCTTATAAGA AGCAGCTTAA AGAGCAAATT CTGGGTCAAT
                                                                                                  4680
                                                                                                  4740
          GAACAGAGGT ATGGAGGAAT TTCCATTGGA GGAAAGCTCC CAGTCGTCCC CATCACGGGG
          GAAGCACTTG TTGGGTTTTT AAGCGACCTT GGCCGGATCA TGAATGTGAG CGGGGGCCCT
                                                                                                  4800
 15
                                                                                                  4860
          ATCACTAGAG AGGCCTCTAA AGAAATACCT GATTTCCTTA AACATCTAGA AACTGAAGAC
          AACATTAAGG TGTGGTTTAA TAACAAAGGC TGGCATGCCC TGGTCAGCTT TCTCAATGTG
GCCCACAACG CCATCTTACG GGCCAGCCTG CCTAAGGACA GGAGCCCCGA GGAGTATGGA
                                                                                                  4920
                                                                                                  4980
                                                                                                 5040
          ATCACCGTCA TTAGCCAACC CCTGAACCTG ACCAAGGAGC AGCTCTCAGA GATTACAGTG
                                                                                                 5100
          CTGACCACTT CAGTGGATGC TGTGGTTGCC ATCTGCGTGA TTTTCTCCAT GTCCTTCGTC
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         CCAGCCAGCT TIGTCCTTTA TTTGATCCAG GAGCGGGTGA ACAAATCCAA GCACCTCCAG
TTTATCAGTG GAGTGAGCC CACCACCTAC TGGGTGACCA ACTTCCTCTG GGACATCATG
AATTATTCGG TGAGTGCTGG GCTGGTGGTG GGCATCTTCA TCGGGTTTCA GAAGAAAGCC
                                                                                                 5160
                                                                                                 5220
                                                                                                 5280
                                                                                                 5340
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GCTTTATCTT GTGCTAATCT GTTCATCGGC ATCAACAGCA GTGCTATTAC CTTCATCTTG
                                                                                                 5400
 25
                                                                                                 5460
                                                                                                 5520
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          ATTGTCTTCC CCCACTTCTG CCTGGGCCGG GGCCTCATTG ACCTTGCACT GAGCCAGGCT
GTGACAGATG TCTATGCCCG GTTTGGTGAG GAGCACTCTG CAAATCCGTT CCACTGGGAC
                                                                                                 5640
          CTGATTGGGA AGAACCTGTT TGCCATGGTG GTGGAAGGGG TGGTGTACTT CCTCCTGACC
                                                                                                 5700
 30
                                                                                                 5760
          CTGCTGGTCC AGCGCCACTT CTTCCTCTCC CAATGGATTG CCGAGCCCAC TAAGGAGCCC
                                                                                                 5820
          ATTGTTGATG AAGATGATGA TGTGGCTGAA GAAAGACAAA GAATTATTAC TGGTGGAAAT
                                                                                                 5880
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AATGGTGCCG GCAAAACAAC CACATTCAAG ATGCTCACTG GGGACACCAC AGTGACCTCA
                                                                                                 5940
                                                                                                 6000
 35
                                                                                                 6060
          GGGGATGCCA CCGTAGCAGG CAAGAGTATT TTAACCAATA TTTCTGAAGT CCATCAAAAT
          ATGGGCTACT GTCCTCAGTT TGATGCAATC GATGAGCTGC TCACAGGACG AGAACATCTT
                                                                                                 6120
                                                                                                 6180
          TACCTTTATG CCCGGCTTCG AGGTGTACCA GCAGAAGAAA TCGAAAAGGT TGCAAACTGG
                                                                                                 6240
          AGTATTAAGA GCCTGGGCCT GACTGTCTAC GCCGACTGCC TGGCTGGCAC GTACAGTGGG
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                                                                                                 6300
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          CTGGATGAGC CCACCACAGG GATGGACCCC CAGGCACGCC GCATGCTGTG GAACGTCATC
                                                                                                 6360
                                                                                                 6420
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         GAGGCACTGT GTACCCGGCT GGCCATCATG GTAAAGGGCG CCTTTCGATG TATGGGCACC
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                                                                                                 6540
                                                                                                 6600
45
                                                                                                 6660
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                                                                                                 6840
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         TGATCTTTCA CACCGCTCGT TCCTGCAGCC AGAAAGGAAC TCTGGGCAGC TGGAGGCGCA
GGAGCCTGTG CCCATATGGT CATCCAAATG GACTGGCCCA GCGTAAATGA CCCCACTGCA
                                                                                                 6900
50
                                                                                                 6960
                                                                                                 7020
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                                                                                                 7080
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                                                                                                 7140
         TTCTCCAGAC CCCAGAACTA GAAACCCCGG GCCATCCCAC TAGCAGCTTT GGCCTCCATA
                                                                                                 7200
         TTGCTCTCAT TTCAAGCAGA TCTGCTTTTC TGCATGTTTG TCTGTGTGTC TGCGTTGTGT
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         GTGATTTTCA TGGAAAAATA AAATGCAAAT GCACTCATCA CAAAAAAAAA AAAAAAAA
                                                                                                7260
         Seq ID NO: C117 DNA Sequence
         Nucleic Acid Accession #: NM_006671.2
         Coding sequence: 138..1820
60
                                                   31
         GGCACGAGGC TGGTGTTTAG CAACTCCGAC CACCTGCCTG CTGAGGGGGCT AGAGCCCTCA
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                                                                                                180
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                                                                                                300
                                                                                                360
70
                                                                                                420
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                                                                                                600
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        AGGAGGCCC TCCTCGGCG ATCCTCATCT ACGGGTCCA GGAGGAAT GGCTCCCATG
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TGCTGGGCCG CATGGGTGAC AGCGGGGCCC CCCTGGTCAG CTTCTGCCAC ATGGCCATCA
                                                                                                660
75
                                                                                                720
                                                                                                780
                                                                                                840
         AGTCGGTCAT GAAGATCGTG GCGGTGGCTG TGTGGTATTT CCCCTTCGGC ATTGTGTTCC
         TCATTGCGGG TAAGATCCTG GAGATGGACG ACCCCAGGGC CGTCGGCAAG AAGCTGGGCT
                                                                                                960
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         TCTACTCAGT CACCGTGGTG TGCGGGCTGG TGCTCCACGG GCTCTTTATC CTGCCCCTGC
                                                                                                1020
         TCTACTTCTT CATCACCAAG AAGAATCCCA TCGTCTTCAT CCGCGGCATC CTGCAGGCTC
                                                                                                1080
        TECTCATCGC GCTGGCCACC TCCTCCAGCT CAGCCACACT GCCCATCACC TTCAAGTGCC TGCTGGAGAA CAACCACATC GACCGGCGCA TCGCTGGCTT CGTGCTGCCC GTGGGTGCCA
                                                                                                1140
                                                                                                1200
                                                                                                1260
        CCATCAACAT GGACGGCACT GCGCTCTACG AGGCTGTGGC CGCCATCTTC ATCGCCCAGG
```

|     | TCAACAACTA   | CGAGCTGGAC                              | TTTGGCCAGA  | TCATCACCAT  | CAGTATCACA   | GCCACTGCAG   | 1380  |
|-----|--------------|---|-------------|-------------|--------------|--------------|-------|
|     | CCAGCATTGG   | GGCAGCTGGC                              | ATCCCCCAGG  | CCGGCCTCGT  | CACCATGGTC . | ATCGTGCTCA   | 1440  |
|     | CCTCCGTGGG   | ACTGCCCACC                              | GATGACATCA  | CCCTCATCAT  | TGCCGTTGAC   | TGGGCTCTGG   | 1500  |
|     | ACCGTTTCCG   | CACCATGATT                              | AACGTGCTGG  | GTGATGCGCT  | GGCAGCGGGG . | ATCATGGCCC   | 1560  |
| 5   | ATATATGTCG   | GAAGGATTTT                              | GCCCGGGACA  | CAGGCACCGA  | GAAACTGCTG   | CCCTGCGAGA   | 1620  |
| -   | CCAAGCCAGT   | GAGCCTCCAG                              | GAGATCGTGG  | CAGCCCAGCA  | GAATGGCTGT   | GTGAAGAGTG   | 1680  |
|     | TAGCCGAGGC   |   |             |             |              |              | 1740  |
|     | TGGAGCGGGA   |   |             |             |              |              | 1800  |
|     | AGCTGGAGAC   |   |             |             |              |              | 1860  |
| 10  | GGGTCCTGAG   | CAAIGICIGA                              | GCCIGCGAG   | CIGCAGGGGC  | CACCCCCCAC   | CCCCCCACCAT  | 1920  |
| 10  |              |   |             |             |              |              |       |
|     | CACACATTCT   | TCTCACCCTT                              | GAGAGGCTGG  | AATTAACCCC  | GCTTGACGGA   | AAATGTATUT   | 1980  |
|     | CAGAGAAGGG   | AAAGGCTGCA                              | TGGGGGAGCC  | CCATCCAGGG  | AGTGATGGGC   | CCGGCATTGC   | 2040  |
|     | CTGAGGCCCC   | GCTGTGACAG                              | TTTCCCCCGGT | GTGAGCCCGG  | TGAGGGCGGC   | AGGCAGGGGT   | 2100  |
| 1.5 |              |   |             | TGAGGCTCTG  |              |              | 2160  |
| 15  |              |   |             | TCAAATCTTT  |              |              | 2220  |
|     |              |   |             | GGCCCAGGCC  |              |              | 2280  |
|     |              |   |             | GCCCAGGGCC  |              |              | 2340  |
|     |              |   |             | CACGTGTCTT  |              |              | 2400  |
|     | GGAGACAGAT   | GTCTTTACTA                              | GAGCTGAAAG  | GCCCCCTTGA  | CACATCCAGG   | CCAACCTCCC   | 2460  |
| 20  | ATGGAATAGG   | TAGGCAAGCC                              | AGGACTCCGG  | GAAGGAGGTG  | CAGCCAGGAT   | GCTCTGGTGG   | 2520  |
|     | AGCTGCCGAT   | GGGGCCCTGG                              | TGTCAGAACT  | CCCCAAAGGC  | CTGTGCGTCC   | AAGTGGAGTC   | 2580  |
|     |              |   |             | TTCAGTGTTA  |              |              | 2640  |
|     |              | AAAAAAAA                                |             |             |              |              | 2663  |
|     |              | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, |             |             |              |              |       |
| 25  | Sea ID NO:   | C118 DNA Se                             | equence     |             |              |              |       |
|     |              |   | #: NM_005   | 689         |              |              |       |
|     |              | ence: 278.                              |             |             |              |              |       |
|     | couring acqu | acineci E.o.                            |             |             |              |              |       |
|     | 1            | 11                                      | 21          | 31          | 41           | 51           |       |
| 30  | ī            | ī                                       | 1           | Ĩ-          | i            | Ĩ            |       |
| 50  | COCCECCA     | TOTAL CARC                              | COTCCCCCC   | CCAGAGCCAG  | CCCCCCCCCTC  | CTCAGACGC    | 60    |
|     |              |   |             | GCGCGTGCGC  |              |              | 120   |
|     |              |   |             |             |              |              | 180   |
|     | CCTGGTCCAC   | GIGCGICCCT                              | TCCCGGGACC  | CCCGCAGCTT  | *CECCCCAGC   | BOOCCERCOCC  |       |
| 35  |              |   |             | CCGAGTGACA  |              |              | 240   |
| 22  |              |   |             | CATTGCCATG  |              |              | 300   |
|     |              |   |             | GATGCAGGAT  |              |              | 360 . |
|     |              |   |             | TCTAGGGACT  |              |              | 420   |
|     |              |   |             | TGCTGATTCG  |              |              | 480   |
| 40  |              |   |             | TCTGGCCACA  |              |              | 540   |
| 40  |              |   |             | CCGGGGGGCC  |              |              | 600   |
|     |              |   |             | CGCCTGTGGC  |              |              | 660   |
|     | GCGGAGCCAG   | GCACGGCAGC                              | GTCTGGCAAT  | GGGCATCTGG  | ATCAAGTTCA   | GGCACAGCCC   | 720   |
|     |              |   |             | TGCAGCTGAG  |              |              | 780   |
|     | GAACAGCCCA   | CAGTGGTGGT                              | GGGCAAGGGC  | AGACTTGGGC  | CAACAGGTTC   | AGTTTAGCCT   | 840   |
| 45  | GTGGGTGCTG   | CGGTATGTGG                              | TCTCTGGAGG  | GCTGTTTGTC  | CTGGGTCTCT   | GGGCCCCTGG   | 900   |
|     | ACTTCGTCCC   | CAGTCCTATA                              | CATTGCAGGT  | TCATGAAGAG  | GACCAAGATG   | TGGAAAGGAG   | 960   |
|     | CCAGGTTCGG   | TCAGCAGCCC                              | AACAGTCTAC  | CTGGCGAGAT  | TTTGGCAGGA   | AGCTCCGCCT   | 1020  |
|     | CCTGAGTGGC   | TACCTGTGGC                              | CTCGAGGGAG  | TCCAGCTCTG  | CAGCTGGTGG   | TGCTCATCTG   | 1080  |
|     |              |   |             |             |              | TCTATAGGAA   | 1140  |
| 50  | CATTGTGAAC   | TTGCTGACTG                              | AGAAGGCACC  | TTGGAACTCT  | CTGGCCTGGA   | CTGTTACCAG   | 1200  |
| ••  |              |   |             |             |              | TCGTGAGCAA   | 1260  |
|     |              |   |             |             |              | TGGAGCTGCT   | 1320  |
|     |              |   |             |             |              | GCACAGGGGA   | 1380  |
|     |              |   |             |             |              | GCTACCTGGT   | 1440  |
| 55  |              |   |             |             |              | TCAGCATGTT   | 1500  |
| 55  |              |   |             |             |              | TCACCCTGAC   | 1560  |
|     |              |   |             |             |              | AGGAGAACGC   | 1620  |
|     |              |   |             |             |              | ATTACAACGC   | 1680  |
|     |              |   |             |             |              | GTTTGGAGTG   | 1740  |
| 60  |              |   |             |             |              | TTGGGCTCGG   | 1800  |
| 00  |              |   |             |             |              | TACAGGTTGG   | 1860  |
|     |              |   |             |             |              |              | 1920  |
|     |              |   |             |             |              | ATTGGTTTGG   | 1980  |
|     | CACCTACTAC   | AGGATGATO                               | AGACCAACT   | CATTGACATG  | GAGAACAIGI   | TTGACTTGCT   | 2040  |
| 65  |              |   |             |             |              | TTCAGAAGGG   |       |
| 05  |              |   |             |             |              | CTCTGCAGGA   | 2100  |
|     |              |   |             |             |              | CTGGGGCAGG   | 2160  |
|     | GAAGAGCACA   | ATTTTGCGC                               | C TGCTGTTTU | CTTCTACGAC  | ATCAGCTCTC   | GCTGCATCCG   | 2220  |
|     |              |   |             |             |              | ACATTGGAGT   | 2280  |
| 70  | TGTGCCCCA    | A GACACTGTC                             | C TCTTTAATG | A CACCATOGO | GACAATATCO   | GTTACGGCCG   | 2340  |
| 70  |              |   |             |             |              | TCCATGATGC   | 2400  |
|     |              |   |             |             |              | TGAAGCTGAG   | 2460  |
|     | CGGCGGGGA    | AAGCAGCGC                               | G TOGCCATTG | C CCGCACCAT | CTCAAGGCT    | CGGGCATCAT   |       |
|     | TCTGCTGGA'   | r gaggcaacg                             | T CAGCGCTGG | A TACATCTAA | r gagagggcci | A TCCAGGCTTC | 2580  |
|     | TCTGGCCAA    | A GTCTGTGCC                             | A ACCGCACCA | C CATCGTAGT | GCACACAGG    | TCTCAACTGT   | 2640  |
| 75  | GGTCAATGC    | T GACCAGATO                             | C TOGTCATCA | A GGATGGCTG | C ATCGTGGAG  | A GGGGACGACA |       |
|     |              |   |             |             |              | C AGCAGGGACA |       |
|     |              |   |             |             |              | A AGTTTGGCCA |       |
|     | CTTCCCTCT    | C AAAGACTAA                             | C CCAGAAGGG | A ATAAGATGT | 3 TCTCCTTTC  | C CTGGCTTATT |       |
|     | TCATCCTGG    | T CTTGGGGTA                             | T GGTGCTAGC | T ATGGTAAGG | 3 AAAGGGACC  | TTCCGAAAAA   | 2940  |
| 80  |              |   |             | G TGAAAAAA  |              |              | 2993  |
|     |              |   |             |             |              |              |       |
|     | CON TO NO    | . C130 DNA                              | Camianca    |             |              |              |       |

|          | 1          | 11                       | 21                | 31         | 41   | 51                          |              |
|----------|------------|--------------------------|-------------------|------------|--|-----------------------------|--------------|
|          | GGGCAATTTG | TTAGTTATCC               | CCCCCACCA         | AGACGCCCA  |  | 10000000000                 |              |
| 5        | CCCCGCGCGG | GCGCGAACTT               | TGGGCTCGGG        | CGAGTGGGTG | GTGCTCCGCC                                   | CAGCCCGAGA                  | 60<br>120    |
|          | CGGGCGGGCG | CGCGGGCCAA               | TGGGTGCCGC        | CTCTTGGCCG | CGGGGGGCCC                                   | CGACCCGTGG                  | 180          |
|          | GTCCCGGCCA | CCAGCGCCCC               | AGCCCCGAGG        | CTCAGAAGCG | GCAGGCGGAG                                   | GCGCGGTCCG                  | 240          |
|          |            | CCATGCCCGG               |                   |            |  |                             | 300          |
| 10       | ACCTCCCCCT | CCGGGGCCCA<br>GGAGCTGGTC | ATOGCOGG          | CCATGCTGCT | GGAGACACAG                                   | GACGCGCTGT                  | 360          |
|          | CCGCGGTGGG | CACGGCGAAC               | ACTCTGCAGA        | CCCCACCAA  | CTACTTCCTG                                   | CTGTGTGTGCG                 | 420<br>480   |
|          | CTGCGGCCGA | CGTGGCCGTG               | GGGCTCTTCG        | CCATCCCCTT | TGCCATCACC                                   | ATCAGCCTGG                  | 540          |
|          | GCTTCTGCAC | TGACTTCTAC               | GGCTGCCTCT        | TCCTCGCCTG | CTTCGTGCTG                                   | GTGCTCACGC                  | 600          |
| 15       | AGAGCTCCAT | CTTCAGCCTT               | CTGGCCGTGG        | CAGTCGACAG | ATACCTGGCC                                   | ATCTGTGTCC                  | 660          |
| 13       | CGCTCAGGTA | TAAAAGTTTG<br>CTTTGGCATC | GTCACGGGGA        | CCCGAGCAAG | AGGGGTCATT                                   | GCTGTCCTCT                  | 720          |
|          | CCACCAACAA | CTGCACAGAA               | CCTGGGATG         | GAACCACGAA | TCANACTCC                                    | AAAGACAGTG                  | 780          |
|          | AGTGTCTCTT | TGAGAATGTG               | GTCCCCATGA        | GCTACATGGT | ATATTTCAAT                                   | TTCTTTGGGT                  | 840<br>900   |
| 20       | GTGTTCTGCC | CCCACTGCTT               | ATAATGCTGG        | TGATCTACAT | TAAGATCTTC                                   | CTGGTGGCCT                  | 960          |
| 20       | GCAGGCAGCT | TCAGCGCACT               | GAGCTGATGG        | ACCACTCGAG | GACCACCCTC                                   | CAGCGGGAGA                  | 1020         |
|          | TCCATGCAGC | CAAGTCACTG               | GCCATGATTG        | TGGGGATTTT | TGCCCTGTGC                                   | TGGTTACCTG                  | 1080         |
|          | GGGCAATGAA | TAACTGTGTC<br>TATGGCCATT | CTTCTCTCAC        | AGCCAGCTCA | GGGTAAAAAT                                   | AAGCCCAAGT                  | 1140         |
| 0.5      | ATGCTTACCG | GAACCGAGAC               | TTCCGCTACA        | CTTTTCACAA | AATTATCTCC                                   | AGGTATCTTC                  | 1200<br>1260 |
| 25       | TCTGCCAAGC | AGATGTCAAG               | AGTGGGAATG        | GTCAGGCTGG | GGTACAGCCT                                   | GCTCTCGGTG                  | 1320         |
|          | TGGGCCTATG | ATCTAGGCTC               | TCGCCTCTTC        | CAGGAGAAGA | TACAAATCCA                                   | CAAGAAACAA                  | 1380         |
|          | AGAGGACACG | GCTGGTTTTC               | ATTGTGAAAG        | ATAGCTACAC | CTCACAAGGA                                   | AATGGACTGC                  | 1440         |
|          | AGGCTCCAAG | CACTTCCCTG<br>GATTGACAAA | TATATTTATC        | ATCTATTCAC | AATATGTATG                                   | TGTCAGTAGT                  | 1500         |
| 30       | ATGCCAACAG | CTTGAATGGA               | TTCTAACAGA        | CTCTTTTGTT | TTTAAAAGTC                                   | TGCCTTGTTT                  | 1560<br>1620 |
|          | ATGGTGGAAA | ATTACTGAAA               | CTATTTTACT        | GTGAAACAGT | GTGAACTATT                                   | ATAATGCAAA                  | 1680         |
|          | TACTTTTTAA | CTTAGAGGCA               | ATGGAAAAAT        | AAAAGTTGAC | TGTACTAAAA                                   | ATG                         | 1733         |
| <u> </u> | Seg ID NO: | C120 DNA Se              | emence            |            | •  |                             |              |
| 35       |            | id Accession             |                   | 932        |  |                             |              |
|          |            | ence: 217                |                   |            |  |                             |              |
|          | 1          | 11                       | 21                | 31         | 41   | 51                          |              |
| 40       | L          | 1                        | 1                 | 1          | 1  | 1                           |              |
| 40       | CCCAGCCCGG | CCCCGCCGCC               | CCGGCTGCGC        | ACGCGACGCC | CCCTCCAGGC                                   | CCCGCTCCTG                  | 60           |
|          | GAAGCGGAGC | GGTCATTCGG<br>CGGCGCCGGC | GGGGCAAGCG        | GCGGGAGGGG | AAACGTGCGC                                   | GGCCGAAGGG                  | 120          |
|          | GAGCCCACGA | GGCTGCCGCA               | TCCTGCCCTC        | GGAACAATGG | GACTICGCCA                                   | CCTCGGCTGG                  | 180<br>240   |
| 40       | TGGGCCGCGC | TGCTCCTGGG               | GACGCTGCAG        | GTGCTAGCGC | TGCTGGGGGC                                   | CGCCCATGAA                  | 300          |
| 45       | AGCGCAGCCA | TGGCGGAGAC               | TCTCCAACAT        | GTGCCTTCTG | ACCATACAAA                                   | TGAAACTTCC                  | 360          |
|          | AACAGTACTG | TGAAACCACC               | AACTTCAGTT        | GCCTCAGACT | CCAGTAATAC                                   | AACGGTCACC                  | 420          |
| •        | ACCRIGAAAC | CTACAGCGGC<br>CCTTAAAGTC | TRORCCORRA        | ACAACACCAG | GGATGGTCTC                                   | AACAAATATG                  | 480          |
| ~~       | ATATCAACAT | CCACAATGAC               | CGTAACCCAC        | AATAGTTCAG | TGACATCTGC                                   | TGCTTCATCA                  | 540<br>600   |
| 50       | GTAACAATCA | CAACAACTAT               | <b>GCATTCTGAA</b> | GCAAAGAAAG | GATCAAAATT                                   | TGATACTGGG                  | 660          |
|          | AGCTTTGTTG | GTGGTATTGT               | ATTAACGCTG        | GGAGTTTTAT | CTATTCTTA                                    | CATTCCCATCC                 | 720          |
|          | AAAATGTATT | ACTCAAGAAG               | AGGCATTCGG        | TATCGAACCA | TAGATGAACA                                   | TGATGCCATC                  | 780          |
|          | TTTGGTTTAT | ATCCATGGAC TAATAGTTTA    | CAAGGATGGA        | ATACAGATIG | ATGCTGCCCT                                   | ATCAATTAAT                  | 840          |
| 55       | GCATATAATG | TACAGTGTAT               | TACGTAAATA        | TGTAAAGATT | CTTCAAGGTA                                   | ACAGGCCAT                   | 900<br>960   |
|          | GGGTTTTGAA | ATAAACATCT               | <b>GGATCTTATA</b> | GACCGTTCAT | ACAATGGTTT                                   | TAGCAAGTTC                  | 1020         |
|          | ATAGTAAGAC | AAACAAGTCC               | TATCTTTTTT        | TTTTTGGCTG | GGGTGGGGGC                                   | ATTGGTCACA                  | 1080         |
|          | TATGACCAGT | AATTGAAAGA<br>GTCACAGCAC | CGTCATCACT        | GAAAGACAGA | ATGCCATCTG                                   | GGCATACAAA                  | 1140         |
| 60       | TCAGTGCTTT | TCAGAGCTGG               | ATATATCTTA        | STACTATA   | CCACACAGAA                                   | ATAAAGAACT                  | 1200<br>1260 |
|          | CAAACTAGAT | CTGAAGCATA               | ATTTAAGAAA        | AACATCAACA | J. J. L. | יייבירים א א בייריי         | 1320         |
|          | AGTAGTTGGT | CTAGAAACAA               | AATACTCCAA        | GAAAAAGAAA | ATTTTCAAAT                                   | AAAACCCAAA                  | 1380         |
|          | ATAATAGCTT | TGCTTAGCCC               | TGTTAGGGAT        | CCATTGGAGC | ATTAAGGAGC                                   | ACATATTTT                   | 1440         |
| 65       | AACTGCAGTG | TTTGAGCTTT<br>TTTAACATAA | TAATGITGAT        | ALCACTTACT | TOTOLOGIGI                                   | AATTTAGGTA                  | 1500         |
|          | GGCATTATAG | GGAAAAAACC               | TCCTAGAAGT        | TAGATTATTT | GCTACTGTGA                                   | GAATATTGTC                  | 1560<br>1620 |
|          | ACCACTGGAA | GTTACTTTAG               | TTCATTTAAT        | TTTAATTTTA | TATTTTGTGA                                   | ATATTTTAAG                  | 1680         |
|          | AACTGTAGAG | CTGCTTTCAA               | TATCTAGAAA        | TTTTTAATTG | AGTGTAAACA                                   | CACCTAACTT                  | 1740         |
| 70       | ACTATACCCT | AACCGCTTGT               | ATGATTTTCA        | AAAGAACATT | TAGAATTCTA                                   | TAGAGTCAAA                  | 1800         |
| . •      | AACCTGCAGG | ATGAAAATGC               | TATITAGEC         | TTCATCCACT | GGACTTCCCC                                   | CICAGATTIG                  | 1860<br>1920 |
|          | GGGAAATGAC | ATTTTTATAC               | TAAAACAAAC        | ACCAAAATAT | TTTAGAATAA                                   | ATTCTTAGAA                  | 1920         |
|          | AGTTTTGAGA | GGAATTTTTA               | GAGAGGACAT        | TTCCTCCTTC | CTGATTTGGA                                   | TATTCCCTCA                  | 2040         |
| 75       | AATCCCTCCT | CTTACTCCAT               | GCTGAAGGAG        | AAGTACTCTC | AGATGCATTA                                   | <b>ፕሬፕሞል አጥር</b> ርል         | 2100         |
| 13       | CATTTTACAC | ACAGTATTGT               | AGAGACACCA        | ATATTAGCTA | ATGTATTTTG                                   | GAGTGTTTTC                  | 2160         |
|          | TGTAGTCACA | TTTATATTCC<br>GTAAATACTA | AGATCCCATT        | TCTATCTCAC | AGGGCCAAAC                                   | AAAAGAGGTA                  | 2220         |
|          | CAGTTTCTGA | AGGTCCTAAA               | AATAGCTCAG        | ATGTCCTAAT | GAACATGCAC                                   | CTACATTAA                   | 2280<br>2340 |
| 80       | TAGGAGTACA | ATAAAACTGT               | TGTCAGCTTT        | TGTTTTACAG | AGAACGCTAG                                   | ATATTAAGAA                  | 2400         |
| 80       | TTTTGAAATG | GATCATTTCT               | ACTTGCTGTG        | CATTTTAACC | AATAATCTGA                                   | TGAATATAGA                  | 2460         |
|          | GGAAATTTTC | CCAAAATATG<br>TGAAAAATAC | GATATGATTG        | GATGTATGTA | ACACATACAT                                   | GGAGTATGGA                  | 2520         |
|          | CIGAGIIGIA | TGTTACTAAC               | TTGGCCCTGA        | CTGGTTGTGC | AACCATTGCT                                   | לושרוי וושרוי עייוון עייוון | 2580<br>2640 |
|          | GCAAAATGTA | GTTAAGATAT               | ACTITATION        | AATGAAGGCC | TTTTAAATTT                                   | GTCCACTGCA                  | 2700         |
|          |            |                          |                   |            |  |                             |              |

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                                                                                    2880
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                                                                                    2940
       TTTTTGTTGT TGTTATCTAT AAAAATTGAG GGAAATGGTT ATGCAAAAAA ATATTTTGCT
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       TTGGACCATA TTTCTTAAGC ATAAAAAAAT GCTCAGTTTT GCTTGCATTC CTTGAGAATG
                                                                                    3060
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       CAGTATATTA TAGTGATAAT TITGTATTIT CAAMAAAAA AAAGTTAAAC TCTTCTTTTC
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       GAGACCCAGC TGCTGCTGGA GGTGCCGCCG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC
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                                                                                    720
                                                                                    726
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       Nucleic Acid Accession #: AK091896.1
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       Coding sequence: 28..1572
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ATCGCCTTCC TGGGGCCCAC GCTGCTGGAC CTGCGTGTC AGACGCACAG CTCGCTGCCC
                                                                                    120
                                                                                    180
        CAGATCTCCT GGGTCTTCTT CTCGCAGCAG CTCTGCCTCC TGCTGGGCAG CGCCCTCGGG
                                                                                    240
        GGCGTCTTCA AAAGGACCCT GGCCCAGTCA CTATGGGCCC TGTTCACCTC CTCTCTGGCC
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                                                                                     1860
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                                                                                     1920
                                                                                     1980
        TTAAGCAAAA CAAGCTGCAA GTTATTCCCT GGCATGCTCA AAGGATTTTC GTGCTTTTCA
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                                                                                     2100
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80
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|           | CTGCAAACCC                              | AGCGCAACTA  | CGGTCCCCCG        | GTCAGACCCA        | GGATGGGGCC        | AGAACGGACA   | 60    |
|-----------|---|-------------|-------------------|-------------------|-------------------|--------------|-------|
|           |   | CGCTGCCGCT  |                   |                   |                   |              | 120   |
|           |   | ACAATGTTGG  |                   |                   |                   |              | 180   |
| •         |   | ATGCAGTGCA  |                   |                   |                   |              | 240   |
| 5         | TCACCCTGGA                              | GTGGCTTTCC  | TGAGAACCGA        | ATGGGAGATG        | TGTATAAATG        | TCCTGTTGAC   | 300   |
|           | CTATCCACTG                              | CCACATGTGA  | AAAACTAAAT        | TTGCAAACTT        | CAACAAGCAT        | TCCAAATGTT   | 360   |
|           | ACTGAGATGA                              | AAACCAACAT  | GAGCCTCGGC        | TTGATCCTCA        | CCAGGAACAT        | GGGAACTGGA   | 420   |
|           | GGTTTTCTCA                              | CATGTGGTCC  | TCTGTGGGCA        | CAGCAATGTG        | GGAATCAGTA        | TTACACAACG   | 480   |
|           | GGTGTGTGTT                              | CTGACATCAG  | TCCTGATTTT        | CAGCTCTCAG        | CCAGCTTCTC        | ACCTGCAACT   | 540   |
| 10        |   | CTTCCCTCAT  |                   |                   |                   |              | 600   |
|           | CCTTGGGATG                              | CAGTAAAGAA  | TTTTTTGGAA        | AAATTTGTAC        | AAGGCCTTGA        | TATAGGCCCC   | 660   |
|           |   | AGGTGGGGTT  |                   |                   |                   |              | 720   |
|           | AACACATATA                              | AAACCAAAGA  | ACADATCATT        | CTACCAACAT        | COCACACATO        | GITIMACTIG   |       |
|           | GGGGACCTCA                              | CAAACACATT  | CCCACCAATT        | CARTAGGA          | CCCAGACATC        | CCAMINIGGI   | 780   |
| 15        | CCTTCTCCTC                              | GGCGACGAAG  | TCCTACCAAA        | CANTAIGCAA        | GAAAATATGC        | CTATTCAGCA   | 840   |
| 10        | CATCATCCTT                              | CARCORCORAG | ACCORCINCARA      | CAMCAAMGGIAG      | TIGIAACIGA        | CGGTGAATCA   | 900   |
|           | TTTCCCCATAC                             | CAATGTTGAA  | AGCIGIGATI        | GATCAATGCA        | ACCATGACAA        | TATACTGAGG   | 960   |
|           | IIIGGCATAG                              | CAGTTCTTGG  | GTACTTAAAC        | AGAAACGCCC        | TIGATACTAA        | AAATTTAATA   | 1020  |
|           | AAAGAAATAA                              | AAGCGATCGC  | TAGTATTCCA        | ACAGAAAGAT        | ACTTTTTCAA        | TGTGTCTGAT   | 1080  |
| 20        | GAAGCAGCTC                              | TACTAGAAAA  | GGCTGGGACA        | TTAGGAGAAC        | AAATTTTCAG        | CATTGAAGGT   | 1140  |
| 20        | ACTGTTCAAG                              | GAGGAGACAA  | CTTTCAGATG        | GAAATGTCAC        | AAGTGGGATT        | CAGTGCAGAT   | 1200  |
|           | TACTCTTCTC                              | AAAATGATAT  | TCTGATGCTG        | GGTGCAGTGG        | GAGCTTTTGG        | CTGGAGTGGG   | 1260  |
|           | ACCATTGTCC                              | AGAAGACATC  | TCATGGCCAT        | TTGATCTTTC        | CTAAACAAGC        | CTTTGACCAA   | 1320  |
|           | ATTCTGCAGG                              | ACAGAAATCA  | CAGTTCATAT        | TTAGGTTACT        | CTGTGGCTGC        | AATTTCTACT   | 1380  |
| 25        | GGAGAAAGCA                              | CTCACTTTGT  | TGCTGGTGCT        | CCTCGGGCAA        | ATTATACCGG        | CCAGATAGTG   | 1440  |
| 25        | CTATATAGTG                              | TGAATGAGAA  | TGGCAATATC        | ACGGTTATTC        | AGGCTCACCG        | AGGTGACCAG   | 1500  |
|           |   | ATTTTGGTAG  |                   |                   |                   |              | 1560  |
|           | GACGTGCTCT                              | TGGTAGGTGC  | ACCAATGTAC        | ATGAGTGACC        | TAAAGAAAGA        | GGAAGGAAGA   | 1620  |
|           | GTCTACCTGT                              | TTACTATCAA  | AAAGGGCATT        | TTGGGTCAGC        | ACCAATTTCT        | TGAAGGCCCC   | 1680  |
| 20        | GAGGGCATTG                              | AAAACACTCG  | ATTTGGTTCA        | GCAATTGCAG        | CTCTTTCAGA        | CATCAACATG   | 1740  |
| 30        | GATGGCTTTA                              | ATGATGTGAT  | TGTTGGTTCA        | CCACTAGAAA        | ATCAGAATTC        | TGGAGCTGTA   | 1800  |
|           | TACATTTACA                              | ATGGTCATCA  | GGGCACTATC        | CGCACAAAGT        | ATTCCCAGAA        | AATCTTGGGA   | 1860  |
|           |   | CCTTTAGGAG  |                   |                   |                   |              | 1920  |
|           | GATTTAAATG                              | GGGATTCCAT  | CACCGATGTG        | TCTATTGGTG        | CCTTTCGACA        | ACTCCTTCAA   | 1980  |
|           | CTCTGGTCAC                              | AAAGTATTGC  | TGATGTAGCT        | ATAGAAGCTT        | CATTCACACC        | ACRARARATO   | 2040  |
| 35        | ACTITIGGTCA                             | ACAAGAATGC  | TCAGATAATT        | CTCABACTCT        | COTTCACTCC        | AAACTTCACA   | 2100  |
|           |   | AAAACAATCA  |                   |                   |                   |              | 2160  |
|           |   | GAGTAACCTC  |                   |                   |                   |              | 2220  |
|           | AAGAATATGG                              | TAGTAAATCA  | ACCACACACAC       | TITAMAGAAA        | VCVVIOVED         | MARK CACCAG  |       |
|           | CCCTCTCATC                              | TTGTCAACTC  | TOCHCAGAGA        | CONCECCIONOC      | TCATCALLIA        | 1A1ACAGGAG   | 2280  |
| 40        | ACTAGCCCTG                              | CCCTTGAAGC  | CTATTCTCAC        | COLOTOGACA        | TCAGICIGGA        | MAACCCTGGC   | 2340  |
|           | AAACACTCTC                              | GTGAGGATGG  | CIMITCIONG        | MCIGCCAAGG        | TCTTCAGTAT        | TCCTTTCCAC   | 2400  |
|           | CCACCTCCTC                              | SIGNOGRIGG  | ACTITICATT        | TCTGATCTAG        | TCCTAGATGT        | CCGACAAATA   | 2460  |
|           | CENGCIGCIC                              | AAGAACAACC  | CITIATIGIC        | AGCAACCAAA        | ACAAAAGGTT        | AACATTITCA   | 2520. |
|           |   | AAAATAAAAG  |                   |                   |                   |              | 2580  |
| 45        | GAAAACTTGT                              | TTTTTGCATC  | ATTCTCCCTA        | CCGGTTGATG        | GGACAGAAGT        | AACATGCCAG   | 2640  |
| 73        | GIGGCIGCAT                              | CTCAGAAGTC  | TGTTGCCTGC        | GATGTAGGCT        | ACCCTGCTTT        | AAAGAGAGAA   | 2700  |
|           | CAACAGGTGA                              | CTTTTACTAT  | TAACTTTGAC        | TTCAATCTTC        | AAAACCTTCA        | GAATCAGGCG   | 2760  |
|           | TCTCTCAGTT                              | TCCAAGCCTT  | AAGTGAAAGC        | CAAGAAGAAA        | ACAAGGCTGA        | TAATTTGGTC   | 2820  |
|           |   | TTCCTCTCCT  |                   |                   |                   |              | 2880  |
| 50        | AATTTTTATG                              | AAATCTCTTC  | GGATGGGAAT        | GTTCCTTCAA        | TOGTGCACAG        | TTTTGAAGAT   | 2940  |
| 50        | GTTGGTCCAA                              | AATTCATCTT  | CTCCCTGAAG        | GTAACAACAG        | GAAGTGTTCC        | AGTAAGCATG   | 3000  |
|           | GCAACTGTAA                              | TCATCCACAT  | CCCTCAGTAT        | ACCAAAGAAA        | AGAACCCACT        | GATGTACCTA   | 3060  |
|           | ACTGGGGTGC                              | AAACAGACAA  | GGCTGGTGAC        | ATCAGTTGTA        | ATGCAGATAT        | CAATCCACTG   | 3120  |
|           |   | AAACATCTTC  |                   |                   |                   |              | 3180  |
| 66        | GAATTGAACT                              | GCAGAACTGC  | TTCCTGTAGT        | AATGTTACCT        | GCTGGTTGAA        | AGACGTTCAC   | 3240  |
| 55        | atgaaaggag                              | AATACTTTGT  | TAATGTGACT        | ACCAGAATTT        | GGAACGGGAC        | TTTCGCATCA   | 3300  |
|           | TCAACGTTCC                              | AGACAGTACA  | GCTAACGGCA        | GCTGCAGAAA        | TCAACACCTA        | TAACCCTGAG   | 3360  |
|           | ATATATGTGA                              | TTGAAGATAA  | CACTGTTACG        | ATTCCCCTGA        | TGATAATGAA        | ACCTGATGAG   | 3420  |
|           | AAAGCCGAAG                              | TACCAACAGG  | <b>AGTTATAATA</b> | <b>GGAAGTATAA</b> | TTGCTGGAAT        | CCTTTTGCTG   | 3480  |
| <b>CO</b> | TTAGCTCTGG                              | TTGCAATTTT  | ATGGAAGCTC        | <b>GGCTTCTTCA</b> | AAAGAAAATA        | TGAAAAGATG   | 3540  |
| 60        | ACCAAAAATC                              | CAGATGAGAT  | TGATGAGACC        | ACAGAGCTCA        | GTAGCTGAAC        | CAGCAGACCT   | 3600  |
|           | ACCTGCAGTG                              | GGAACCGGCA  | GCATCCCAGC        | CAGGGTTTGC        | TGTTTGCGTG        | CATGGATTTC   | 3660  |
|           |   |             |                   |                   |                   | ATTTTAAGAG   | 3720  |
|           | AAAACTGCAG                              | GTCAGTTTGG  | ATGAAGAAAT        | TGTGGGGGGT        | GGGGGAGGTG        | CGGGGGGCAG   | 3780  |
| 10        | GTAGGGAAAT                              | AATAGGGAAA  | ATACCTATTT        | TATATGATGG        | GGGAAAAAA         | GTAATCTTTA   | 3840  |
| 65        | AACTGGCTGG                              | CCCAGAGTTT  | ACATTCTAAT        | TTGCATTGTG        | TCAGAAACAT        | GAAATGCTTC   | 3900  |
|           | CAAGCATGAC                              | AACTTTTAAA  | GAAAAATATG        | ATACTCTCAG        | ATTTTAACCC        | GGAAAACTCT   | 3960  |
|           | TCTCTTTAAA                              | ATATTTGTCT  | TTARACAGCA        | ACTACAGAAG        | TEGRACIECT        |              | 4020  |
|           | GTACTTCCAC                              | TTYSTGTATAT | TTTAATCAAT        | ATTCATCTTA        | ACARGACCCC        | AAAACAAAAC   | 4080  |
|           | ACAGGTTTTT                              | TCAATTTATG  | CTCCTCATCC        | AAACTTCCCA        | CACATCATAC        |              |       |
| 70        | TAATTTTATT                              | TATAAACTAG  | CLVVVVVV          | Target Tocol      | Calculate yas and | * I CONNOTON | 4140  |
|           | CTTCCACACC                              | CCATCTTCTAG | CENTRACTURE       | NANCARCOTTE       | CITITATACC        | GCTTAGAGTA   | 4200  |
|           | TACCTCCTAT                              | AMALICITACI | DACTTACCAC        | AGGGGGGGT         | GAATAACIGA        |              |       |
|           | delabel contract a                      | WAGICOWILL  | WANT TARRAR       | TOTALLE           | ALAGAGACTA        | MUGCACAAAA   | 4320  |
|           |   | AACTCAGAAT  |                   |                   |                   |              | 4380  |
| 75        | CONCURSORS                              | GAAGGAAAAG  | GAGGAAATTT        | COLLECTOR         | TAGGAGGCA         | CAACAGTTCT   | 4440  |
|           | TOTAGGAT                                | TTGTTTGGCT  | GACTUGCAGT        | MACCTAGTGA        | ATTITIGAAA        | GATGAGTAAT   | 4500  |
|           | TATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | ACCTTCCTCC  | TCCCTTACTG        | AACCACTCTC        | CCACCTCCTG        |              | 4560  |
|           | ATTATAGAA                               | GCCCTCTACA  | GCCTGACTTT        | CTCTCCAGCG        | GTCCAAAGTT        |              | 4620  |
|           | TACCCCTCA                               | 1 CCAAAGTTC | CCACTCCTTC        | AGGACAGCTG        | CTGTGCATTA        |              | 4680  |
| 80        | GGGAAAGTCA                              | TCTGTTTAAT  | TTACACACTT        | GCATGAATTA        | CTGTATATAA        | ACTCCTTAAC   | 4740  |
| UU        | TTCAGGGAGC                              | TATTTTCATT  | TAGTGCTAAA        | CAAGTAAGAA        | AAATAAGCTA        | GAGTGAATTT   | 4800  |
|           | CTAAATGTTG                              | GAATGTTATG  | GGATGTAAAC        | AATGTAAAGT        | AAAACACTCT        | CAGGATTTCA   | 4860  |
|           | CCAGAAGTTA                              | CAGATGAGGC  | ACTGGAAACC        | ACCACCAAAT        | TAGCAGGTGC        | ACCITCIGIG   | 4920  |
|           | GCTGTCTTGT                              | TTCTGAAGTA  | CTTTTTCTTC        | CACAAGAGTG        | AATTTGACCT        | AGGCAAGTTT   | 4980  |
|           | GTTCAAAAGG                              | TAGATCCTGA  | GATGATTTGG        | TCAGATTGGG        | ATAAGGCCCA        | GCAATCTGCA   | 5040  |
|           |   |             |                   |                   |                   |              |       |

| 5                               | ATTTCTACTT<br>CTTAGATTAA<br>AAACTTCAGA<br>TTTAGTTTTA   | CACCCCAGTC<br>TTTGCACCTT<br>AATTCACAGA<br>GTCCTCATTA<br>AAAGTCTATG<br>ACTTGGAAAA   | ATTTTCTCTG<br>CACTACATAT<br>TAAAATGGGA<br>ATCTGATCTG   | TTCCTGAGCC<br>CTAAAGCTTT<br>AGACTGAGCT   | CCCACATTCT<br>GACAAGTCCT<br>GGAGTTCAGC  | CTAGGAGAAA<br>TGACCTCTAT<br>AGTGATGCTT   | 5100<br>5160<br>5220<br>5280<br>5340<br>5361  |
|---------------------------------|--|--|--|--|---|--|---|
| 10                              | Nucleic Aci  | Cl24 DNA Se<br>d Accession<br>ence: 103  | า#: NM_0314  | 60 .   |   |  |   |
|                                 | 1  | 11<br>   | 21   | 31   | 41  | 51<br>I  |   |
| 1.0                             | AGCAGGCGTT   | TGCGAGAGGA   | GATACGAGCT   | GGACGCCTGG   | CCCTTCCCTC  | CCACCGGGTC   | 60  |
| 15                              |  | GCTCCCGGCG   |  |  |   |  | 120   |
|                                 | CGGGCGGCTC   | CCGAGGGCAG   | GGTCCGGGGC   | TGCGCGGTGC   | CCAGCACCGT  | GCTCCTGCTG   | 180   |
|                                 | GCGCCTACC  | TGGCTTACCT<br>ACTCCAGCCG   | CAGCTTCCAG   | CCCGCCGTGT   | TCTGGACGCT  | GGAGGGCCGC   | 240<br>300  |
|                                 |  | ACCGCCCGGC   |  |  |   |  | 360   |
| 20                              | AACGGAGCCA   | GCCTCCTCAG   | CAACACCACC   | AGCATGGGGC   | GCTGGGAGCT  | CGTGGGCTCC   | 420   |
|                                 |  | CTGTGTCCAC   |  |  |   |  | 480   |
|                                 |  | GCCTCTTCTG<br>GACTGGGGCA   |  |  |   |  | 540   |
|                                 |  | GGCAGGATCC   |  |  |   |  | 600<br>660  |
| 25                              |  | TGCTCTTCCT   |  |  |   |  | 720   |
|                                 | AGCTACACAG   | AGGGCTTCTA   | CTTCGCCTTC   | ATCACCCTCA   | GCACCGTGGG  | CTTCGGCGAC   | 780   |
|                                 | TACGTGATTG   | GAATGAACCC   | CTCCCAGAGG   | TACCCACTGT   | GGTACAAGAA  | CATGGTGTCC   | 840   |
|                                 | CTGTGGATCC   | TCTTTGGGAT<br>CAGGGAGGGT   | ATCTTCCTCC   | GCCTTGATCA<br>TGCCACCACA   | TCAAACTCAT  | CCTCTCCCAG   | 900   |
| 30                              |  | GGAGACAGGG   |  |  |   |  | 960<br>1020   |
|                                 | TGCTATCCAG   | AGGGACCCAT   | GGGAATCATA   | CAGCATCTGG   | AACCTTCTGC  | TCACGCTGCA   | 1080  |
|                                 | GGCTGTGGCA   | AGGACAGCTA   | GTTATACTCC   | ATTCTTTGGT   | CGTCGTCCTC  | GGTAGCAAGA   | 1140  |
|                                 |  | TAAGCTTTGC<br>GGTGCAGCTA   |  |  |   |  | 1200  |
| 35                              |  | TGGGATGTGA   |  |  |   |  | 1260<br>1320  |
|                                 |  | CGGGCTGCAA   |  |  |   |  | 1380  |
|                                 | GCACCATGAA   | GTAGCGGCAA   | TGTTTGAGCG   | <b>GCACAATTAG</b>  | ATAGGAAGAG  | TCTGGATCTC   | 1440  |
|                                 | TGATGATCAC<br>GAAATAAACA   | AGAGCCATCC   | TAACAAACGG   | AATATCACCG   | ACCCTCCTTT  | ATGTGAGAGA   | 1500<br>1519  |
| 40                              | Nucleic Ac   | C125 DNA Sold Accession  | n.#:NM_004:  | 154  |   |  |   |
|                                 |  |  |  |  |   |  |   |
| 45                              | •  | ••   | 0.1  |  |   |  |   |
| 45                              | 1  | 11   | 21<br>   | 31<br>1  | 41  | 51<br>i  |   |
| 45                              | l .  | 1  | 1  | ì  | 1   | 1  | 60  |
| 45                              | AAGGACAGAG<br>CGGAAGAACT   | <br>GAGGGGCCCT<br>GGTTCTGTGG   | <br>TCCTGTCAGC<br>AATTTGTGCT   | <br>TGGCTGGGAG<br>TATTTCCCAT   | CAGAGGTGGC<br>CAAGGATCAA  | <br>TTTGTCTTTT<br>GGACCTGCTC   | 60<br>120   |
|                                 | AAGGACAGAG<br>CGGAAGAACT<br>TGGGGCTACC   | GAGGGGCCCT<br>GGTTCTGTGG<br>TCAGGGCCCC   | TCCTGTCAGC<br>AATTTGTGCT<br>ACAGGATGAG   | <br>TGGCTGGGAG<br>TATTTCCCAT<br>GGGCTGGTTT   | CAGAGGTGGC<br>CAAGGATCAA<br>TCAGATGAGT  | TTTGTCTTTT<br>GGACCTGCTC<br>TTTCTGCTTG   | 120<br>180  |
| <ul><li>45</li><li>50</li></ul> | AAGGACAGAG<br>CGGAAGAACT<br>TGGGGCTACC<br>CCTGTCATCT   | GAGGGGCCCT<br>GGTTCTGTGG<br>TCAGGGCCCC<br>GGATAGTGTC   | TCCTGTCAGC<br>AATTTGTGCT<br>ACAGGATGAG<br>TAAAAATTTG   | <br>TGGCTGGGAG<br>TATTTCCCAT<br>GGGCTGGTTT<br>CAAACTGCCT   | CAGAGGTGGC<br>CAAGGATCAA<br>TCAGATGAGT<br>TCTTGTCAGT  | TTTGTCTTTT GGACCTGCTC TTTCTGCTTG GTCTTGCTCA  | 120<br>180<br>240   |
|                                 | AAGGACAGAG<br>CGGAAGAACT<br>TGGGGCTACC<br>CCTGTCATCT<br>TTCTTCATGA   | GAGGGGCCCT<br>GGTTCTGTGG<br>TCAGGGCCCC<br>GGATAGTGTC<br>CACTCCTGAT   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA   | TGGCTGGGAG<br>TATTTCCCAT<br>GGGCTGGTTT<br>CAAACTGCCT<br>GTTTCCTCAT   | CAGAGGTGGC<br>CAAGGATCAA<br>TCAGATGAGT<br>TCTTGTCAGT<br>CTGCTGCCTC  | TTTGTCTTTT<br>GGACCTGCTC<br>TTTCTGCTTG<br>GTCTTGCTCA<br>TCCAGACTTC   | 120<br>180<br>240<br>300  |
|                                 | AAGGACAGAG<br>CGGAAGAACT<br>TGGGGCTACC<br>CCTGTCATCA<br>TTCTTCATGA<br>TGCCAGAACA<br>CACGAGTGGG   | GAGGGGCCCT GGTTCTGTGG TCAGGGCCCC GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC   | TGGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAG   | CAGAGGTGGC<br>CAAGGATCAA<br>TCAGATGAGT<br>TCTTGTCAGT<br>CTGCTGCCTC<br>ACTGGCAGCA<br>CGAGGCACTT  | <br>TTTGTCTTTT<br>GGACCTGCTC<br>TTTCTGCTTG<br>GTCTTGCTCA<br>TCCAGACTTC<br>GGGGCTGCTC<br>GCTAACTCTT   | 120<br>180<br>240   |
| 50                              | AAGGACAGAG<br>CGGAAGAACT<br>TGGGGCTACC<br>CCTGTCATCT<br>TTCTTCATGA<br>TGCCAGAACA<br>CACGAGTGGG<br>GGATAACAAG   | GAGGGGCCCT GGTTCTGTGG TCAGGGCCCC GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCCA  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT  | TEGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAG GGCTTTGGAA  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGGTTC  | TTTGTCTTTT GGACCTGCTC TTTCTGCTCA GTCTTGCTCA TCCAGACTTC GGGGCTGCTC GCTAACTCTT AGGCTGAGGA  | 120<br>180<br>240<br>300<br>360<br>420<br>480   |
|                                 | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACGAGTGGG GGATAACAAG GATGGGTGCC   | GAGGGGCCCT GGTTCTGTGG TCAGGGCCCC GGATAGTGTC CACTCCTGAT TTGCACGGGA AATTTGCTCC ACCTCTGCCA GTCCTCAGTG   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAG GAAGCACTCA AGCCCCTGCC   | TGGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAG GGCTTTGGAA TCCCTGAACA   | CAGAGGTGGC CAAGGATGAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCACTT GGCGGAGTACT TAGGAAACCC   | TTTGTCTTTT GGACCTGCTC TTTCTGCTTG GTCTTGCTCA TCCAGACTTC GGGGCTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGGCAG   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
| 50                              | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GATGGGTGCG CCATGGAATG  | GAGGGGCCCT GGTTCTGTGG TCAGGGCCCC GGATAGTGTC CACTCCTGAT TTGCACGGGA AATTTGCTCC ACCTCTCGCT ACCTCTCAGTG GGACAATGGC   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG  | TGGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAG GGCTTTGGACA TCCCTGAACA CTCTGGGCTT   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTCT TAGGAAACCC GCCACCCACC   | TTTGTCTTT GGACCTGCTC GTCTGCTCG GTCTTGCTCA GTCTTGCTCA GCGGCTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGGCAG ACCTGTGTCT  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600   |
| 50                              | AAGGACAGAG<br>CGGAAGAACT<br>TGGGGCTACC<br>CCTGTCATCT<br>TTCTTCATGA<br>TGCCAGAACG<br>GATAACAAG<br>GGATAACAAG<br>GATGGGTGCG<br>CCATGGAATG<br>ACCGCGAGAA<br>GCCTGCCGCT  | GAGGGGCCCT GGTTCTGTGG TCAGGGCCCC GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCCA GTCCTCAGTG GGACAATTGG CTTCAAGCAA GAACATCTGT  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG CTGCTGCTGCC GTCATTACCC  | TEGCTGEGAE TATTTCCAT GEGCTGETT CAAACTGCCT GTTTCCTCAT CACAGAACTG EGACTGCAAG GEGCTTGGAA TCCCTGAACA CTCTGGACT CACCTGTTTA AGATCTGCAC   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGTG GTCCGCCGG  | TTTGTCTTT GGACCTGCTC TTTCTGCTTG GTCTTGCTCA TCCAGACTTC GGGGCTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGGCA ACCTGGGCAG GCCCTGGCTC GGCCTGACCCC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
| 50<br>55                        | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACGAGTGGG GGATAACAAG GATGGGTGCG CCATGGAATA ACCGCGAGAA GCCTGCCGCT GCACGGCCT  | GAGGGGCCCT GGATAGTGTC GCATAGTGTC GCATAGTGTC GCATAGTGTC TTGCACGCGA AATTTGCTCC ACCTCTGCCA GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA  | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG CTGCTGCTGCTGC GAACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  | TEGCTEGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT GCACGAACTG GGCTTGGAA TCCCTGAAC TCCCTGAAC CTCTGGGCTT CACCTGTTTA AGATCTGCAC TGGCTGACT   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAAACCC GCCACCCACC TTCGGGGGG GTCCCGCCGG GCTATATGCC   | TTTGTCTTTT GGACCTGCTC TTTCTGCTTG GTCTTGCTCA TCCAGACTTC GGGGGTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGGCAG ACCTGGTCT CTGGCGCTG GCCCTGACCC TGCTCCCTGC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780   |
| 50                              | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGT TGCAGAACA CACGAGTGGG GGATAACAAG GATGGGTGCG CCATGGAATA ACCGCGAGAA ACCGCGGAGAA GCCTGCCGCT CCATGCCTCAT   | GAGGGCCCT GGATAGTGTC CACTICCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCCA GTCCTCAGTG GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACAACTAT  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTG ATGTCTCTCA CAGGACCATCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG CTGCTGCTGCTGCTATTACCC GACCTTGCTC GCCAAGGTG GCCTAGGTG   | TEGCTEGEAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGCTTGGAA GGCTTTGGAA CTCCTGAACA CTCTGGGCT CACCTGTGTA AGATCTGCAC TGGCTGCAC ATCACTGCC  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT TCTTGTCAGT CTGCTGCCTC GAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGTG GTCCGCCGG GCTATATGCC CTTTGGGAA  | TTTGTCTTTT GGACCTGCTC GTCTGCTCG GTCTTGCTCA GTCTTGCTCA GCGACCTCC GCTAACTCTT AGGCTGAGGA ACCTGGGCAG ACCTGGTCCT CTGGGGGCTG GCCCTGACCC TTGGCGCTGC TTCGCCTGCC  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840   |
| 50<br>55                        | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GATGGGTGCG CCATGGAATG ACCGCAGAAA GCCTGCCGCT GCACGCCGT GCACGCCGT  | GAGGGGCCCT GGATAGTGTC GCATAGTGTC GCATAGTGTC GCATAGTGTC TTGCACGCGA AATTTGCTCC ACCTCTGCCA GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTG ATGTCTCACA CAGTTTCAGG AAGAACCAT AGCCCCTGCCC ACAGGCCAGG CTGCTGCTGCTGCTCAC GCCAAGGTGTGCTAACCCTAACCTTGCTC TATGCCAAACCTTAACCC   | TEGCTEGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG CACAGAACTG GGCTTTGGAA TCCCTGAACA CTCTGGGCTT AGATCTGCAC TGCTGACA TGCACTGACC TGCACGGCAG TGCACGGCAG TGCACGGCAG  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCAC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TTAGGAAACCC GCCACCCACC TTCGGCGGT GTCCGCCGG GCTATATGCC CATCCTCTTC  | ITTIGICITIT GGACCIGCTC GTTTCTGCTTG GTCTTGCTCA TCCAGACTTC GGGGCTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGGCA ACCTGGGCA CCTGGCTC CTGGCGCCT GCTTACCCTGC TCGCCTGCC TCGCCTGCC TCCCCTGCC TCCCCTGCC TCCCCTGCC TCCCCTGCC TCCCCTGCC TCCCCTGCC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900  |
| 50<br>55                        | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGT TGCCAGAACA CACGAGTGGG GATAACAAG GATGGGTGCG CCATGGAATA ACCGCGAGAA GCCTGCCGT CCCTGCTCAT GCACGGCGT TCAGCTTCCA TCAGCTTCCA GCCCCGGGG   | GAGGGGCCCT GGATAGTGTC CACTCCTGAT TTGCAGGGGA AATTTGCTCC ACTCTCAGTG GGACAATGGC CTTCAAGGA GAACATCTGT GTACACCCTA CTACAACTAT CTTCCTCTCTC GCGCTACCTG TGCCTACCTA  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGACCAGG CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC  | TEGCTEGEAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGCTTTGGAA TCCCTGAACA CTCTGGGCT CACCTGTGTA AGATCTGCAC TGGCTGACCT ATCACTGCC ATCACTGCC ATCACTGCC CGCTGCC CGCCTGCC CCCTGTGCC CCCTGTCC CCCTCC CCCTGTCC CCCTCC CCCTCC CCCTCC CCCTCC CCCTCCC CCCTCC CCCTCC CCCTCC CCCTCC CCCTCC CCCTCC CCCC CCCTCC CCCTCC CCCTCC CCCC CCCTCC CCCC CCCTCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT TCTTGTCAGT CTGCCTGCCTC TAGGAAACCC GCCACCCACC TTCGGCGGTG GCTATATGCC CTTTGGCAGC CTTTGGCAGC CTTTGGCAAC CTTTGGCAAC CCTTTGGCAAC CCTCTCTTC CCCCTGGAC GGCCCTGACA GGCCCTGACA GGCCCTGACA   | TTTGTCTTTT GGACCTGCTC GTCTTGCTCTG GTCTTGCTCTC GCCTACTCTT AGGCTGACGA ACCTGGGCAG ACCTGTGTCT CTGGCGGCTG GCCCTGACCCTGCT TTCGCCTGCC TTCGCCTGCC CTCACCTGCA AAACGTGGGG ACCCAGTGCC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840   |
| 50<br>55<br>60                  | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GATGGGTGC CCATGGAATA ACCGCGAGAA GCCTGCCGCT GCACGCCGT TCAGCTTCCA GCCTGCTCCAT GCCCGCGGGC TCAGCTCCAGGC  | GAGGGGCCCT GGATAGTGTC CACTCCTGAT TTGCAGGGA AATTIGCTCC ACCTCTGACT GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACCAACTAT CTTCCTCTCTC GCGCTACCTG TGCCTGCCTA CACCTCTCCTCT  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTG ATGTCTCTCA CAGATTCAGC GAAGAACCAT AGCCCCTGCC GCCAAGGC GTCATTACCC ACCTTGCTC ACCTTGCTC GCCCAAGGTG TATGCCAACC GGCATCTGCC GTGTGTTGCG GTGTGTTGCG GTCCAGGCA  | TEGCTEGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGCTTGGAA TCCCTGAACA GCTTTGGAA TCCCTGACCA AGATCTGCAC AGATCTGCAC TGGCTACCT ATCACTGCAC TGGCTACCT TCCAGCGTGGCT TCCAGCGTGGCT TCCAGCGTAGCT TCCAGCGTTAC TCCAGCGT   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT TCTTGTCAGT CTGCTGCCTC CAGAGCACTT GGCGAGGTTC TAGGAAACCC TTCGGCGGTG GTCCCGCCGG GCTATATGCC CTTTGGCAC CATCCTCTTC CCCCTGGCAC GGCCGTGACA CCGCACTGTC   | TTTGTCTTTT GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTCA GTCTTGCTCA GCGGACCTCT GGGGACCTCT AGGCTGAGGA ACCTGGGCAG GCCTGACCC TGCTCCCTGC CTCACCTGCA AAACGTGGGG ACCCAGTGCC TGCTATGACC TGCTACTGCA TGCACTGCA TGCACTGCA TGCACTGCA TGCACTGCA TGCACTGCA TGCACTGCA TGCACTGCA TGCACTGCA TGCATTGACC TGCTATGACC TGCTATGACC TGCTATGACC  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020   |
| 50<br>55                        | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GATGGGTGCG CCATGGAATG ACCCGAGAA GCCTGCGCT GCACGGCCGT TCAGCTTCCA GCCGCGGGC TCAGCTCCAGC TCAGCCCGCC   | GAGGGCCCT GGATAGTGTC CACTOCTGAT TTIGCACGCGA AATTTGCTCC ACCTCTGCA GGACAATGGC CTTCAAGCAA GAACATCTGT GTACAACCAT CTACCAACTAT CTTCCTCTCTC GCGCTACCTG TGCCTGGCT TGCCCTGGCT TGCCCTGGCCT   | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG CTCCTGCCC ACCTTGCTC GCCCAAGGTG TATGCCCAACG GGCATCTGCC GGCATCTGCAACC GGCATCTGCAACC ACCCACAGGAACCATAAA   | TEGCTEGGAE TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTTTGGAA CTCCTGGACA CTCTGGGCTT CACCTGTGTA AGATCTGCAC TGGCTGACA ACCCTGCCA ACCACTGCCA ACCACTTGCAC ACCACTGCCA   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TTAGGAAACCC GCCACCCACC GTCCGCCGG GCTATATGCC CATCCTCTC CCCTGGCAC CGCCCTGCAC CGCCCTGCCAC CGCCCTGCCAC CGCCCTGCCAC CCCTGGCAC CCCTGGCAC CCATCCTCTC CCCTGGCAC CCATCCTGCCAC CCATCCTGCCAC CCATCCTGCCAC CCATCCTGCCAC CCATCCTGCCAC CCATCGCACTGTCC CATGGCTCTC  | I TTTGCTTTT GGGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTCC GGGGCTGCTC GCTAACTCT AGGCTGAGGA ACCTGGGCA ACCTGGCTC TCGCGGCTC TCGCCTGCC TCCCTGCC TCCCTGCC TCCCTGCA AAACGTGGGG ACCCAGTGCC TGCTATGACC ACCTGTCATCA   | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>840<br>900<br>960<br>1020<br>1140   |
| 50<br>55<br>60                  | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATCT TTCTTCATGA CACGAGTGGG GGATAACAAG GCTGCGGTGGACACACGCGGTGCCTCAT CCCTGCTCAT GCCTGCTCAT GCCTGCTCAT GCCCGGGGC TCAGCCACAGC TCAGCCCGGC TCAGCCCGCC TCAGCCCGCC TCAGCCCGCC TCAGCCCGCC TCAGCCCGCC TCAGCCCGCC TCAGCCCGCC TCAGCCCGCC   | GAGGGGCCCT GGATAGTGTC GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGACT GGACAATGGC CTTCAAGTG GAACATCTGT GTACACCCTA CTACAACTAT CTTCCTCTTC GCGCTACCTG TGCCTGGCTA CATCTTCGCTT CCTCTCGCTT CCTCTGCCTA CATCTTCGCTT CCTCTCGCT  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGCACTTCAC GAAGAACCAT AGCCCTGCC ACAGGCCAGG CTGCTGCTGC GCCAAGGTG TATGCCAACC GGCATCTGCC GCCACAGGTA ACCCACAGGCA ACCCACAGGCA ACCCACATATA GCCCTGCTGG  | TEGCTEGEAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT GGACTGCAAG GGCTTTGGAA TCCCTGAAG CTCTGGGCT CACCAGAGCT AGACTGCAC TCAGGCT ATCACTGCC TGCACGCAG ACCGCTGGC CCGTTGGCT TCCAGGCTT TCCAGGCTT TCCAGGCTT TCCAGGCTT TCCAGGCTT TCCAGCTT   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCTC ACTGGCAGCA CGAGGCACTT GGCGAGAACCC TTCGGCGGGG GTCCCGCCGG GCTATATGCC CCTTGGCAC CCCCGCGGAC CCCCGGGAC CCCCGGGAC CCCCGGGAC CCCCTGGCAC CCGCTGACA CCGCACTGTC TCTCCTGCC   | TTTGTCTTTT GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTCA GGGGCTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGCAG ACCTGGCAG ACCTGACCC TGCTCCCTGC TTCGCCTGCC TCGCCTGCC TCACCTGCA AAACCTGGGA ACCTGGCA CCTAACAC TGCTACTGCA TGCTGCC TGCTATGACC TGCTATGACC ACTGTCATCG TGCCGCCTGT  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200   |
| 50<br>55<br>60                  | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GATGGGTGGG CCATGGAATA ACCGCGAGAA ACCGCGCGGC GCACGCCGGC TCAGCTCCA TCAGCTTCCA GCCGCCAGGC TCAGCCCGGC GCTTCCTGCT GCCCCGCCGGC GCTTCCTGCT GCCCCCGGCAGAC TCAGCCCGGCC GCTTCCTGCT GCCCCCGGCAGAC TCAGCCCGGCAGAC TCAGCCCGGCAGAC TCAGCCCGGCAGAC TCAGCCCTGGCT GCCCCCAGGAC TGCCCCAGGAC TGCCCCTGGTT   | GAGGGGCCCT GGATAGTGTC CACTOCTGAT TTIGCACGCGA AATTTGCTCC ACCTCTGCAG GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACAACCAT CTTCCTCTC GCGCTACCTG TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGCCAGCCAGCCT TGCCCTGCCAGCCACCTC TGCCCTGCCC   | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTCACG AGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG GTCATTACCC AACCTTGCTC GCCCAAGGTG TATGCCCAACG GGCATCTGCC GCCATGTTAGC GCCACAGGCA ACCCTGCTAGC GCCACAGGCA ACCCTGCTAGC GCCACTATA GCCCTGCTGG GAGCCTGTGGG GAGCCTGTGGG GAGCCTGTGGG GAGCCTGTGGG  | TEGCTGGAG TEGCTGGAG GGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTTGGAA CTCTGGGCT CACCTGTGTA AGACTGCCC TGGCTGACA CTCTGGGCA ACCCTGGCA ACCCCTGGC ACCCCTGGC CCGTGTGGCA ACCCCTGGC CCGTTGGCA ACCCCTGGC CCGTTGGCT TCCAGCGTAA TGCCCTATGG CCTGGCTACGC CCTGGCC CCTGGCC CCTGGCC CCTGGCC TCAGCTTCCT TCAGCTTCT TCAGCTTCT TCAGCTTCT TCAGCTTCT   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCAGCA CGAGGCACTT GGCGGAGTTC TTAGGAAACCC GCCACCCACC GTTCGGCGGG GCTATATGCC CATCCTCTC CCCTGGCAC CGGCCGTGACA CCGCACTGTC CATCGCTGTC CATGCTCTC  | TTTGTCTTTT GGGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTCA GTCTTGCTCC GGGGCTGCTC GCTAACTCT AGGCTGAGGA ACCTGGGCA ACCTGGTCT CTGGCGCTGC TCTCCCTGC TTCCCTGC TCTCCCTGC AAACCTGGGG ACCCAGTGCC TGCTATGACC ACTGTCATCA TGCGCCCGCA ATCACCAAGA   | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>840<br>900<br>960<br>1020<br>1140   |
| 50<br>55<br>60<br>65            | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACGAGTGGG GGATAACAAG GCTGCAGAACA GCCTGCAGAACA GCCTGCCGCT GCACGACGAC TCACGCCGCC GCCCACGCC GCCCCACGC GCTCCCACGC GCTCCCACGC GCTCCCAGGA TGCCCACGC GCTCCCAGGA TCACCCGCCAGGA TCACCCGCCAGGA TCACCCGCCAGGA TGCCCACGC GCTCCCTGCT GCCCCACGC GCTCCCTGCT GCCCCACGC CCTCCTGCT GCCCCACGC CCTCCCTGCT CCCCCACGC CCTCCCTGCT CCCCCACGC CCTCCCTGCT CCCCCCACGC CCCCCACGC CCCCCACGC CCCCCACGC CCCCCACGC CCCCCCACGC CCCCCCCC  | GAGGGCCCT GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC GGATAGTGTC CTCCTCAGTG GGACAATGGC CTTCAAGCAA GAACATCTGT GTACAACCTA CTACAACTAT CTACAACTAT CTACAACTAT CTCCTCTTC CGCGTACCTG CGCCTACCTG TGCCTGGCTA CATCTTCCCTTT CCCCTTTCCTCTTC TGCCTGGCTA CATCTTCCCTTT CGCCTGGCTA CACTCTGCCT GGCCTGGCTG GCCCTGGCTG GCCCTGGCTG GCCCTGCCTG  | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCTGCC ACAGGCCAGG GTCATTACCC AACCTTGCTC GCCCAAGGTG TATGCCCAAC GGCATCTGCC GGCATCTGCC GGCACAGGCA ACCCTCTATA GCCCTGCTGC GAGCCTGTGGC GAGCCTGTGGC GAGCCTTGCC CTGTTTGCC CTGTTTGCC CTGTTTGCC CTGTTTGCC CAGCCC CTCTTGCC CAGCCC CAGCCC CACAGCC CACACGCC CACACGC CACACGCC CACACGCC CACACGCC CACACGCC CACACGC CACACGCC CACACGC CACACGCC CACACGC CACACC C | TEGCTEGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGCTTCGAAC CTCTGGGCT CACCTGGAAC CTCTGGGCT ACACTGGAC TGCACGAG AGATCTGCAC TGCACGCAG ACCGCTGGC CCTGTGGCT TCCAGGAT TCCAGGAGA CCGCTGGC CCTGTGGCT TCCAGGTAG CCTGCTAGG CCTGCTAGG CCTGCTAGG CCTGCTAGG CCTGCTAGG CCTGCTAGG CCTGCTAGG CCTGCTAGG CCTGCTAGG CCTGCTACT CCAGGAGGG TCAGCTTCCT CCAGGAGGG TCAGCTTCCT CCAGGACCT CCGCTCCCCTG CCTCCCCTG  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGGTTC TTCGGCGGTG GTCCCCCCGC CTTTGGCAGC CATCCTCTTC CCCCTTGGCAC CCCTTGGCAC CCGCCTGGCAC CCGCCTGCCAC CCTTCCTCTCC CCTTTCCTCCTCC CCTTTCCTCCTC  | TTTGTCTTTT GGACCTGCTC GTCTTGCTCTG GTCTTGCTCTG GTCTTGCTCTC GCTACTCTT AGGCTGAGGA ACCTGTGCTC TCGCGGCTG GCCCTGACCC TTGCCTGC TGCATGCC TGCTATGACC ACTGCATGC TGCCGCCAA   | 120<br>180<br>240<br>300<br>360<br>420<br>420<br>600<br>660<br>720<br>780<br>960<br>960<br>1020<br>1080<br>1140<br>1200   |
| 50<br>55<br>60                  | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGT TTCTTCATGG CACGAGTGGG GGATAACAAG GCTGCGGGGAGA ACCGCGAGAA GCCTGCCGT CCCTGCTCAT GCACGGCGGC TCAGCCTGCC GCTTCCTGCT GCCTGCTGCT GCCCGGGGC TCAGCCTGCC GCTTCCTGCT GCCTGCTGCT  | GAGGGGCCCT GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC ACCTCTCAGTA ACTTCTCAGTG GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACACTAT CTTCCTCTCTC GCCCTACCTG TGCCTGGCTA CATCTTGCT TGCCTGGCTA CATCTTGCT TGCCTGGCTA CATCTTGCT TGCCCTGGCTA CATCTTGCT TGCCCTGGCTA CATCTTGCT TGCCCTGGCTA CATCTTGCT TGCCCTGGCTA CATCTTGCT TGCCCTGGCTA CATCTTGCT TGCCCTGGCCA CGCCCTTTGCT TGGCCCGGCA CGCCAGTGCCC CAAAGGCACG   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGCACTTCAC GAAGAACCAT AGCCCTTGCC GCCAAGGGC CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC  | TEGCTEGEAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGCTTGGAA CTCCTGAACA CTCTGGGCT CACCTGAACA AGATCTGCAC TTGCTGACT ATCACTGACT ATCACTGACT ATCACTGCC CCGTGTGCT CCCAGGAGGC CCTGCTCACC CCTGTTACTG CCCAGGAGCG CCTGCTCCCTGC CCAGGACCG CCAGTGCCCCTGC CCAGTGCCCCTGC CCAGTGCCCCAGC CCAGTGCCCCAGC CCAGTGCCCAGC CCAGTGCCCAG  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT TCTTGTCAGT CTGCCTGCTC TAGGAACCC TCGCGCACC TTCGGCGGTG GCTATATGCC CTTTGGCAC CATCCTCTTC CCCCCGGAC CCCTGGCAC CCCTGGCAC CCTTGGCAC CCTTTGGCAC CCCTGGCAC CCCTGGCAC CATCCTTTTC CATGGCTTC  | I TTTGTCTTTT GGACCTGCTC GTTTGCTTG GTCTTGCTTG GTCTTGCTTC GCGGCTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGGCAG ACCTGGTCT CTGGCGGCTG GCCCTGACCTGC TTCGCCTGCC TTCGCCTGCC TCACCTGCA AAACGTGGGG ACCAGTGCC TGCTATGACC ACTGTCATCG TGCCGCCTGT GCGGCCCGCA ATCACCAGAG AGGCCCTTT GCGGCCCGCA ATCACCAAGA GAGGCCTTTT   | 120<br>180<br>240<br>300<br>360<br>420<br>420<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1220<br>1320<br>1380                                   |
| 50<br>55<br>60<br>65            | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAA GACGGGTGCG CCATGGAATG ACCGCGGGCT GCACGCCGGCT TCAGCTTCCA TCAGCCTGCG TCAGCCCGGCG TCAGCCCGGCC GCTTCCTGCT GCCGCGGGC TCAGCCTGCC GCTTCCTGCT CAGCCTAGCT CAGCCTAGCT CAGCCTACT CAGCCTACT CAGCCTACT CAGCCTACT CAGCCTACT CAGCCCTACT CAGCCCTACT CAGCCCTACT CAGCCCTACT CAGCCCTACT CAGCCCTACT CAGCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCCTACT CAGCCCCCTACT CAGCCCCCTACT CAGCCCCTACT CAGCCCCTACT CAGCCCCCTACT CAGCCCCCTACT CAGCCCCCTACT CAGCCCCCTACT CAGCCCCCTACT CACCGCCCCTACT CACCGCCCCTACT CACCGCCCCTACT CTTCTACTT TCTTCTACTT TTCTTCTACTT   | GAGGGCCCT GGATAGTGTC CACTOCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCA GGACAATGGC CTTCAGGGG GACAATGGC CTTCAGGGG GACAATGGC CTTCAGGGA GAACACTGT GTACACCCTA CTACAACTAT CTTCCTCTCTC GCGCTACCTG TGCCCTGGCT TGCCCTGGCT TGCCCTGGCC GCCCTTTGCT TGCCCTGGCC GCCAGGCGCA CGTGGCTGCT CGCCAGAAGCCACC CAACCAAAG  | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ACACTTCACC GAAGAACCAT AGCCCCTGCC ACAGGCCAGC GTCATTACCC AACCTTGCTGC GCCCAAGGTTG TATGCCAACC GGCATCTGCC GCCTGCTGC GCCAAGGTG GCCACGGCA ACCCTGCTGC GCCATGTATA GCCCTGCTGC GCCTGCTGGC GCATCTGCC TCGGCCTGTG GCCCTGCTGG GCGCCTTTGCCA TCGACCCGG CGGCCTTTTGCCA TCGACCCGCG TCGACCCCGC TCGACCCCGC TCGACCCCGC TCGACCCCGC TCGACCCCCCC ACCTTTCCCCC ACCTCTTTGCCA TCGACCCCGC TCGACCCCGCTTTG AGGTTCCCCCC  | TEGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTGGCTT CACAGGACT GGACTGCAAC TCCTGGACA TCCTGGACA TCACTGGCC TGCACGGCAG ACCCCTGGC TCCAGGGAGA ACCCCTATGGA TCCAGGCAG ACCCCTGGC TCCAGGGAGCG TCCAGGAGCG TCAGGTTAC TCCAGGAGCG TCAGGTTCCT GGTTCCCTG GGTCCCCTG GGGTCCCCTG GGGTCCCCTG GGGCGCAGCC GGGCACCACA   | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TTAGGAAACCC GCCACCCACC GTCCGCCGG GCTATATGCC CATCCTCTC CCCTGGCAC CGAGCCTTTCCCGCCG GGCTGACA CCGCACTGTC CATGGCTCTC CATGGCTCTC CATGGCTCTC CATGGCTCTC CATGGCTCTC CACGCTGTCACA GCCTTTTCAC CACCTGTTCAC CACCTGTTCAC CACCTGTTCAC CACCTGTTTCAC CACCTGTTTC CACCTGCTCT TGAGCTCCTA  | TTTGTCTTTT GGGACCTGCTC GGGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTCA GTCTTGCTCC GGGGCTGCTC GCTAACTCT AGGCTGAGGA ACCTGGGCA ACCTGGTCT TCGCCTGCC TCCCCTGC TTCGCCTGCC CTCACCTGCA AAACGTGGGG ACCCAGTGCC TGCTCATCG TGCGCCCGCA ACTGTCATCG TGCGCCCGCA ATCACCAAGA GAGGCCTTT GCGCCCCCCA CAGAAACTCA  | 120<br>180<br>240<br>300<br>360<br>420<br>420<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500                   |
| 50<br>55<br>60<br>65            | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGT TTCTTCATGG TGCCAGAACA CACGAGTGGG GGATAACAAG GCTGCGGTGCG CCATGGAGAA GCCTGCTCAT GCACGCGGT TCAGCTCAT GCCCAGGAGA TCAGCCAGGC TCAGCCGGC TCAGCCGGC TCAGCCGGC TCAGCCAGGA TGGCCTAGT CAGCCTACT CAGCCAAGA TGGCCTACT CAGCCAAATG CACCAATGTGT  | GAGGGGCCCT GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCTA GTACAATGGC CTTCAAGTGA GAACATCTGT GTACACCCTA CTACAACTAT CTTCCTCTTC TGCCTGGCTA CACTCTTGGCT TGCCTGGCTA CACTCTTGGCT TGCCTGGCTA CACTCTTGCT TGCCTGGCCA CACCTGGCCA CACCTAGAGCACC CACCAGAGGCACC CACCAGAAGCACC CACCAGAAGCACC CCAGAGGCACC  | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTG ATGTCTCTCA CAGCACTTCAC GAAGAACCAT AGCCCTGCC ACAGGCAGG CTGCTGCTGCG GCCAAGGTG TATGCCAACC GGCATTGCC GCCACAGGCA ACCCTGCTGCG GGCATTGCC GCCACAGGCA ACCCTGCTGGG GCCACTGCT GCCCACAGGCA ACCCCTGCTGG GCCCTTTGCA CCCCTTTTGCACC CGGCACTTGGC GCCCTTTTGCAACCC CGGCCCTTTGGAGGCCCCG CGGCCGCTTGGAGGCCCCCAAGGCCAAGGCAACCCCCCCC  | TEGCTEGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT GGACTGCAAG GGCTTGGAA TCCCTGAAC TCCTGGACT CACCAGAGCT ACACTGGCCT ATCACTGCC TGCACGCAG ACCGCTGCC CCGTGTGCC CCGTGTGCC CCGCTACTG CCCAGGAGGCG CCGGCTACTG CCCAGGAGCG CCGGCTACTG CCCAGGACCAC TCACGCAG GGCGACCACA TCCCCCAG  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCAGATGAGT TCTTGTCAGT CACTGCACC CGAGGCACTT GGCGAGATCC TTCGGCGGGTG GTCCCGCCGG GCTATATGCC CATCCTCTTC CCCCTGGCAC CATCCTTCTC CCCCTGGCAC GCCATGTCT CATGGCTTCT CATGGCTTCC CATGGCTTCT CATGGCTTCC TCTCCTGGCC GCGTGCAAG GCCTTTTCAC GCCTTTCAGCCT TCTCCTGGCCA GCCTTTCAC CACTGTATTC CACTGTATTC CACGCTGCTCT TGAGCTCCT TGAGCTCCTG CACTGTCCTGCACA CACTGTATTC CACTGGCACAC CACTGTCTCT TGAGCTCCTG  | TTTGTCTTTT GGGACCTGCTC GTTTGCTTG GTCTTGCTTG GTCTTGCTTC GGGGCTGCTC GCTAACTCTT AGGCTGAGGA ACCTGGGCAG ACCTGGCAG ACCTGGCAC TCGCCGCC TCGCCTGCC TCGCCTGCC TCGCCTGCC TCGCTGCC TCGCTGCC TGCTACTCC TGCTACTCC TGCTACTGCC TGCTACTGCC TGCTATGACC ACTGTCATCC GCGCCCGTT GCCGCCTGT GCGGCCCGCA ATCACCAAGA GAGGCCTTTC GAGCCCATCC CAGAAACTCA CTTCATATTT TGAATTAGAGT  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1560   |
| 50<br>55<br>60<br>65<br>70      | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAA GATGGGTGCG CCATGGAATG ACCGCGGGT GCACGGCTGCT TCAGCTTCCA TCAGCCAGAG TCAGCCAGAG TCAGCCAGGC TCAGCCAGGC TCAGCCTACCT CAGCCAGGC TCAGCCAGAC TCAGCCAAATG GCCATAGTT CAGCCAAATG GCCATAGTT TCAGCTCAGC  | GAGGGCCCT GGATAGTGTC CACTCCTGAT TTGCACGCA AATTTGCTCC ACTCTCAGTG GGACAATGGC CTTCAGGGG CTTCAGGGG GACAATGGC CTTCAGGTA GAACACTGT GTACACCTA CTACACCTA CTACACCTA CTACACCTA CTACACTAT CTCCTCTTC GCCTACCTG TGCCTGGCT TGCCTGGCT TGCCTGGCT GGCCTGGCC GCCCTTTGCT TGGCCTGGCC GCCATTGCGC CAAAGGCACG CACCCAGAAG GCAGGGCACC TGGGCCACC TGGGCCACC TGGGCCACC TGGGCCACC TGGGCCACC TGGGCCACC TGGGCCACC TGGGCCACC TGGGCCACC   | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG AGCACTTCACC GAAGAACCAT AAGCACCATGCC ACAGGACAGC GTCAGCTGCC ACAGGACAGC ACACGTGCC ACAGGACAGC ACCCTGCTGC ACACGTGCC ACCCTAGCT ACCCTAGCT GCCCAAGGTC ACCCTGCTGC GCCAAGGTC ACCCTGCTGC GCCATGTTAGAC GCCACTGTAG GCCACTGTGC GGCGCTTTGCCA ACCCTGCTGGG GAGCCTGTGGG GAGCTCTGCG GGTCGCTGGG AGGACCCCA AGGTCAGCAG AGGACCCCA AGGAGCCCCA AGGAGCCCCA AGGAGCCCCA AGGAGCCCCA AGGAGCCCCA AGGAGCCCCA AGGAGCCCCA AGGAGCCCCA   | TEGCTEGGAE TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGCTGCTAGACA TCCCTGAACA TCCTGGACA TCCCTGAACA TCACTGCAC TGGCTGCACA ACACTGCAC TGCACGGCAG ACCCCTAGG TCACGGCAG TCACGGCT TCCAGGGTAA TGCCTATGG TCCAGGGTAA TGCCTATGG TCCAGGGTAA TGCCTATGG TCCAGGGTAC TCCAGGAGCG TCAGCTCCCTG CCAGTGCCAA TCCTCCAGGT TCACAGGAC TCCTCCAGGT TCACAGGAC TCCTCCAGGT TCACAGGAC TCTCCAGGT TCACAGGAC TCTCCAGGAC TCACAGGAC TCACAGAC TCACAG | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT TCTGTCAGT CTGCTGCAGCA CGAGGCACTT GGCGGAGTTC TTAGGAAACCC GCCACCCACC GCCACCCACC CATCCTCTC CCCTGGCAG CGCTGACA CGCACTGTC CATGGCTGC CATCCTCTTC CATGGCTGTC CATGGCTGTC CATGGCTGC CATCCTTTC CATGGCTGC CATGCTTTC CATGGCTGC CATGGCTAACA GCCTTTTCAC CACTGTTATTG CAGCGTGTC CAGCGTGTC CAGCGTGCC CACTGTCC CACTGTCC CACTGTCC CACTGTCC CACTGTCC CACTGTCC CACTGTCC CACTGTCAC CACTGTCAC CACTGTCAC CACTGCAGC ACCATGCAGC ACCATGCAGC ACCATGCAGC CCACAGCGCAGC CCACAGCGCAGC CCACAGCGCAGC CCACAGCGCACC CCACAGCAGCTCC CACAGCAGCTCC CCACAGCAGCC CCACAGCAGC CCACAGC CCACAGCAGC CCACAGCAGC CCACAGCAGC CCACAGCAGC CCACAGCAGC CCACAGC | ITTIGICITIT GGACCIGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTCA GTCTTGCTCC GCGACCTCC GCTAACTCT AGGCTGAGGA ACCTGGGCA ACCTGGCCT GCTCACCTGC TCCGCCTGC TCCGCCTGCC CTCACCTGCA AAACGTGGGG ACCCAGTGCC TGCTACCGCA ACTGCCTGC ACTGCCTGCC TGCTACCCTGCA AAACGTGGGG ACCCAGTGCC TGCTACCTGCA ACTGCCAGAGA AGGCCTTTG GACCCACCAAGA CAGGCCCTTT GAAATTGAGCT ACCAAAAACT CTCATATTT GAATTAGAGT ACCAAAAACT   | 120<br>180<br>240<br>300<br>360<br>420<br>420<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500                   |
| 50<br>55<br>60<br>65            | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAA GCCTGGGATGG GCATGGAATG GCCTGCTCAT TCCTGCTCAT GCCTGCTCAT TCAGCCCGCC GCCCCAGGA TCAGCCCGCC GCTCCCACGC TCAGCCCGCC GCTCCCACGC TCAGCCTACT TCAGCCTACT CAGCCCTACT CAGCCCAAATG GCCATTGTGT TCAGCTCAGC   | GAGGGGCCCT GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCCA ACCTCTGCCA ACCTCTGCCA GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACAACCAT CTACCACCTGGCT GCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGCC   | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG CTGCTGACGC GTCATTACCC AACCTTGCTC GCCCAAGGTG TATGCCAACC GGGATCTGCC GGCATCTGCC GGCATCTGCC GCCTTTGCC GCCCTTTGCC GCCCTTTGCC GCCCTTTGCC GGTCGCTGGG GCCCTTTGCCA AGGTCCCCG GGTCGCTGGG GCCCTTTGCCA AGGTCCCCG GGTCGCTGAG AGGTCCCCCG GGTCCCTGAG AGGAGCCCCC GGTCCCTAAGATCC GGCCCAGACC   | TEGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTTGGAAC CTCTGGGCTT CACCTGTGTA AGATCTGCAC TGCTGGCT TGCACGAGCAG ACCCCTGGC CCTGTGGCT TCCAGGCTA TCCAGGACC CCTGTGTACA TCCAGGACC CCAGGACC CCAGC CCAGGACC CCAGC CCAGGACC CCAGC CCAGGACC CCAGC CCAGC CCAGC CCAGC CCAGC CCAGC CCACGC CCACGC CCACGC CCACGC CCACG CCACG CCACG CCACGC CCACG CCACG CCACG CCACG CCACG CCACG CCACG CCACG CCACC CCACG CCACC CCACG CCACC CCACG | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGG GCTATATGCC CATCCTCTTC CACTGGCAC CATCCTCTTC CATGGCTCTC TCTCCTGGCAC GCCTTGCAC GCCTTGCAAC CATGCTTTC CATGGCTCTC TCTCCTGGCAC CACTGTTCTC TCTCTGGCAC CACTGTATTG CACGGTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTGCTAAC CACTGTATTG CAGCATGCTAAC CCAGGAAGCTC CCAGAAGCTC GGAAAGCTC GGAAAGGTA   | TTTGTCTTTT GGACCTGCTC GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTTG GTCTTGCTCC GCGACCTCC GCTAACTCT AGGCTAAGACT CTGGCGCTG CCTGCCTGC TTCGCCTGC TTCGCCTGC CTCACCTGCA AAACCTGGA ACCTGGAC ACCTGTATCACC GCGCCCGCA ACTGTCATCC GCGCCCGCA ATCACCAGAA GAGGCCTTT GAACCCATCC CAGAAACTCA CTTCATATTT GAATTAGAGT AGACCTGGGC AGAAACTCA CACAAAACT AGACCTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAACACT ACCACACC ACC | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1220<br>1320<br>1380<br>1440<br>1500<br>1560<br>1680<br>1680<br>1740         |
| 50<br>55<br>60<br>65<br>70      | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GCTGCAGAACA GCCTGCCGCT GCACGACGGC TCACGCCGCC GCTCCACGCCGCC GCTCCACGCC GCTCCACGCC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC CAGCACCT CAGCCGCAGAACC CAGCGCCTACCT CAGCCAACC CAGCGCCTACCT CAGCCAACT CCTCTCTACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCC CCACT CCAGCCCCCC CCAGCCCCC CCACCC CCACCCC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACC CCACC CCACC CCACC CCACC CCACC CCACCC CCACC CCACC CCACC CCACC CCACC CCACC | GAGGGCCCT GGATAGTGTC CACTCTGGAT TTGCACGCGA AATTTGCTCC ACCTCTGCA ACCTCTCAGT GGACAATGGC CTTCAAGCAA GAACATCTGT CTACAACTAT CTACAACTAT CTACAACTAT CTACAACTAT TGCCCTGGCA GCCCTTGCT TGCCCTGGCC GCCCTTTGCT TGCCCGGCA CACCCAGAAG GCAGGCACC CACCAGAAG CCCGGGCACC TGGGCATGGA CCCGGGCACC AGGGGCACC AGGGGCACC AGGGCACC AGGCACC AGGGCACC AGGCACC AGGGCACC AGGCACC AGGCAC | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCTGCC ACAGGCCAGG CTGCTGCTGCG GCCAAGGTG TATGCCAACC GGCATCTGCC GGCACAGGCA ACCCTGTTGCA GCCTGCTGCG GGCCTTTGCA TCGACCCGG GGCCTTTGCA AGCTTCCCG GGCCTTTGCA AGCTTCCCG GGCCTTTGCA AGGTTCCCGG CGGCCTTTGCA AGGTTCCCGG CGGCCTTTGCA AGGAGCCCA GGTTAAGATCC GGTCAGCCCAG CGGCCCAAGCC GGTCAGCCCAG CGGCCCAAGCC GGCCCAAGCC GGTCAGCCCAACC GGCCCAACC GGCCCAACC GGCCCAACC GGCCCAACC GTCAGCCCAACC GGCCCAACC GGCCCAACC   | TEGCTEGGAE TATTTCCCAT GEGCTEGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTE GEACTGCAAC GECTTTGGAAC CTCTEGGCTT CACCTGTTTA AGATTGCAC TGCACGAGA ACCCCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT CCAGGAGG CCGTGGCCT CCAGGAGGC CCGTCCCCT CCAGGACCAC GGCGACCACA CCCACCCCA CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACCCCAA CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTGTGCGCAT GAGAGCTCGG  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGG GCTATATGCC CATCCTCTTC CACTGGCAC CATCCTCTTC CATGGCTCTC TCTCCTGGCAC GCCTTGCAC GCCTTGCAAC CATGCTTTC CATGGCTCTC TCTCCTGGCAC CACTGTTCTC TCTCTGGCAC CACTGTATTG CACGGTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTGCTAAC CACTGTATTG CAGCATGCTAAC CCAGGAAGCTC CCAGAAGCTC GGAAAGCTC GGAAAGGTA   | ITTIGICITIT GGACCIGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTCA GTCTTGCTCC GCGACCTCC GCTAACTCT AGGCTGAGGA ACCTGGGCA ACCTGGCCT GCTCACCTGC TCCGCCTGC TCCGCCTGCC CTCACCTGCA AAACGTGGGG ACCCAGTGCC TGCTACCGCA ACTGCCTGC ACTGCCTGCC TGCTACCCTGCA AAACGTGGGG ACCCAGTGCC TGCTACCTGCA ACTGCCAGAGA AGGCCTTTG GACCCACCAAGA CAGGCCCTTT GAAATTGAGCT ACCAAAAACT CTCATATTT GAATTAGAGT ACCAAAAACT   | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1550<br>1620<br>1620<br>1620<br>1620<br>1620 |
| 50<br>55<br>60<br>65<br>70      | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GCTGCAGAACA GCCTGCCGCT GCACGACGGC TCACGCCGCC GCTCCACGCCGCC GCTCCACGCC GCTCCACGCC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC GCTCCACGC CAGCACCT CAGCCGCAGAACC CAGCGCCTACCT CAGCCAACC CAGCGCCTACCT CAGCCAACT CCTCTCTACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCAACT CAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCACT CCAGCCCCC CCACT CCAGCCCCCC CCAGCCCCC CCACCC CCACCCC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC CCACC CCACCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACCC CCACC CCACC CCACC CCACC CCACC CCACC CCACCC CCACC CCACC CCACC CCACC CCACC CCACC | GAGGGGCCCT GGATAGTGTC CACTCCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCCA ACCTCTGCCA ACCTCTGCCA GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACAACCAT CTACCACCTGGCT GCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGGCT TGCCCTGCC   | I TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCTGCC ACAGGCCAGG CTGCTGCTGCG GCCAAGGTG TATGCCAACC GGCATCTGCC GGCACAGGCA ACCCTGTTGCA GCCTGCTGCG GGCCTTTGCA TCGACCCGG GGCCTTTGCA AGCTTCCCG GGCCTTTGCA AGCTTCCCG GGCCTTTGCA AGGTTCCCGG CGGCCTTTGCA AGGTTCCCGG CGGCCTTTGCA AGGAGCCCA GGTTAAGATCC GGTCAGCCCAG CGGCCCAAGCC GGTCAGCCCAG CGGCCCAAGCC GGCCCAAGCC GGTCAGCCCAACC GGCCCAACC GGCCCAACC GGCCCAACC GGCCCAACC GTCAGCCCAACC GGCCCAACC GGCCCAACC   | TEGCTEGGAE TATTTCCCAT GEGCTEGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTE GEACTGCAAC GECTTTGGAAC CTCTEGGCTT CACCTGTTTA AGATTGCAC TGCACGAGA ACCCCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT TCACCTGGCT CCAGGAGG CCGTGGCCT CCAGGAGGC CCGTCCCCT CCAGGACCAC GGCGACCACA CCCACCCCA CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACCCCAA CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTCACAGGAC CTGTGCGCAT GAGAGCTCGG  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGG GCTATATGCC CATCCTCTTC CACTGGCAC CATCCTCTTC CATGGCTCTC TCTCCTGGCAC GCCTTGCAC GCCTTGCAAC CATGCTTTC CATGGCTCTC TCTCCTGGCAC CACTGTTCTC TCTCTGGCAC CACTGTATTG CACGGTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTGCTAAC CACTGTATTG CAGCATGCTAAC CCAGGAAGCTC CCAGAAGCTC GGAAAGCTC GGAAAGGTA   | TTTGTCTTTT GGACCTGCTC GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTTG GTCTTGCTCC GCGACCTCC GCTAACTCT AGGCTAAGACT CTGGCGCTG CCTGCCTGC TTCGCCTGC TTCGCCTGC CTCACCTGCA AAACCTGGA ACCTGGAC ACCTGTATCACC GCGCCCGCA ACTGTCATCC GCGCCCGCA ATCACCAGAA GAGGCCTTT GAACCCATCC CAGAAACTCA CTTCATATTT GAATTAGAGT AGACCTGGGC AGAAACTCA CACAAAACT AGACCTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAACACT ACCACACC ACC | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1220<br>1320<br>1380<br>1440<br>1500<br>1560<br>1680<br>1680<br>1740         |
| 50<br>55<br>60<br>65<br>70      | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGT TTCTTCATGA TGCCAGAACA CACGAGTGGG GGATAACAAG GCTGCCGCT CCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT TCAGCCAGGA TGGCCTAGCA TCAGCCAGGA TGGCCTACTCT CAGCCAGGA TGGCCTACTCT CAGCCAAATG CAGCCTACTC CAGCGGCCTA CTTCTTCACTT CAGCCAAATG CCAGCAAATAGC ATTTCTTCAGC ATTTCTTCAGC ACTTCTTCT ACACAAAAATAC Seq ID NO: Nucleic AC   | GAGGGCCCT GGATAGTGTC CACTCTGGAT TTGCACGCGA AATTTGCTCC ACCTCTGCA ACCTCTCAGT GGACAATGGC CTTCAAGCAA GAACATCTGT CTACAACTAT CTACAACTAT CTACAACTAT CTACAACTAT TGCCCTGGCA GCCCTTGCT TGCCCTGGCC GCCCTTTGCT TGCCCGGCA CACCCAGAAG GCAGGCACC CACCAGAAG CCCGGGCACC TGGGCATGGA CCCGGGCACC AGGGGCACC AGGGGCACC AGGGCACC AGGCACC AGGGCACC AGGCACC AGGGCACC AGGCACC AGGCAC | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTG ATGTCTCTCA CAGCACTTCAC GAAGAACCAT AGCCCTGCC ACAGGCCAGG GTCATTACC AACACTTGCTC GCCAAGGTG TATGCCAACC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCACAGGCA ACCCCACTATA GCCCTGCTGG GAGCCTGTGG GCCCTTTGCC GGTAGGTAAGATCC GGCCCGATCGC GGTAGGAGCCCCA GTTAAGATCC GCCCCAGGC GTACGCCATG GTACGCCATG GTACGCCATG GTACTCTCAA  | TEGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTTGGAAC CTCTGGGCTT CACCTGTGTA AGACTGCAC TGCAGCAGC TGCAGCAC ACCACGAGCAG ACCCCTGGCT TCCAGGCTTA CCCGAGACAC CCGAGCAGC CCGAGCACAC CCAGGACAC CCAGGACAC TCAGGACAC TCAGGACAC TCACAGCACA CCCACCCAA CCCACCCAA CCCACCCAA CCCACCCAA CCACACCCAA CCACACCCAA CCACACCCCAA CAGCACCCCAA CAGCACCACAC CAGCACCACAC CAGCACCACAC CAGCACCACAC CAGCACCACAC CAGCACCACAC CACACCACAC CACACCCCAA CACCACCAC  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGG GCTATATGCC CATCCTCTTC CACTGGCAC CATCCTCTTC CATGGCTCTC TCTCCTGGCAC GCCTTGCAC GCCTTGCAAC CATGCTTTC CATGGCTCTC TCTCCTGGCAC CACTGTTCTC TCTCTGGCAC CACTGTATTG CACGGTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTGCTAAC CACTGTATTG CAGCATGCTAAC CCAGGAAGCTC CCAGAAGCTC GGAAAGCTC GGAAAGGTA   | TTTGTCTTTT GGACCTGCTC GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTTG GTCTTGCTCC GCGACCTCC GCTAACTCT AGGCTAAGACT CTGGCGCTG CCTGCCTGC TTCGCCTGC TTCGCCTGC CTCACCTGCA AAACCTGGA ACCTGGAC ACCTGTATCACC GCGCCCGCA ACTGTCATCC GCGCCCGCA ATCACCAGAA GAGGCCTTT GAACCCATCC CAGAAACTCA CTTCATATTT GAATTAGAGT AGACCTGGGC AGAAACTCA CACAAAACT AGACCTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAACACT ACCACACC ACC | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1550<br>1620<br>1620<br>1620<br>1620<br>1620 |
| 50<br>55<br>60<br>65<br>70      | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGT TTCTTCATGA TGCCAGAACA CACGAGTGGG GGATAACAAG GCTGCCGCT CCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT GCCCTGCTCAT TCAGCCAGGA TGGCCTAGCA TCAGCCAGGA TGGCCTACTCT CAGCCAGGA TGGCCTACTCT CAGCCAAATG CAGCCTACTC CAGCGGCCTA CTTCTTCACTT CAGCCAAATG CCAGCAAATAGC ATTTCTTCAGC ATTTCTTCAGC ACTTCTTCT ACACAAAAATAC Seq ID NO: Nucleic AC   | GAGGGGCCCT GGATAGTGTC CACTCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCA AGTCCTCAGTG GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACAACTAT CTACAACTAT CTACAACTAT CTACAACTAT TGCCCTGGCT GGCCTACCTG GCCTACCTG TGCCTGGCT TGCCCTGGCC GCCCTTTGCT TGCCCTGGCC GCAGTGCGC CAAAGGCACG CACCAGAAG CCAGGAGCAG CCAGGAGCAG CCGGGCCACCT AGAGGTCCCA AGTGTGACGT CCCTTCCT AGAGGTCCCA AGTGTGACGT CC126 DNA S id Accessio uence: 18   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTG ATGTCTCTCA CAGCACTTCAC GAAGAACCAT AGCCCTGCC ACAGGCCAGG GTCATTACC AACACTTGCTC GCCAAGGTG TATGCCAACC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCACAGGCA ACCCCACTATA GCCCTGCTGG GAGCCTGTGG GCCCTTTGCC GGTAGGTAAGATCC GGCCCGATCGC GGTAGGAGCCCCA GTTAAGATCC GCCCCAGGC GTACGCCATG GTACGCCATG GTACGCCATG GTACTCTCAA  | TEGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTTGGAAC CTCTGGGCTT CACCTGTGTA AGATCTGCAC TGCACGAGCAG ACCCCTGGCT TCCAGGCTT TCCAGGCTTACA ACCCCTGGCT TCCAGGCTTACA TCCAGGACC CCTGTTGGAC TCCAGGACC CCAGGACC CCAGGACC CCAGGACC CCAGGCAC TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA CTCCAGGACC CCTGTGGCAT CCAGGACC CCAGGCCC CCTGTGCCAA CCCCAGGACC CCAGGCCAA TCCTCCAGGT CCAACCCCAA CTCCCAGGAC CCTGTGGCAT GAGACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGAC CCAGGCC CCAGCC CCAGCC CCAGCC CCAGCC CCAGCC CCAGCC CCAGCC CCACGC CCACCC CCACC CCACCC CCACC CCACCC CCACCC CCACCC CCACCC CCACCC CCACC CCACCC CCACC CCACC CCACCC CCACC | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGG GCTATATGCC CATCCTCTTC CACTGCACC GCCCTGGCAC GGCCATGACA CCGCATGTC CATGGCTCTC TCTCCTGGCC GCTTGCCAAG CACTGTTCTC CACTGTCTC TCTCCTGGCC GCCTTGCCAAG CCCTTTTCAC CACTGTATTG CAGCTTCTC TCACTGGCC CACTGTCTCAC CACTGTATTG CAGCATGCTAC CACTGTATTG CAGCATGCTAC CACTGTATTG CAGCATGCAGA CCAGAAGCTC CGGAAAGCACAT  | TTTGTCTTTT GGACCTGCTC GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTTG GTCTTGCTCC GCGACCTC GCTAACTCT AGGCTGAGCA ACCTGGCAC TCTGCCTGC TCTCCCTGC TTCGCCTGCC TCCCTGCC TCCCTGCA AAACCTGGAA ACCTGGAACCC TGCTCCTGCA ACCCAGTGCC TGCTCATCAC ACCGCCCGTA GCGCCCCGTA GCGCCCCGTA GCGCCCCGTA GCACCCAACAC CTCAAAACTTA GAATTAGAGT ACAAAAACT ACACCAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAACT ACACCAACACC TAAGGTGCTC  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1550<br>1620<br>1620<br>1620<br>1620<br>1620 |
| 50<br>55<br>60<br>65<br>70      | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACCAGTGGG GGATAACAAG GCTGGCGGC GCACGGCCGGC TCAGCTCCAGACA GCCCGCCAGGA TCAGCCCGCCCAGGA TCAGCCCGCCCAGGA TCAGCCCGCCCAGGA TCAGCCTACT TCAGCCACAGC CTTCTCTACT CAGCCACAGC ATTTCTTCAG CAGCTACCT CAGCCACAGC ATTTCTTCAG CTGGCTCTG ACAAAAATAC Seq ID NO: Nucleic Ac Coding seq  | GAGGGGCCCT GGATAGTGTC GGATAGTGTC GGATAGTGTC GGATAGTGTC TTGCACGCGA AATTTGCTCC ACCTCTGCA GGACAATGGC CTTCAAGCA GAACATCTGT GTACACCCTA CTACAACTAT CTTCCTCTTC GCGCTACCTG GCCCTACCTG GCCCTACCTG GCCCTACCTG TGCCCTGGCC CACCTAGGGC CACCCAGAGG CACCCAGAGG CACCCAGAGG CAGGGCACC CACCCAGAGG CACCCAGAGG CCCGTTCCT TGCCTGCT TGCCCTGCT CACCCAGAGG CCCCTCCTC CAAGGCACC CACCCAGAGG CCCCTCCTC AGAGGTCCCA AGTGTGACGT CCACCTCCCA AGTGTGACGT CCACCTCCCA AGTGTGACGT CCACCTCCCA AGTGTGACGT CCACCTCCCA AGTGTGACGT CCACCGCCCCCCCCCC   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG CTGCTGCTGC GCCCAAGGTTG TATGCCAACC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATTTGC AACCTTGCTG GACCCTGTGG AACCTTGCCA TCGACCCGG GGCCTTTGC AAGTTCCCC GGTCTGCAACC GGTCAGCACC GTTAGAACC GGTCAGCACC GTCAGCCATAA AGGAGCCCCAGACC GTCAGCCATACC GGCCCATTAGACC GGTCAGCCAGCC GTCAGCCAGCC GTCAGCCAGCC GTCAGCCATGCC GTCAGCCC GTCAGCCATGCC GTCAGCCATGCC GTCAGCCATGCC GTCAGCCATGC GTCAGCCATGCC GTCAGCCATGC GTCAGCC GTCAGCCATGC GTCAGCC GTCAGCCATGC GTCAGCC GTCAGC | TEGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTTGGAAC CTCTGGGCTT CACCTGTGTA AGACTGCAC TGCAGCAGC TGCAGCAC ACCACGAGCAG ACCCCTGGCT TCCAGGCTTA CCCGAGACAC CCGAGCAGC CCGAGCACAC CCAGGACAC CCAGGACAC TCAGGACAC TCAGGACAC TCACAGCACA CCCACCCAA CCCACCCAA CCCACCCAA CCCACCCAA CCACACCCAA CCACACCCAA CCACACCCCAA CAGCACCCCAA CAGCACCACAC CAGCACCACAC CAGCACCACAC CAGCACCACAC CAGCACCACAC CAGCACCACAC CACACCACAC CACACCCCAA CACCACCAC  | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTTC TAGGAAACCC GCCACCCACC TTCGGCGGG GCTATATGCC CATCCTCTTC CACTGGCAC CATCCTCTTC CATGGCTCTC TCTCCTGGCAC GCCTTGCAC GCCTTGCAAC CATGCTTTC CATGGCTCTC TCTCCTGGCAC CACTGTTCTC TCTCTGGCAC CACTGTATTG CACGGTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTTGCTAAC CACTGTATTG CACGCTGCTAAC CACTGTATTG CAGCATGCTAAC CCAGGAAGCTC CCAGAAGCTC GGAAAGCTC GGAAAGGTA   | TTTGTCTTTT GGACCTGCTC GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTTG GTCTTGCTCC GCGACCTCC GCTAACTCT AGGCTAAGACT CTGGCGCTG CCTGCCTGC TTCGCCTGC TTCGCCTGC CTCACCTGCA AAACCTGGA ACCTGGAC ACCTGTATCACC GCGCCCGCA ACTGTCATCC GCGCCCGCA ATCACCAGAA GAGGCCTTT GAACCCATCC CAGAAACTCA CTTCATATTT GAATTAGAGT AGACCTGGGC AGAAACTCA CACAAAACT AGACCTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC AGCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAAAACT AGACTGGGC ACCAACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAAAACT AGACTGGGC ACCACACC ACCAACACT ACCACACC ACC | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1550<br>1620<br>1620<br>1620<br>1620<br>1620 |
| 50<br>55<br>60<br>65<br>70      | AAGGACAGAG CGGAAGAACT TGGGGCTACC CCTGTCATCT TTCTTCATGA TGCCAGAACA CACGAGTGGG GGATAACAAG GCTGCCGCT CCCTGCTCAT GCCCGCGAGAA GCCTGCCCAT GCCTGCCAGA GCCTGCCCAGA TCAGCCCGC TCAGCCCGC TCAGCCAGC TCAGCCAATC CAGCGCCTAC CAGCGCTTACT TCAGCTCAGC  | GAGGGGCCCT GGATAGTGTC CACTCTGAT TTGCACGCGA AATTTGCTCC ACCTCTGCA AGTCCTCAGTG GGACAATGGC CTTCAAGCAA GAACATCTGT GTACACCCTA CTACAACTAT CTACAACTAT CTACAACTAT CTACAACTAT TGCCCTGGCT GGCCTACCTG GCCTACCTG TGCCTGGCT TGCCCTGGCC GCCCTTTGCT TGCCCTGGCC GCAGTGCGC CAAAGGCACG CACCAGAAG CCAGGAGCAG CCAGGAGCAG CCGGGCCACCT AGAGGTCCCA AGTGTGACGT CCCTTCCT AGAGGTCCCA AGTGTGACGT CC126 DNA S id Accessio uence: 18   | TCCTGTCAGC AATTTGTGCT ACAGGATGAG TAAAAATTTG ATGTCTCTCA CAGTTTCAGG AGCACTTCAC GAAGAACCAT AGCCCCTGCC ACAGGCCAGG CTGCTGCTGC GCCCAAGGTTG TATGCCAACC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATCTGCC GGCATTTGC AACCTTGCTG GACCCTGTGG AACCTTGCCA TCGACCCGG GGCCTTTGC AAGTTCCCC GGTCTGCAACC GGTCAGCACC GTTAGAACC GGTCAGCACC GTCAGCCATAA AGGAGCCCCAGACC GTCAGCCATACC GGCCCATTAGACC GGTCAGCCAGCC GTCAGCCAGCC GTCAGCCAGCC GTCAGCCATGCC GTCAGCCC GTCAGCCATGCC GTCAGCCATGCC GTCAGCCATGCC GTCAGCCATGC GTCAGCCATGCC GTCAGCCATGC GTCAGCC GTCAGCCATGC GTCAGCC GTCAGCCATGC GTCAGCC GTCAGC | TEGCTGGGAG TATTTCCCAT GGGCTGGTTT CAAACTGCCT GTTTCCTCAT CACAGAACTG GGACTGCAAC GGCTTGGAAC CTCTGGGCTT CACCTGTGTA AGATCTGCAC TGCACGAGCAG ACCCCTGGCT TCCAGGCTT TCCAGGCTTACA ACCCCTGGCT TCCAGGCTTACA TCCAGGACC CCTGTTGGAC TCCAGGACC CCAGGACC CCAGGACC CCAGGACC CCAGGCAC TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA CTCCAGGACC CCTGTGGCAT CCAGGACC CCAGGCCC CCTGTGCCAA CCCCAGGACC CCAGGCCAA TCCTCCAGGT CCAACCCCAA CTCCCAGGAC CCTGTGGCAT GAGACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGT CCAACCCCAA TCCTCCAGGAC CCAGGCC CCAGCC CCAGCC CCAGCC CCAGCC CCAGCC CCAGCC CCAGCC CCACGC CCACCC CCACC CCACCC CCACC CCACCC CCACCC CCACCC CCACCC CCACCC CCACC CCACCC CCACC CCACC CCACCC CCACC | CAGAGGTGGC CAAGGATCAA TCAGATGAGT TCTTGTCAGT CTGCTGCCTC ACTGGCAGCA CGAGGCACTT GGCGGAGTT GTAGGAAACCC GCCACCCACC TTCGGCGGG GCTATATGCC CTTTGGCAGC CATCCTCTTC CCCCTGGCAC CGCACTGCAC CGCACTGTC CCTTCCTGGCC GCGTGGCAC GCCATGTCT CATGGCTCTC TCTCCTGGCAC CACTGTATTG CAGCTTGCTAC CACTGTATTG CAGCATGCTC TGCAGGCACTGC TGAGCACTCT TGCAGGCACTGCAC GCATGATATG CACTGTATTG CAGCATGCTCA CCACTGTACTA CCACTGTACTA CACTGTATTG CAGCAGAACCACAT   | TTTGTCTTTT GGACCTGCTC GGACCTGCTC GTCTTGCTCA GTCTTGCTCA GTCTTGCTTG GTCTTGCTCC GCGACCTC GCTAACTCT AGGCTGAGCA ACCTGGCAC TCTGCCTGC TCTCCCTGC TTCGCCTGCC TCCCTGCC TCCCTGCA AAACCTGGAA ACCTGGAACCC TGCTCCTGCA ACCCAGTGCC TGCTCATCAC ACCGCCCGTA GCGCCCCGTA GCGCCCCGTA GCGCCCCGTA GCACCCAACAC CTCAAAACTTA GAATTAGAGT ACAAAAACT ACACCAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAACT ACACCAAAAACT ACACCAAAAACT ACACCAAAACT ACACCAACACC TAAGGTGCTC  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500<br>1550<br>1620<br>1620<br>1620         |

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                                                                                   480
        CCTGCACTGC CTCCCCCTCC AGACGCCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC CCACGCTCAC GGGCCGAGCG CCGGGGGGCG CCCCAGCCTG CTACTCTTGC TGCCCTGCGC
                                                                                  540
                                                                                   600
40
        ACTOCTGCAC OGCOTOCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC
                                                                                   660
        CGTCCTCCAG CGGGAGCGGC GCCCCTGCGG AAGGCCGGGA CTTGGGCATC GCCTTTAATT
                                                                                   720
        TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA
                                                                                   780
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        AAAAAA
45
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        Nucleic Acid Accession #: NM_006533.1
        Coding sequence: 72..467
50
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                                            31
                                                                    51
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        CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT
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        TCTCCGGACC TGGTGTCAGG GGTGGTCCTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG
                                                                                   180
55
        CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC
        CCGACTGCOG ATTCCTGACC ATTCACOGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA
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        AGGCCGTGG GCGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG
                                                                                   360
        CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG
                                                                                   420
        GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG
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        CTGGCCCTGC CGTTTCCCCT CCTTGGGTTT ATGCAAATAC AATCAGCCCA GTGCAAAC
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        Nucleic Acid Accession #: AB064272
        Coding sequence: 1..708
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        AAAACCACAA GAACCCCAGA AAAGCCTACG CTATACTCAG AGAAGACCAT ATGCACCAAA
 70
        GGGAAAAACA CACCAGTCCC AGAAAAGCCT ACAGAAAACC TGGGGAACAC CACACTGACC
                                                                                   180
        ACTGAGACCA TAAAAGCCCC AGTAAAGTCC ACAGAAAAACC CAGAAAAAAC AGCAGCAGTC ACAAAGACTA TAAAACCTTC AGTCAAGGTC ACAGGAGACA AATCTCTCAC TACTACCTCT
                                                                                   240
                                                                                   300
        TCTCATCTAA ATAAAACTGA AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCCTCATT
        ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAGCCA CAGGAAACGA GAGCCATCCA
                                                                                   420
 75
        TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCACGCTG GACAGATGGG AGAGAATGAT
                                                                                   480
         TCATTCCCTG CATGGGCCAT AGTTATTGTG GTCCTGGTGG CTGTGATTCT CCTCCTGGTG
                                                                                   540
         TTCCTTGGCC TGATCTTCTT GGTCTCCTAT ATGATGCGGA CACGCCGCAC ACTAACCCAG
        AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGCCCCA ATTCCTACCC GGTCTACCTG
ATGGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA
                                                                                   560
                                                                                    70B
 80
         Seq ID NO: C133 DNA Sequence
```

|   | 1  | 11   | 21   | 31   | 41   | 51   |   |
|---|--|--|--|--|--|--|---|
|   | A CATTON CACA  | 1  | A D CT CCD CD C  | NACACCACACA  | )  | TC>> CC> C>C   | 60  |
| 5   |  |  | AAGTCCACAG<br>GAAAAGCCTA   |  |  |  | 60<br>120   |
| •   |  |  | CCAGAAAAGC   |  |  |  | 180   |
|   |  |  | CCAGTAAAGT   |  |  |  | 240   |
|   |  |  | TCAGTCAAGG   |  |  |  | 300   |
| 10  | CTTCTCATCT   | AAATAAAACT   | GAAGTTACTC   | ATCAGGTGCC   | CACTGGTTCT   | TTCACCCTCA   | 360   |
| 10  |  |  | AGTTCTATCA   |  |  |  | 420   |
|   |  |  | TCACAGAAAG   |  |  |  | 480   |
|   |  |  | ATAGTTATTG   |  |  |  | 540   |
|   |  |  | TTGGTCTCCT   |  |  |  | 600   |
| 15  |  |  | GCAGAGGATG<br>GGCATGGGCC   |  |  |  | 660<br>720  |
| 10  |  |  | CCATGCTCTG   |  |  |  | 780   |
|   |  |  | CAGGAAGGGC   |  |  |  | 840   |
|   |  |  | GGTTGGGGAA   |  |  |  | 900   |
| 20  |  |  | TGAATAATAC   |  |  |  | 960   |
| 20  |  |  | GATGGACATG   |  |  |  | 1020  |
|   |  |  | GGAGCCTTAT   |  |  |  | 1080  |
|   |  |  | GACTGAGGGC   |  |  |  | 1140  |
|   |  |  | TTAAGAGTTT   |  |  |  | 1200  |
| 25  |  |  | CATTTTTTA  |  |  |  | 1260<br>1320  |
|   |  |  | CTCTCATCTA   |  |  |  | 1380  |
|   |  |  | CAGTGGACGC   |  |  |  | 1440  |
|   |  |  | TTTATTTGGC   |  |  |  | 1500  |
| 20  |  |  | TCAGCATTTA   |  |  |  | 1560  |
| 30  |  |  | TTACCCATCT   |  |  |  | 1620  |
|   |  |  | TTTCCTCCTT   |  |  |  | 1680  |
|   |  |  | TGGCCATTTC   |  |  |  | 1740  |
|   | AGGAGAATGA   | TGATGATAGT   | TTCCTTCTGT   | CTATTGACCT   | TTTTTATAAT   | AAAGTATAAC   | 1800  |
| 35  | AIGII  |  |  |  |  |  | 1805  |
| -   |  |  |  |  |  |  |   |
|   | Seq ID NO:   | C134 DNA S   | equence  |  |  |  |   |
|   | Nucleic Ac   | id Accession   | n #: FGENESI   | i predicted  |  |  |   |
| 40  | Coding seq   | uence: 11  | 0674   |  |  |  |   |
| 40  |  |  |  |  |  | a.   |   |
|   | 1  | 11   | 21   | 31   | 41   | 51   |   |
|   |  | 1  |  | 1  |  | 1  |   |
|   | ע האישאיים ער ביינים ער  | COURSE COMME   | THE PROPERTY CANADA  | COTOTOCOCO   | ***********  | CIRCOCOCO NOC  |   |
|   |  |  | TTGTTGCTGG   |  |  |  | 60  |
| 45  | TTTCAGCAGA   | TGTCCCCGTC   | GCGCAATTTC   | AGCTTCCGCC   | TCTTCCCCGA   | GACCGCGCCC   | 120   |
| 45  | TTTCAGCAGA<br>GGGGCCCCCG   | TGTCCCCGTC<br>GGAGTATCCC   | GCGCAATTTC<br>CGCGCCGCCC   | AGCTTCCGCC<br>GCTCCTGGCG   | TCTTCCCCGA<br>ACGAAGCGGC   | GACCGCGCCC<br>GGGGAGCAGA   |   |
| 45  | TTTCAGCAGA<br>GGGGCCCCCG<br>GTGGAGCGGC   | TGTCCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC   | GCGCAATTTC   | AGCTTCCGCC<br>GCTCCTGGCG<br>CGCGTGCGGC   | TCTTCCCGA<br>ACGAAGCGGC<br>TGCTGCGGGA  | GACCGCGCCC<br>GGGGAGCAGA<br>GCTCAGCGAG   | 120<br>180  |
| 45  | TTTCAGCAGA<br>GGGGCCCCCG<br>GTGGAGCGGC<br>CGCCTGGAGC<br>AGCGAGCTCA   | TGTCCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC<br>TTGTCTTCCT<br>TGTTCGTCCG   | GCGCAATTTC<br>CGCGCCGCCC<br>GTTCCGGCGA<br>GGTGGATGAT<br>CAAGCTGCTG   | AGCTTCCGCC<br>GCTCCTGGCG<br>CGCGTGCGGC<br>TCGTCCAGCG<br>TCCGACTTCC   | TCTTCCCGA<br>ACGAAGCGGC<br>TGCTGCGGA<br>TGGGCGAAGT<br>CCGTGGTGCC   | GACCGCGCCC<br>GGGGAGCAGA<br>GCTCAGCGAG<br>CAACTTCCGC<br>CACGGCCACG   | 120<br>180<br>240   |
|   | TTTCAGCAGA GGGGCCCCCG GTGGAGCGGC CGCCTGGAGC AGCGAGCTCA CGCGTGGCCA  | TGTCCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC<br>TTGTCTTCCT<br>TGTTCGTCCG<br>TCGTGACCTT   | GCGCAATTTC<br>CGCGCCGCCC<br>GTTCCGGCGA<br>GGTGGATGAT<br>CAAGCTGCTG<br>CTCGTCCAAG   | AGCTTCCGCC<br>GCTCCTGGCG<br>CGCGTGCGGC<br>TCCGACTTCC<br>AACTACGTGG   | TCTTCCCGA ACGAAGCGGC TGCTGCGGGA TGGGCGAAGT CCGTGGTGCC TGCCGCGCGT   | GACCGCGCCC<br>GGGGAGCAGA<br>GCTCAGCGAG<br>CAACTTCCGC<br>CACGGCCACG<br>CGATTACATC   | 120<br>180<br>240<br>300<br>360<br>420  |
| 45<br>50  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGGC CGCCTGGAGC AGCGAGCTCA CGCGTGGCCA TCCACCCGCC   | TGTCCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC<br>TTGTCTTCCT<br>TGTTCGTCCG<br>TCGTGACCTT<br>GCGCGCGCCCA  | GCGCAATTTC<br>CGCGCCGCCC<br>GTTCCGGCGA<br>GGTGGATGAT<br>CAAGCTGCTG<br>CTCGTCCAAG<br>GCACAAGTGC   | AGCTTCCGCC<br>GCTCCTGGCG<br>CGCGTGCGGC<br>TCGTCCAGCG<br>TCCGACTTCC<br>AACTACGTGG<br>GCGCTGCTCC   | TCTTCCCGA<br>ACGAAGCGGC<br>TGCTGCGGA<br>TGGGCGAAGT<br>CCGTGGTGCC<br>TGCCGCGCGT<br>TCCAAGAGAT   | GACCGCGCCC<br>GGGGAGCAGA<br>GCTCAGCGAG<br>CAACTTCCGC<br>CACGGCCACG<br>CGATTACATC<br>CCCTGCCATC   | 120<br>180<br>240<br>300<br>360<br>420<br>480   |
|   | TTTCAGCAGA GGGGCCCCG GTGGAGCGGC GGCTGGAGC AGCGAGCTCA CGCGTGGCCA TCCACCCGCC TCCTACCGAG  | TGTCCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC<br>TTGTCTTCCT<br>TGTTCGTCCG<br>TCGTGACCTT<br>GCGCGCGCCA<br>GTGGCGCGCAC  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTCGTCCAAG GCACAAGTGC CTACACCAAG  | AGCTTCCGCC<br>GCTCCTGGCG<br>CGCGTGCGGC<br>TCGTCCAGCG<br>TCCGACTTCC<br>AACTACGTGG<br>GCGCTGCTCC<br>GGCGCCTTCC   | TCTTCCCGA ACGAAGCGGC TGCTGCGGGAAGT CCGTGGTGCC TGCCGCGCGT TCCAAGAGAT AGCAAGCCGC   | GACCGCGCCC<br>GGGGAGCAGA<br>GCTCAGCGAG<br>CAACTTCCGC<br>CACGGCCACG<br>CGATTACATC<br>CCCTGCCATC<br>GCAAATTCTT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
|   | TTTCAGCAGA GGGGCCCCG GTGGAGCGGC CGCCTGGAGC AGCGAGCTCA CGCGTGGCCA TCCACCCGCC TCCTACCGAG CTTCATGCTA  | TGTCCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC<br>TTGTCTTCCT<br>TGTTGTCCT<br>TCGTGACCTT<br>GCGCGCGCCA<br>GTGGCGGCACA<br>GAGAAAACTC   | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTCGTCCAAG GCACAAGTGC CTACACCAAG AACAAAGTT  | AGCTTCCGCC GCTCCTGGCG CGCGTGCGGC TCCGACTTCC AACTACGTGG GCGCTGCTCC GGCGCCTTCCC GTATTTCTCA   | TCTTCCCGA ACGAAGCGGC TGCTGCGGGAAGT CGGTGGTGCGCGCT TGCCGCGCGT TCCAAGAGAT AGCAAGCGC TCACTGATGG   | GACCGCGCCC GGGGAGCAGA GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600   |
| 50  | TTTCAGCAGA GGGGCCCCCG GTGGAGCCC CGCCTGGAGC AGCGAGCTCA CGCGTGGCCA TCCACCCGCC TCCTACCGAC CTTCATGCTA GGGGGAGACCC  | TGTCCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC<br>TTGTCTCCT<br>TGTTCGTCCG<br>TCGTGACCTT<br>GCGCGCGCCC<br>GTGGCGCCAC<br>GAGAAAACTC<br>CTAGACCAAT  | GCGCAATTTC CGCGCCGCCC GTTCCGGCCGC GGTGGATGAT CAAGCTGCTG CTOGTCCAAG GCACAAGTGC CTACACCAAG AACAAAAGTT TGCAGCGTCA   | AGCTTCCGCC GCTCCTGGCG CGCGTGCGGC TCCGACTTCC AACTACGTGG GCGCTGCTCC GGCGCCTTCCC GTATTTCTCA CTGCGAGATT  | TCTTCCCGA ACGAAGCGGC TGCTGCGGGC TGCTGCGGCGAGT TCCAAGAGAT AGCAAGCGG TCACTGATGG CAGGAGTGGA   | GACCGCGCCC GGGAGCAGA GCTCAGCGAG GCACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600   |
|   | TTTCAGCAGA GGGGCCCCCG GTGGAGCGCC CGCCTGGAGC CGCGTGGCCA TCCACCCGCC TCCTACCGAG CTTCATGCTA GGGGGAGACC TTTGGCATAT  | TGTCCCCGTC GGAGTATCCC TGGGCCAGGC TTGTTCTTCCT TGTTCGTCCG TCGTGACCTT GCGCGCGCCA GTGGCGGCACCC GAGAAAACTC CTAGACCAAT GGCAAGGGAA  | GCGCAATTTC CGCGCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTCGTCCAAG GCACAAGTGC CTACACCAAG AACAAAAGTT TGCAGCGTCA CATTCGAGAG  | AGCTTCCGCC GCTCCTGGCG CGCGTGCGGC TCGTCCAGCG TCCCACTTCC AACTACGTGG GCGCTGCTCC GGGGCCTTCC GTATTTCTC CTGCAGATT CTGAATGACA   | TCTTCCCGA ACGAAGCGGC TGCTGCGGGA TGGGCGAAGT CCGTGGTGCC TGCCGCGGT TCCAAGAGAT AGCAAGCCGC TCACTGATGG TCACTGATGGA TGGCTTCCAC  | GACCGCGCCC GGGGAGCAGA GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600   |
| 50  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGGC CGCCTGGAGC AGCGAGCTCA TCCACCGGCC TCCTACCGAG CTTCATCGTA GGGGAGACC TTTGGCATAT GAGCACTGTT  | TGTCCCGTC<br>GGAGTATCCC<br>TGGGCCAGGC<br>TTGTCTCCT<br>TGTTCGTCAG<br>TCGTGACCTT<br>GCGCGCGCCA<br>GTGGCGGCAC<br>GAGAAAACTC<br>CTAGACCAAT<br>GGCAAGGAA<br>ACCTGCTACA  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTC CTCGTCCAAG GCACAAGTGC CTACACCAAG AACAAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA  | AGCTTCOGCC<br>GCTCCTGGCG<br>CGCGTGCGGC<br>TCGTCCAGCG<br>TCCGACTTCC<br>AACTACGTGG<br>GCGCCTTCC<br>GGCGCCTTCC<br>GTATTTCTCA<br>CTGCAGAGATT<br>CTGAATGACA<br>GAATTTGAGG   | TCTTCCCGA ACGARGCGGC TGCTGCGGGA TGGGGGAAGT CCGTGGTGCC TGCCGGGGT TCCAAGAGAT AGCAAGCGC TCACTGATGG CAGGAGTGGA TGGCTTCCAC  | GACCGOGCCC GGGGAGCAGA GCTCAGCGAG GCACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720   |
| 50  | TTTCAGCAGA GGGGCCCCCG GTGGAGCCC AGCGAGCTCA AGCGAGCTCA ACCCAGCC TCCTACCGAG CTTCATGCTA GGGGGAGACC TTTGGCATAT GAGCACTGTT CATGAAGAAT CATGAAGAAT TGTGAATGAAA  | TGTCCCGTC GGAGTATCCC TGGGCCAGGC TTGTCTTCCT TGTTGGTCG TGGGCGGCCC GTGGCGGCCC GTGGCGGCCC CTGGCCGCCC GGCAAGGGAA ACCTGCTACA TACCTTCTGC GCAAGGGACT GCCAAGGACTG   | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTCCTCCAAG GCACAAGTGC CTACACCAAG AACAAAAGTT TGCAGCGTCA CATTCGAGGA CAGTTTTGAA GAGTTTTATT CTGTGACCGA  | AGCTTCCGCC<br>GCTCCTGGCG<br>CCGCTGCGCC<br>TCGTCCAGCG<br>TCCGACTTCC<br>AACTACGTGG<br>GGCCCTTCC<br>GGCCCTTCC<br>GTATTTCTCA<br>CTGCAGGATT<br>CTGAATGACA<br>GAATTTGAGG<br>CAAGATGATA<br>ATGGGAAGCT   | TCTTCCCGA ACGAAGCGGC TGCTCGGGA TGGCGGAAGT TCCAAGAGGT TCCAAGAGAT AGCAAGCCGC TCACTGATGG TCACTGATGG TCACTGATGG TCACTGATGG TCACTGATGC TTAGCTCAC TGTTAGCTCAC GCAAATGTGG GCAAATGTGG  | GACCGOGCCC GGGGAGCAGA GCTCAGCGAG GCACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGGCATTG CTCAAATCTT GAACACACACA   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780   |
| 50  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGC CGCCTGGAGC AGCGAGCTCA TCCACCCGCC TCCTACCGAG CTTCATGCTA GGGGGAACC TTTGGCATAT GAGCACTGTT CATGAAAGATC TGTGATAAAG GGCCATTTTG   | TGTCCCGTC GGAGTATCCC TGGGCCAGC TTGTTCTTCT TGTTCGTCG TCGTGACCTT TGTGGCGCCA GTGGCGGCCA GTGGCGGCA GGGAAAACTC CTAGACCAAT GGCAAGGAA ACCTGCTACA TACCTTCTCG AGGAAGGAA AGGAAGGACTG AGTGCAACGACTG AGTGCAACGACTG AGTGCAACTACA  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTGC CTCCTACAAG GCACAAGTGC CTACACCAAG AACAAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTAAA TGTGACCGA TGAAAAGGGG   | AGCTTCCGCC GCTCCTGGGG CCGCTTCCGGCTCCGC TCCGACTTCC AACTACGTGG GCGCTCCC GGCGCTTCC GTATTTCTCA CTGCAGATT CTGAATGACA GAATTTAGGG CAAGATGATA ATGCGGAAGCT TATTACGGA  | TCTTCCCGA ACGAAGCGGC TGCTGCGGAAGT TGGGGAAGT TCCAGAGGAT AGCAAGCGC TCACTGATGG CAGGAGTGGA TGGCTTCCAC CTTTAGCTCG TGTCCACTGATGG CAGAAGTGGA AGGAAGTGGA AGGAAGTGGA AGGAAGTGGA AAGGTCACTG  | GACCGOGCCC GGGGAGCAGA GCTCAGCGAG GCTCAGCGAG CAACTTCCGC CACGGCCACC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGCATTG CTCATATCTT GACACACACAC GTATGAATGC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960  |
| 50<br>55  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGGC CGCCTGGAGC AGCGAGCTCA TCCACCGGC TCCTACCGAG CTTCATCGTA GGGGAGACC TTTGGCATAT GAGCACTGTT CATGAAGATC AGGCACTTTTG GGGCATATT GAGCACTTTTA  | TGTCCCGTC GGAGTATCCC TGGGCCAGC TTGTCTTCCT TGTTCGTCCG TCGTGACCTT GCGCGCCCA GCGACACCAC GCAACACAC GCCAACCACT TACCTTCTGC GCAAGGCAA ACCTGCTACA TACCTTCTGG GCAAGGACTAC CATCGCGCAC CATCGCGGCAC CATCGCGGAC CATCGCGGAC CATCGCGGAC CATCGCGGAC CATCGCGGAC CATCGCGGAC CATCGCGGGAC CATCGCGGGAC  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTCGTCCAAG GCACAAGTGC CTACACCAAG AACAAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTATT CTGTGACCGA ATGAAAAGGG ATACAAACCT  | AGCTTCCGCC GCTCCTGGGG CCGCTTCCGGCT TCGTCCAGCG TCCGACTTCC AACTACGTGG GCGCGTTCCC GTATTTCTCA CTGCGAGATT CTGAATGATCA GAATTTGAGG CAAGATGATA ATCGGAAGCT TATTACGGAA GAAGCTCAC   | TCTTCCCGA ACGAAGCGGC TGCGCGGAAGT TGGGGGAAGT CCGTGGTGCC TGCCGCGGGT AGCAAGAGAT AGCAAGCGC TCACTGATGG CAGGAGTGGA CGGTCCACTG TGGTCCAC TGGTCCACTG TGGTCCACTG TGGTCCACTG TGGTCCACTG TGGTCCACTG TGGTCACTGCACTG   | GACCGOGCCC GGGGAGCAGA GCTCAGCGAG GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCAAGATTCTT ATATTCCAAT GATCTTCACT CCCAAAGAG CCGGGCATTG CTCATATCTT GACACACACAC GTATGAATGC CAGCAGTTGC CAGCAGTTGC CAGCAGTTGC CAGCAGTTGC CAGCAGTTGC CAGCAGTTGC CAGCAGTTGC  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>900<br>1020   |
| 50  | TTTCAGCAGA GGGGCCCCCG GTGGAGCCA CGCCTGGAGC AGCGAGCTCA CGCGTGGCCA TCCACCGGCC TCCTACCGAG CTTCATGCTA GGGGGAGACC TTTGGCATAT CATGAAGATC TGTGATGAAG GGCCATTTTG ACAGCTTGCC ATTCCATGTC ACACCTGCC ACTCCATGCC ATTCCATGTC ACTCCATGTC ACTCCATGTC   | TGTCCCGTC GGAGTATCCC TGGGCCAGGC TTGTCTTCCT TGTTCGTCG TCGGCGCCC GGGCACGCA GGCAAAACTC CTAGACCAAT GCCAGGAAACTC GCAAGGAAA CCTGCTACA GCAAGGAAC GCAAGGACT ACCTTCTCG GCAAGGACT AGTGCATCT CATCGCGCAC CTGATGAAAA CCTGATGAAAA CCTGATGAAAA  | GCGCAATTTC CGCGCCGCCC GTTCCGGCA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTATT CTGTGACCGA TGAAAAGGGG ATACAAACCT TGAACCCT TGAACCT TGAACCCT TGAACCCT TGAACCCT TGAACCCT TCACACCTCT   | AGCTTCCGCC GCTCCTGGCG GCGCTGCAGCG TCCGACTTCC AACTACGTGG GCGCTTCC GGCGCTTCC GTATTTCTCA CTGCAGGATT CTGAATGACA GAATTTGAGG AACTTACGGAAGCT TATTACGGAA CCACCTGGAA CCACCTGCAC CCACCTCCACCTCCAC CCACCTCCACCTCCAC CCACCTCCACCTCCAC CCACCTCCACCTCCACCTCCAC CCACCTCCACCTCCACCTCCACC | TCTTCCCGA ACGAAGCGGC TGCTGGGCA TGGGCGAAGT TCCTGGTGCC TCCCAGAGAGT TCCAAGAGAT AGCAAGCGC TCACTGATGG TCACTGATGG TCACTGATGG TCACTGATGA TGGCTTCCAC TGTTCCACT GCAAATGTGG AAGGTCTAC AAGGTCTCAC AAGGTCTACAC GCAAATGTGG AAGGTAAT GCACATCCCC  | GACCGCGCCC GGGGACCAGA GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGCATTG CTCAAATTCTT GACACACACA GTATGAATGCT TGACACACTC CAGCAGTTGC TGAAGACTGT TGAAGACTGT  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080   |
| 50<br>55  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGC CGCCTGGAGC AGCGAGCTCA TCCACCCGCC TCCTACCGAG CTTCATGCTA GGGGGAGACC TTTGGCATAT GAGCACTGTT CATGAAGAT CATGAAGAT GGCCATTTTG ACAGCTTGCC ATTCCATGTC ATTCCATGTC GTCTGCAGAG   | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCCT TGTTCGTCGG GGCGCGCCA GTGGCGGCCC GTGGCGGCC GTGGCGGCA GGAAAACTC GGCAAGGGAA ACCTGCTACA TACCTTCTGC GCAAGGACT AGTGCATCTC CATCGGGGAC CATGGAACTACA AGGGATGAAAA AGGGATACAA  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTC CTCCAAG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGGAG CAGTTTTAAT CTGTGACCGA TGAAAAGCG ATACAAACCT TCACACCTCT CGCATCTGG  | AGCTTCCGCC GCTCCTGGGG CTCGTCCAGCG TCCGACTTCC AACTACGTGG GGGCGCCTTCC GGGCCTTCC GTATTTCTCA CTGCAAGAGT CTGCAAGAGT CTGAAAGAGA GAATTTGAG GAATTTACGGA GAAGCTCAC GAAGCCTCAC CCACCTGCAA CAGACCTGTAC  | TCTTCCCGA ACGAAGCGGC TGCTGGGGAAGT CCGTGGTGCC TGCCGCGGT TCCAGAGGAGT AGCAAGCGG CACTGATGG CAGGAGTGGA CAGGATGGA TGGCTCCACT CTTTAGCTCG CTTTAGCTCG AGGAGGAAT AGGAAGCAACCCC CAGGAAGAAA  | GACCGOGCCC GGGGACCAG GCTCAGCGAG GCTCAGCGAG CAACTTCCGC CACGCCACC GCATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCAGT GCCAAAGGAG CCGGGCATTG CTCATATCTT GACACACCA GTATGAATGC CAGCAGTTGC TGAAGACTGT TGAAGACTGT TGCCCTGCC  | 120<br>180<br>240<br>360<br>420<br>540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080  |
| 50<br>55  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGGC CGCCTGGAGC AGCGAGCTCA CGCGTGGCCA TCCACCGGG CTCATCGAG CTTCATCGTA GGGGAGACCC TTTGGCATAT GAGCACTGTT CATGAAGATC ACAGCTTGCATGAT ACAGCTTGCC ATTCCATGTG GTCCATGTG CTTGCATGAGGAG CCTGCATGAGGAGC CTGCAAGAGC CTGAAGCCTCC CTGCAAGAGC CTGAAGCCTCC   | TGTCCCGTC GGAGTATCCC TGGGCCAGC TTGTCTTCCT TGTTCGTCCG TCGTGACCTT GGCGGCGCA GGGAAAACTC CTAGACCAAT ACCTTCTGG GGCAAGGGAA ACCTGCTACA TACCTTCTGG AGTGCATCTACA CTGCTACA ACCTGCTACA CTGCTACA ACCTGCTACA CTGCTACA AGGGAAACA CCGAAAAACG  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTACACAAG ACAAAAGTT TGCAGCGTCA CAGTTTTGAA GAGTTTTTGAA GAGTTTTATT CTGTACCCG ATACAAACCT TCACACCTCT TCACACCTCT TCACACCTCT TCACACCTCT TCACACCTCT TTACACTCTGGC TTACTTTGTA  | AGCTTCCGCC GCTCCTGGGG CCGCTTCCGGCT TCGTCCAGCG TCCGACTTCC AACTACGTGG GCGCCTTCC GTATTTCTCA CTGCAGATT CTGAATGACA GAATTTAGGG CAAGATGATA ATGGAACCT TATTACGGAA GAAGCTCAC CCACCTGGAA CCACCTGGAA CAAACACTT CAAAACACTT CAAAACACTT   | TCTTCCCGA ACGAAGCGGC TGCTGCGGAAGT TGGGGGAAGT TCCAGGGGAT AGCAAGGAT AGCAAGCGC TCACTGATGG CAGTGGA TGGCTCCAC TGGTCCACTG TGGTCCACTG TGGTCCACTG TGGTCCACTG TGGTCCACTG TGACTCGCA AACGTTGCAC AACGTTGTCAC CAGGAGGAAT CAGGACAACCCA AACTTGTCCA  | GACCGOGCCC GGGGAGCAGA GCTCAGCGAG GCTCAGCGAG CAACTTCCGC CACGGCCACG GGATTACATC CCCAAGATCCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGGCATTG CTCATATCTT GACACACACA CAGAGAGTGC TGAAGACTGC CAGCAGTTGC TGAAGACTGC CTGCCCTGCC   | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1140  |
| 50<br>55<br>60  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGC AGCGAGCTCA AGCGAGCTCA TCCACCCAGC TCCTACCAG CTTCATGCTA GAGCACTGTT CATGAAGATC TATGAAGATC TATGAAGATC ATTCAAGATA GCCATTTTG ACAGCTTCATGAAGATC GCCATTTTG ACTGACAAGATC GTCTGCAGAG CTTGAAGAGCCTCACCCCATGCCCCCCCCCC   | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCT TGTTCGTCG TGGCGCGCCA GTGGCGGCCA GTGGCGGCCA GTGCCGCCA GTGCAGGCAA ACCTGCTACA TACCTTCTGG GCAAGGGAA ACTGCTACA AGTGCATCTC AGTGCATCTC CGTCAGGAAA AGGGATACAG CTGATGAAAA AGGGATACAG CCGAAAATGG TCCGATGTCA GTTCTGGTC GTTTCTGGTC GTTTTTGGTC  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTTT TGCAGCGTCA CATTCGAGAG GAGTTTTGAA GAGTTTTATT CTGTCACCGA TGAAAAGCG ATACAAACCT TCACACCTCT GGCATCTGGC TTACTTTACT   | AGCTTCCGCC GCTCCTGGGG CTCGTCCAGCG TCCGACTTCC AACTACGTGG GCGCTGCTCC GGCGCTTCC GTATTTCTCA GCATTTCCTAGG CAAGATGTA ATGGGAAGCT TATTACGGA GAAGCTCAC CCACCTGGAA CAGACCTTG CAAAACACTT GATCTTGTTG AGCTACTC  | TCTTCCCGA ACGAAGCGGC TGCTGGGGAAGT TCCAGGGAAGT TCCAGGAGGAT AGCAGCGGAGGAGAGCGC TCACTGATGG CAGGAGTGA TGGCTCCAC TTTAGCTCG CTTAGCTCG GCAATGTGG AAGGTCTGCA AGGTTCCAC AGGAAGAAT AGGAAGAAC AGGAAGAAC AACTTGTCCA GCAACAACCA GAAGCACGCA GAAGCAACA  | GACCGOGCCC GGGGAGCAGA GCTCAGCGAG GCTCAGCGAG CCACTTCCGC CACGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCAGT CCCAAAGGAG CCGGGCATTG CTCATATCTT GACACACACA GTATGAATGC CAGCACTTGC TGACGCACTTGC CTTCAATGCC CTTCAATGCA CATCTTCATTGC CTTCAATTGCA CATCTTCATTGCACACCC CTTCAATTGCACACCC CTTCAATTGCACACCC CTTCAATTGCACACCC CTTCAATTGCACACCC CTTCAATTGCACACCC CTTCAATTGCACACCC CTTCAATTGCACACCC CTTCAATTGCACACCCC CTTCAATTGCACACCCC CTTCAATTGCACACCCC CTTCAATTGCACACCCCC CTTCAATTGCACACCCCC CTTCAATTGCACACCCCC CTTCAATTGCACACCCCCCCC CTTCAATTGCACACCCCCCC CTTCAATTGCACACCCCCCCCCC  | 120<br>180<br>240<br>360<br>420<br>540<br>600<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080  |
| 50<br>55  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGC CGCCTGGAGC AGCGAGCTCA ACCGGGC TCCTACCGAG CTTCATGCTA GGGGAGACC TTTGGCATAT GAGCACTGTT CATGAAGATC ATGAAGATC ACAGCTTGCCA ACTCCAGGG CTCCTACGAG CTCCAGAGGCCTCCCAAGGCCTCCCAAGGCCTCCCCAAGCCTCCCCCAGC   | TGTCCCGTC GGAGTATCCC TGGGCCAGC TTGTTCTTCT TGTTCGTCG TCGTGCGCT TGGGCGCCC GGGAAAACTC CTAGACCAAT GGCAAGGGAA ACCTGCTACA TACCTTCTGC CATCGGGGAC CATCGGGGAC CATCGGGGAC CATCGAGAAAACTC CTGATGAAAAACGC CTGATGAAAAACGC CTGATGAAAAACGC CCGAAAATGG CCGAAAATGG CCGAAAACGC CGTTGTGGGAC CGTTGTGGGAC CGGAAACATGG   | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTACACAAG GCACAAGTGC CTACACAAG AACAAAGTT TGCAGGGTCA CATTCGAGAG CAGTTTTGAA CAGTTTTATA TCAGCCCA TGAAAACCT TCACACCTCT TCACACCTCT TCACACCTCT CGCATCTTTATC CCCTGGATTT CGCTTCAGAG CCACATCAGC  | AGCTTCCGCC GCTCCTGGGG CTCGTCCAGGG TCGACTTCC AACTACGTGG GGGCGCTCC GGGCCTTCC GTATTTCTCA CTGCAAGTGTC CTGAATGACA GAATTTCAGGAAGT TATTACGGAAGCT TATTACGGAAGCT TATTACGGAAGCT CCACCTGGAA CAGACCTGTA CAGACCTGTA CAGACCTTGACAC GTCTTACTACAC TGTTCTACACA TCTTCTCACAC TCTCTCTCCACA TGTTCTACACA TGTTCTACACA TCTTCTACCAC TCTCTCCACAC TCTCTCTC  | TCTTCCCGA ACGAAGCGGC TGCTGCGGAAGT TGGGGGAAGT CCGTGGTGCC TGCCGCGGT TCCAAGAGAT AGCAAGCGC CACTGATGG CAGGAGTGGA CAGGAGTCGA CTTTAGCTCCACTG TGGTTCCACTG CGAATGTGC AAGGTCTGCA CAGAAGCAG AAGGTCTGCA CAGAAGCAG AACTGTGCA GCAAATGTGG AAGGTCTGCA CAGGAGGAAT GCACATCCCC GCAACACCA GCAACACCA GCAACACCA GCAACAACCA GCAACAACCA GAGCAGCAT GGGAAATGTTG GGGAACAACCA GGGGAATGTTG  | GACCGOGCCC GGGGAGCAGA GCTCAGCGAG GCTCAGCGAG CCACTTCCGC CACGGCCACC GCATTACATC GCAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGCATTG CTCATATCTT GACACACAC GTATGAATGC CAGCAGTTGC TGAAGACTGT TGACCCTGCC CTTCAATGCA CATCTTTATGT ATGTTCATT  | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>960<br>960<br>1020<br>1080<br>1140<br>1200   |
| 50<br>55<br>60  | TTTCAGCAGA GGGGCCCCCG GGGGGCCCCCG CGCCTGGAGC AGCGAGCCA CGCGTGGCCA TCCACCCGCC TCCTACCGAGC TTTCATGCTA GAGGACTCTA CATGAAGACC TTTGGCATAT TGTGATGAAG GGCCATTTTG GCCATTTTG GTCTGCAGAG CTTCAGCAGAG CTCTACCAATG CTCACCAATG CTCCCCAGC   | TETCCCGTTE GGAETATCCC TEGGCCAGGC TTGTCTTCGTCG TCGTGACCTT GCGCGCCCC GGGCACGCCA GGCAAGGCAA   | GCGCAATTTC CGGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTATT CTGTGACCGA TGAAAAGCT TCACACCTCT GGCATCTGGC CTTACTTTATC CCGTGATTTATC CCGTTCAGAG CCACATCAGC TGAAGGGTTAGAC CAGTTTTAGA   | AGCTTCCGCC GCTCCTGGCG GCGCTCCAGCG TCCGACTTCC GACTTCC GACGCTTCC GGCGCTTCC GGACTTCC GGAGTTTC GGAGGCTTCC GAATTACGGA GAATTAGAGG GAAGTTATACGGAA GAAGTTACAGAA CAGACCTGGA GAGCTCAC CCACCTGGAA CAGACCTGGA AGCTACTCC AAACACTCT AACTTCTACAA AGCTTACTGAA AGACTAGTACA AGACTAGTACA AGACTAGAAA AGACTAGAAAA AGACTAGAAAAAAAA AGACTAGAAAAAAAAAA   | TCTTCCCGA ACGAAGCGGC TGCTGGGAAGT TGGGCGAAGT TCCAAGAGAT TCCAAGAGAT TCCAAGAGAT TCCAAGAGAT TCCAAGAGAT TCCAAGAGAT TCACTGATGG CAGGATTGACTCG TCTTAGCTCG GCAAATGTGG AAGTCTCACA ACGTCTCCACA ACGTCTCCCC AACTTGTCCA GCAACAACA CAGAACAACA GAAACAACA GAAACAACA GAGAACAACA GAGAACAACA GAGAACAACA GAGAACAACA GAGAACAACA CAGGAACAACA CAGGAACAACA CAGGAACAACA CAGGAACAACA CAGGAACAACA CAGGAACAACA CAGGAACAACA CAGGAACAACA CAGGAAACAC CAGGAACACAC CAGGAAACAC CAGGAACAC CAGGAAACAC CAGGAAACAC CAGGAAACAC CAGGAAACAC CAGGAACAC CAGGAAC CA | GACCGCGCCC GGGGAGCAGA GCTCAGCGAG CAACTICCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGCATTG GTCAATACTT GACACACAC GTATGAATGCT TGAAGACTGT TGAAGACTGT CTGCCTTGCC CTTCAATGCA CATCTTATGT ATATTACTAT ATATAAGACA CGCTTACTTT ATGTCCTTATT  | 120<br>180<br>300<br>360<br>420<br>440<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440   |
| 50<br>55<br>60  | TTTCAGCAGA GGGGCCCCG GTGGAGC CGCCTGGAGC AGCGAGCTCA AGCGAGCCA TCCACCGGCC TCCTACCGAG CTTCATGCTA GGGGAGACC TTTGGCATAT CATGAAGATC ATTCATGCTA ACCGTTGCC AGCCCTTCATGCT ACCCAGAGC CTTCATGCT ACCCAGAGC CTACCCAATG CTACCCAATG CTACCCAATG CTACCCAATG CTACCCAATG CTACCCAATG CAAGCATTTGG CTACCCAATG CTACCCAATG CAAGCATTTGC ACAGTTTTGG CAAGCAAACA   | TETCCCGTE GGAETATCCC TEGGCCAGGC TTGTCTTCCT TGTTCGTCGG GGGCGCA GGGAAACTC GCAAGGAAACTC GCAAGGATA ACCTCTCCAC AGTGCATCAC CATCGGGAC CTGATGAAAACATC CTGATGAAAACATC GCAAAACATC GCAAAACATC GCAAAACATC GCAAAACATC GCAAAACATC GCAAAACATC GCAAAACATC GCAACGGCA CCGATGCAC GCAACGAC GCAAACATC GCAAACATC GCAAACATC GCAACGAC GCAACGAC GCAACGCAC GCACGGCAC GCACGGCAC GCCACGGCAC GCCACGGCAC GCCACGCACG  | GCGCAATTTC CGCGCCGCCC GTTCCGGCA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG AGGTTTATT CTGTGACCGA TGAAAAGGGG ATACAAACCT TCACACCTCT GGCATCTGG CCTTGGTCCCCTCGGTTACTTCACTCATC CCCTGGATTT CCGTTCAGAG CCACATCAGGC TGAGGGTAC TGAGGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC   | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG TCCGACTTCC AACTACGTGG GCGCTTCC GGCGCTTCC GGCGCTTCC GTATTTCTCA GAATTGACA GAATTTGAGG AACTAGAGGAAGCT TATTACGGAAGCT CACACAGGAGAT CAGAACACTT CATCTGGCAACC CACCTGGAA CAGACCTGGC AACACTGGC AACACTGGC CACCTGGAA CAGACCTGGC CACCTGGGAA CAGACCTGGC CACCTGGGAA CAGACCTGGC CACCTGGGAA CAGCCTGGCA CAGCCTGGAC CACCTGGAAC CACCTGGAAC CCCCGGGAGC CCCCGGGGGCC CCCCGGGGGCC CCCCGGGGAC CCCCGGGGGCC CCCCGGGGCC CCCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCGGGCC CCCCCC   | TCTTCCCGA ACGAAGCGGC TGCTGGGGA TGGGCGAAGT TCCAAGAGAT TCCAAGAGAT AGCAAGCGC TCACTGATGG CAGGAGTGA TGGCTCACTGATGG CAGGAGTGA TGGCTCACC TGGTCCACTG GCAAATGTGG AAGGTCTGCA CAGGAGGAAT GCACATCCC AACTTGTCCA GCAACAACCA GAACCACCA GAAGCAGCAT GAGTAAGAAC GGGAAATGTG GAGTAAGAAC TGGAGGAAT TGGAGGCCA TGGAGGAAT TGGAGGCCC  | GACCGCGCCC GGGGACAGA GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT CCCAAAGGAG CCGGCATTG CTCAAATCGT GACACACAC GTATGAATCGT TGAAGACTGT CAGCACTGC CTGAAGCTGC CTGCACTGC CTTCAATGCA CATCTTAGT ATATAAGACA ATGTCCACT ATATAAGACA CTTTTATTTGT ATGTCCACC CTTCAATTGT ATGTCCACC CTTTCATTGT ATGTCCACC CTTTCATTGT CTTCTCATCTCT CTTCTCACCC  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500   |
| 50<br>55<br>60  | TTTCAGCAGA GGGGCCCCCG GTGGAGCGC CGCCTGGAGC AGCGAGCTCA ACCGAGC TCCTACCGAG CTTCATCATA GGGGGAAACC TTTGGCATAT CATGAAGAT CATGAAGAT CATGAAGAT CATGAAGAT CTTCATGTA ACAGCTTGCC GTCTGCAGAG CTTGCAGAG CTTGCAGAG CTGAAGCCTC GCCTGTCGG CTACCCAATG CTACGCAGAACA CAAGGAAACA TTTCAGATGC   | TGTCCCGTC GGAGTATCCC TGGGCCAGGC TTGTCTTCT TGTTCGTCG TGGCGGCCCC GTGGCGGCCC GTGGCGGCCC GTGGCGGCCC GTGGCGGCCC GTGGCGGCC GTGGCGGCC GTGGCGGCC GTGGCGGCC GTGGCGGCC GTGGCGGCC GTGGCGCC GTGGCGCC GTGGCGCC GTGGCGCC GCAAGAAACT CCGAAAATGG TCCGATGCC GTTTCTGGT CGAAACT GCCAGTGGCA CCCAAGATT CCCAAGATT  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG CTCCAAG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CAGTTTTGAA GAGTTTTATT CTGTGACCGA TGAAAACCT TCACACCTCT GCATCTGGC TTACTTTACT   | AGCTTCCGCC GCTCCTGGGG CTCGTCCAGCG TCCGACTTCC AACTACGTGG GCGCTCCC GGGGCCTTCC GGGGCCTTCC GTATTTCTCA GAATTTGAGG CAAGATGTT ATTGAGAAGCT TATTACGGA AGACCTGCA CAACCTGGAAACCT GAACTTGTGAC GACTTGCACGAACCT GATCTTGTCG GACTTGCACACCT CCCCCGGTGTG CCCCCACACT CCCCCCACACT  | TCTTCCCGA ACGAAGCGGC TGCTGGGGAAGT TGGGGGAAGT TGCGGGAAGT TGCAAGAGAG AGCAAGCGG TCACTGATGG TGCTCCAC TTTAGCTCG TTTAGCTCG TGTTAGCTCCAC TGGAAGAGAT AGGATCAC AAGTTCCA AGGAAGAAC GAACAACC GAACAACC GAACAACC GAACAACC GAGGAAT GGGAATGTG GAGTGAT GGGAATGTC GAGTGATGC TGGAACACC TGGGAACACC TGGGAAATGTC TGGGAAATGTC TGGGAAATGTC TGGGAAATGTC TGGGAAATGTC TGGGAAATGTC TGGGAAACAC TGGGAAACAC TGGGAAAGCAC TGGGAAAGCAC TGGGAAGCAC TGGGAAGCAC TGGGAAGCAC TGGCAAGCA   | GACCGOGCCC GGGGACCAG GCTCAGCGAG GCTCAGCGAG CCACTTCCGC CACGCCACC CCATTCCATC GCAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGCCATG GCACACACAC GTATGAATGC TGAACACTC TGAAGACTGC TGAAGACTGC CTTCAATGCA CTTCAATGCA ATATCTTATTGT ATATCTCAT ATATCTCAT ATATAAGACA GCTTACTTGT CTGCTCCTCC CTTCAATGCA CTTCAATGCA CTTCAATTGCA CTTCAATTGCA CTTCAATTGT ATATAAGACA GCTTACTTGT CTGTTCCACC GCCAGCCAAA   | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | TTTCAGCAGA GGGGCCCCG GGGGCCCCG CGCCTGGAGC AGCGAGCTCA AGCGAGCTCA CCTACCGAG CTTCATGCTA GGGGAGAACC TTTGGCATAT CATGAAGATC ATTCATGTA GGCCATTTTG ACACTTGCA ATTCCAGAG CTTCAGAGA CCTGCAGAG ACACTTTTC GTCTGCCAGAG CTGAAGCCTC GCCTGCCAGC ACATTTTG CAAGAAACA TTTCAAAGAT TTTCAGAAGA TTTCAGAAGG TTTGGGAAGAA  | TETCCCGTE GGAETATCCC TEGGCCAGGC TTGTCTTCGTCG TCGTCGCGCGCCC GGGCGCCC GGGCGCCC GGGCGCCC CTGGCGCCCC CTGGCGCCCC CTGGCGCCCC CTGGCGCCC CTGACCTAT GCCATCTCTG GCAAGGACT ACCTCTCTGG GCAAGGACT AGTGCATCTC CTGATGAAAA AGGGATACAG TCCGAAGACT TCCGTTCA GTTTTGGTC CGAACATCG TTGCCTGTGA GCCAGTGGGA CCCAAGACATCG TTGCCTGTGA CCCAAGACATCG TTGCTGTGA CCCAAGAGAT TCTGCTATCT TCTGCTATCT TCTGCTATCT   | GCGCAATTTC CGGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTCT CAAGCTGCTCAAG GCACAAGTGC CTACACCAAG AACAAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTATT CTGTGACCGA TGAAAACCT TCACACCTCT GGCATCTGGC TTACTTTATC CCCTGGATTT CGGTTCAGAG TGAAGGGTAC TGAAGGTAC TGAAGGGTAC AGTTGCCGC   | AGCTTCCGCC GCTCCTGGCG GCGCGTCCCAGCT TCCGACTTCC GCGCGTCTCC GGCGCTTCC GGCGCTTCC GGAGTTTC GGAGCTTCC GAATTCCAAA AATACACA GAATTACAGA GAATTACAGAA CAAGATGATA ATGGGAAGCT TATTACGGAA GAAGCTGAC CCACCTGGAA AGCCTGTGA AGCTTATCACAA AGCTTATCACAA AGCTTATCACAA CCCCGGTGTGCCCCCACACCT CAAGGGTTCA  | TCTTCCCGA ACGAAGCGGC TGCTGGGGA TGGGCGAGT TCCAGGGAGT TCCAGGGGT TCCAGGGGT TCCAGGGGT TCCAGGGTGTCCC CTTTAGCTCG CCAGTTTCCAC CTTTAGCTCG CCAAATGTGG AAGGTCTCCAC AAGGTCTCCCC AACTTGTCCA GCACATCCCC AACTTGTCCA GCACAACCC GAAGCAGCAT GCGCAAATGTG CGGAAATGTT CCGGGAAGCAC GGGAAATGTT CCAGTGAGCAC TTTTATCTCG TGCCAGGC   | GACCGCGCCC GGGGAGCAGA GCTCAGGGGG CAACTTCCGC CAGGGCCACG CGATTACATC CCCAAAGTCT CCCAAAGGAG CCGGCATC GCAAATTCTT ATATTCCAAT GCACACACA GTATGATGT GACACACAC GTATGATGC CTGCATGC CTGCATGC CTGCATGC CTTCAATGCA CATCTTATGT ATATCCTATT ATATACACA CATCTTATGT ATATACACA CATCTTATGT CTGCTTCCCT CTTCCATCCAC CATCTTATGT CTGTTCCACC CGCTACCAAA AGTCAAAGAA  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560<br>1620  |
| 50<br>55<br>60  | TTTCAGCAGA GGGGCCCCG GTGGAGC CGCTGGAGC AGCGAGCTCA AGCGAGCTCA CGCTGGCCA TCCACCGCC TCCTACCGAC TTTCATGCTA GGGGAGACC TTTGGCATAT CATGAAGATC ATTCATGCAGAG GCCATTTTG ACAGCTTGCC GCCTGTGCGG CTACCCAAGC CTACCCAAGC CTACCCAAGC TTTCAGCAGAG CTACCCAAGC TTTCAGCAGAG CTACCCAAGC TTTCAGCAGAG CTACCCAAGC TTTCAGAGAC TTTCAGAGAC TTTCAGATGC CAAGGAAACA TTTCAGATGC TTTGGAGAGAA   | TETCCCGTE GGAETATCCC TEGGCCAGGC TTGTCTTCCT TGTTCGTCGG GCGCGCA GGGAAACTC GCAAGGAAA CCTGCTCCTC AGTGCACTT AGTGCACCAT GCAAGGAAA ACTGCACCAC CCGAAGGAAA AGGGATACAG CTGATGAAA AGGGATACAG CTGATGAAA TCCGTACC GCAAAATGC CCGAAGGAC CTGATGAAA GGGAAACATC GCAAGACATC CCAAAGATTC TGCCGTGTA GCCAGTGCA CCAAAGATTC TTGCCGTATG CCAAAGATTC CCAAAGATTC TCTGCTATGT CCAATGCAC CCAAAGATTC CCAATGCAC CCAACC CCAACC CCAACC CCAACC CCACC CC | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTATT CTGTGACCGA ATACAAACCT TCACACCTCT GGCATCTGGC TTACTTGATC CCCTGGATTC CCCTGGATTC CCGTTCAGAG CACATCAGGC CACATCAGGC TGAAGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC TGAGGGTAC AGGTTCCGCAAAATGGC AAGTTGCCGC TGGAAAATGGG   | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG TCCGACTTCC ACTACGTGG GCGCTTCC GGCGCTTCC GGCGCTTCC GTATTTCTCA GAATTACGGA CAAGATGATA ATGGGAAGCT TATTACGGAA CCACCTGGA CAACACT CAACACT CCCCCGCTGTG CCCCCACACT CCCACAGCT CAAGGGTTCA CCCACCTGGAA CCCCCCCACACT CCCACAGGTTCA CAAGGGTTCA CCCACACT CCACGGGATCA CCCACACT CCACGGGTTCG CCACAGCT CAAGGGTTCA AATGTCGGAG AATGTCGGAG CCACAGCT CAAGGGTTCA CAAGGGTTCA CAAGGGTTCA AATGTCGGAG AATGTCGGAG AATGTCGGAG CCACACT CAAGGGTTCA CAAGGGTTCA AATGTCGGAG   | TCTTCCCGA ACGAAGCGGC TGCTGGGCA TGGGCGAAGT TCCAAGAGAT AGCAAGCCGC TCCCTGATGG TCCACTGATGG TCACTGATGG TCACTGATGG TCACTGATGG TCACTGATGG TCACTGATGG TCACTGATGG TGGCCACTG TGGCCACTG TGGCCACTG TGGAATGTCCAC TGGAATGTCCAC TGGAAATGTCCA TGGAAATGTCCA TGGAAAACACCA TGAACAACCA TGAACAACCA TGAAGAAACT TGAAGAACT TGAGAGAATT TGCAGGGAAATT TGCAGGGCAACA TGGCAAGAC TGGCAAGAC TTTTTATCTGG TTTCAGGCACC  | GACCGCGCCC GGGGACAGA GCTCAGCGAG CAACTTCCGC CACGGCCACC CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CTCAATACTT GACACACAC GTATGAATGCT TGAAGACTGT CAGCAGCTGC CAGCAGTTGC TGAAGACTGT CAGCACTGC CATCATTGAT ATATAAGACA CTTTCATTGC CTTCATTGC CTCATTCATTGC CTCCTCATCC CTCATCCATCC CTCTCATCC CTCTCTCAT ATATAAGACA CTTTCTCACC GCCAGCCAAA AGTTACATAA  | 120<br>180<br>360<br>420<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1320<br>1440<br>1500<br>1500<br>1680  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | TTTCAGCAGA GGGGCCCCCG GTGGAGCGC AGCGAGCTCA AGCGAGCTCA TCCACCCGCC TCCTACCGAG CTTCATCATA GAGCACTGTT CATGAAGATC TATGAAGATC ATTCAAGATC GTCTGCAGAG CTTCATGAAGATC GTCTGCAGAG CTTCATGAAGATC TTTGATGAAGATC TTTCAATGAAG TTTCAATGAAG CTCAAGCATCC GCCTGTCGGG CCTACCCAATG CTAACCCAATG CTAAGCATCA TTTCAGATGA ATTCTAGATGA ATTCTGAAGAT TTTGGAACA ATTCTGAAGAT ATTCAGATGA ATTCTGAAGAT ATTCAGATGA ATTCTGAAGAT AGATTGAAGAT AGACTTGAAGAT AGA | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCT TGTTCGTCG TGTGCGGCCCC GGGCGCCA GGGAGCCA GGCAGGCA GGCAGGGAA ACCTGCTACA TACCTTCTGG GCAAGGGAA ACCTGCTACA AGGGATCTG CGTCAGAAATGG CTGATGAAAA AGGGATCTG TCCGGGAC TCCGTGTACA TCCGTGTACA TTGCTGTGGT CGAAGATGG CCCAAGATGT TTGCTGTGGT CCCACAGT TCTGCTATGT CTGCTATGT CTGCTATGT CTCCTCAAAT CGCAAGATGT CCCACATGCCA  | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG GAGTTTTGAA GAGTTTTATT CTGTCACCGA TGAAAAGCGT TTACACCTCT GGCATCTGGC TTACTTTATC CCCTCGGATTT CCGTTCAGAG CACATCAGC TGAAGGGTAC CACATCAGC TGAAGGGTAC CACATCAGC TGAAGGGTAC CACATCAGC TGAAGGGTAC CACATCAGC TGAAGGGTAC CACATCAGC TGAAAATGG CACATCACC TGGAAAATGC CACATCACC TGGAAAATGG  | AGCTTCCGCC GCTCCTGGGG CTCCTCGGGG TCCGACTTCC AACTACGTGG GCGCTGCTCC GGGGCCTTCC GGGGCCTTCC GTATTTCTCA GAATTTGCGGA GAATTTGCGGA CAGAAGCT TATTACGGA CAGACCTGG CACACCTGGAACCC CACCTGGAACCC CACCTGGAACCC CCCCCGGAT CCCCCCCACACCT CAAGGGTTCA AATGTCGGAA CAGGGTTCA AATGTCGGAA CCCCCCACACCT CAAGGGTTCA AATGTCCGAACA AAAGCACTTC AAAGGACTTCA AAAGCACTTCA AAAGCACTCA AAAGCACTCA AAAGCACTCA AAAGCACTCA AAAGCACACCA AAAGCACTCA AAAGCACACCA AAAGCACACCACCACCACCACCACCACCACCACCACCACC  | TCTTCCCGA ACGAAGCGGC TGCTGGGGAAGT TGCGGGAAGT TGCGGGAAGT TGCAGAGGAT AGCAAGCGG TCACTGATGG CAGGAGTGAA TGGCTCCAC TTTAGCTCG GCAATGTGC AACTTGTCCA ACTTGTCCA GCAACACCA AACTTGTCCA GGAACAACCA GAGGAAT GGACAGCAGCA TGGGCAGGAAT TGGACGGCAC TGGGCAGGAC TTTTACTGG TTTACTGG AGGTAAGAC TTTTACTGG TTTTACTGG   | GACCGOGCCC GGGGACCAG GCTCAGCGAG GCTCAGCGAG CCACTTCCGC CACGCCACG CGATTACATC CCCTGCCATC GCAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGGCATTG CTCATATCTT GACACACACA GTATGAATGC CAGCACTTGC CTTCAATGCA CATCTTAATGC CATCATTCTT CTGCCCTGCC   | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1560<br>1560<br>1620<br>1680<br>1740   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | TTTCAGCAGA GGGGCCCCG GTGGAGC CGCTGGAGC AGCGAGCTCA AGCGAGCTCA CGCTGGAGC TCCTACCGAG CTTCATGCTA GGGGAGACC TTTGGCATAT CATGAAGATC ATTCATGTA ACAGCTTGCA ATTCCATGTG GCCTTTCATGCCA ATTCCATGTG CTCAGCAGA CTTACCCAATG CTCACCAATG CTCACCAATG CTCACCAATG CTCACCAATG CTTCACGCAGA ACATGTTTGG CAAGGAAACA TTTCAGATGC TTTCAGCAGG CAAGGAAACA TTTCAGATGC CAAGGAAACA TTTCAGATGC CAAGATCTCAGAGA CAAGATTCTCGCCAGC CAAGATCAGATG CAAGATCAGATC  | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCGTCG TCGTGCGCCAGGC GGGCAGGCA GGGAAAACT GCCAGGCAGGCA GCAAGGGAA ACTGCTCTCAG GCAAGGAAA ACTGCATCAG CCTGATGAAAA AGGGATACAG CTGATGAAA AGGGAAAACT GCAAAATGTAC GCCAAGGAC TTGCTGTCACA GTTGCTCACAG TTGCCTGTCACA GTTGCATCT GCAAAACATCT GCAAGACT TCTGCTGTAG CCCAAAGATTT TCTGCTATGT GTACCACTT CTCCCAAAT TCTGCTAATG CCCAATGTCA CCCAATGTCA CCCCAATGTCA CCCAATGTCA CCCAATGTCAC CCCAAAGTTTA CCCAATGTTAC CCCAATGTTAC CCCAATGTTAC CCCAATGTTAC CCCAAATGTTAC CCCAATGTTAC CCCAATGTTAC CCCAATGTTAC CCCAATGTTAC CCCAATGTTAC CCAATGTTAC CCAA | GCGCAATTTC CGGCCGCCC GTTCCGCGCA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTAT CTGTGACCGA ATACAACCT TGAAAAGGGG ATACAACCT TCACACCTCT GGCATCTGGC TTACTTTGAC CCCTGGATTT CCGTTCAGAG CACATCAGG CACATCAGG CACATCAGG CACATCAGG CACATCAGG CACATCAGG CACATCAGG CACATCAGG CACATCAGG CAGAAAATGG CAACATGCCC TGGAAAATGG CAACATGCCC TGGAAAATGG CAACATGCCC TGGAAAATGG CAACATTCCC CTGGAATT CTGGCAGATT CTGGCAGATT CTGGCAGATT  | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG TCCGACTTCC AACTACGTGG GCGCTTCC GGCGCTTCC GGCGCTTCC GTATTTCTCA GAATTACAGAG CAAGATGATA ATGGGAAGCT TATTACGGAA CCACCTGGCA AGCTCAC CACCTGGCA AGCTCAC CCACCTGCA AGCTTCACAA CCCACCTGCA AGCTTCACAA AGCCTACACACACACACACACACACACACACACACACACA   | TCTTCCCGA ACGAAGCGGC TGCTGGGAAGT TGGGGAAGT TCCAAGAGAGT TCCAAGAGAT AGCAAGCCGC TCACTGATGG CAGGAGTGAA TGGCTCCAC TCACTGATGG CAGAATCTCAC CAGGAGTGAA AGGTTCACAC CAGGAGTCAC CAGAATCTCCAC AACTTGTCCA CAGGAGAAT CGAACAACCAC CAGAACACCAC GAAGAAGCAC TCGCCAGGGAATGTT TCGCAGGCAGCA TGGCAGCAC TTTTACTCG TTTTAGCTAGC AAGCAACAC AAGAACAACAC TTTTAGCCAGC TTTTAGCTAGC AAGCAACACA AAGACAACAC AAGACAACAC AAGACAACAC TTTTAGCCAGC TTTTAGCCAGC AAGCACACAC AAGACAACAC AAGACAACAC TTTTCCCAAT TTTTACCCAAT TTTTCCCAAT TTTCCCAAT TTTTCCCAAT TTTCCCAAT TTTTCCCAAT TTTCCCAAT | GACCGCGCCC GGGGACCAGA GCTCAGCGAG CAACTTCCGC CACGGCCACC CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CTCAATACT CCAAAGGAG CTCAATACT GACACCACA GTATGAATGC TGAAGACTGT CAGCACTGC CAGCAGTTGC TGAAGACTGT ATATAAGACA ATATAAGACA CTTTATGT ATATAAGACA TATTAAAGACA TATTAAAGACA TTTTAATGCA CACCTCCTCAT ATATAAGACA TTTTAATGCA TTTTAATGCA TTTTAATGCA TTTTAATGCA TTTTTAATAAGACA TTTTTTAATAAGACA TTTTTTAATAAGACA TTTTTTAAAC TTTTTTAAAC TTTTTTAAAC TTTTTTTT  | 120<br>180<br>360<br>420<br>540<br>600<br>660<br>720<br>780<br>840<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1320<br>1430<br>1500<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | TTTCAGCAGA GGGGCCCCG GTGGAGC CGCTGGAGC CGCTGGAGC AGCGAGCTCA ACCCGCC TCCTACCGAG CTTCATCCTA GGGGAGACC TTTGGCATAT CATGAAGATC ATTCATGTA ACAGCTTGC ATTCCATGTC GTCTGCAGAG CTTGAAGAAC ATTCCATGTC GCCTGTGGGG CTACCCAATG CAAGAATCCTG GCTACCCTACT GCTACCCTACT GCTACCCTACT GCTACCCTACT CCACCCCCACG CCACCCCCCC CCACCCCCCC CCACCCCCCCC  | TETCCCGTE GGAETATCCC TEGGCCAGGC TTGTCTTCCT TGTTCGTCGG TCGTGCGCCAGGCAG GGGAGGCAG GGGAGGCAG GGGAGGGA   | GCGCAATTTC CGCGCCGCCC GTTCCGGCA GGTGGATGAT CAAGCTGCTG GCACAAGTGCC CTACACCAAG AACAAAGTTT TGCAGCGTCA CATTCGAGAG GATTTGAAC AGATTTTATT CTGTGACCGA TGAAAAGGGT TTACACCTCT GGCATCTTGAC GCATCTTGAC GCATCTGGC TTACTTTATC CCCTGGATTT CCGTTCAGAG CACATCAGGC TGAAGGGTCA CACATCAGC TGAAGGTCC TGAAGATTCCC AAGTTTCCC AAGTTTCCC TGGCAGATT CACCTTCC TGGCAGATT CACCTTCCC TGGCAGATT CACCTTCCC TGGCAGATT CACCTTCCC TGGCAGATT CACCTTCCC TGGCAGATT CACCTTCCC TGACCTTCCC TGACCGTTCCC TGGCAGATT  | AGCTTCCGCC GCTCCTGGGG CTCCTGGGG TCCGACTTCC AACTACGTGG GCGCTGCTCC GGGGCCTTCC GGGGCCTTCC GGAGATT CTGAATGACA GAATTTGAGGA CAAGAAGATTAAATGGGAAGCTTAC CCACCTGGAAACACTTAC CCCCCGGTGTC CCCCCGGTGTC CCCCGGTGTG CCCCACAACT CAAGACGCTAC CAAGACGCTAC CAAGACGCTAC CAACAGCTAC CCAACAGCTAC CCAACAGCTAC CCAACAGCTAC CCAACAGCTAC CCAACAGCTAC CCACAACAC CCACACACC CCACACACC CCCCGGTGTCGC CCCACACC CCCCGGTGTCGC CCCCCGCACACC CCCCCGCACC CCCCGCACACC CCCCCGCACC CCCCCCCC   | TCTTCCCGA ACGAAGCGGC TGCTGGTGCC TGCGGGAAGT TCCAAGAGAT AGCAAGCGCC TCCCAAGAGAT AGCAAGCGCC TCACTGATGG CAGGAGTGAA TGGCTCACCG TGGTCCACCG CAGAGTCACCG CAGAGTCACCG AACTTCCCA AACTTGTCCA GCAAATCTCC AACTTGTCCA GCAAATCTC GCAACAACCA CAGGGAT TGGACGGCAT GAGTAAGAAC TTTTACTCGA TCGACGCCC AACTTGTCCA AGCTCATACCC AACTTGTCCA AACTTGTCCA AGCACACCA CAGGCAAGACA TTTTACTCGA AGCACCC AAGCACCC TTTTACTCGC AAGCACCC AAGCAACCC TTTTACTCGACC AAGCAACCC TTTTACTCGACCC TTTTACTCCAAT TTTCCCAAT CCACCTGCAT CCACCT | GACCGOGCCC GGGGACAGA GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT CCCAAAGGAG CTCATACTCT GACACACACA GTATGAATGC CTGACACTC CTGAAGGAG GTATGAATGC TGAAGACTGT CTGCCTGC CTTCAATGCA ATTTCTATTCT ATATACTCAT ATATACACA CATCTTAGT ATATACACA CTTTCATTCT CTGCTCCC CTTCAATGCA TCTTCATCTT TTCATTCTT TTTCCACC GCCAGCCAAA AGTCAAAGAA TTGTGTAAAAG TTGTGTAAAAG TTGTGTAAAAG TTGTGTGAAAAG TTGTGAAAAGT TTGTGAAAAGT TTGTGAAAAGT TTGTGAAAAGT TTGTGAAAAGT TTGTGAAAAGT TTGTGAAAAGT TTTTCCATTC   | 120<br>180<br>360<br>420<br>540<br>600<br>660<br>720<br>780<br>840<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1320<br>1430<br>1500<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | TTTCAGCAGA GGGGCCCCG GGGGCCCCG CGCCTGGAGC AGCGAGCTCA AGCGAGCTCA TCCACCGGC TCCTACCGAG CTTCATGCTA GGGGAGACC TTTGGCATAT GAGCACTGTT CATGAAGATC ATTCCAAGAG ACTCTACCAAGA CCTGACCAAGAAC TTTCAGATGC ACTGTTCAGAGAC TTTCAGATGC CTACCAATG CCCAGC ACATGTTTGG CAAGGAAAC TTTCAGATGC CTACCAATG CCCAGC ACATGTTTGG CAAGGAATC TTTGGGACGA CAGATTCTG GCAGCGGGG CAAGATTCTG GCAGCGAGGGAGG CAAGATTCTG GCATACCTATA   | TGTCCCGTTC GGAGTATCCC TGGGCCAGGC TTGTCTTCGTCGG GGGGCGCC GGGGGGCCC GGGGGGCCC GGGGGGCCC CTGGGGCCAGGC CTGAGACATC CTAGACCATT GCTCTGCT GGAAGGAA ACCTGCTACA ACGGAAACTC CGAAGGATCA AGGGATACAG TTGCTTTGGTC CGAAGAACTC CGAAGAACTC TTGCTTTGGTC TTGCATCTG TTGCATCTG TTGCATCTG TTGCATCTAGT TCGAAGAACT TCGCATGCA TTGCCTGTAA CCAAGAACT TCGCAAGA TCGCAAGATC TCTCCTAATT CCAATGTTAA CCCAATGTTAA CACGCCAAC ACACGGCAAC  | GCGCAATTTC CCGCGCCGCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCCAGAG GCAGTTTTGAA GAGTTTTGAA GAGTTTTGAA GAGTTTTGAA GAGTTTTGAA GTTACACCAT TCACACCTCT CGCATCTGGC TTACTTTATC CCCTGGATTT CCGTTCAGAG TGAAGGGTAC TGAAGGGTAC TGAAGGGTAC TGAAGGGTAC TGAAGGGTAC TGAAGGGTAC TGAAGTTCCCC AGGTTCCGC TGAAATTGC TGAAAATGG TGAAATTGCCG TGAACTGTCCT CTGCCAGATT AGCTTTCACC TGACCTTCATCC TGACCTATCC TGTCATCA   | AGCTTCCGCC GCTCCTGGCG GCGCTGCCGCTCCC GCGCGCTTCCC GCGCGCTTCCC GGCGCTTCCC GGCGCTTCCC GGCGCTTCCC GGCGCTTCCC GGCGCTTCCC GGAATTTCCA GAATTTCACG GAATTTCACG CAACATGATA ATGGGAAGCT TATTACGGAA GAAGCTGTA AGCCTGGAA AGCCTGGAA CCCCGGGTTCC CAACACCCC CAACACCC CCAACACC CCACCTTACC CAACCT CCACCTTACC CACCTTACC CA | TCTTCCCGA ACGAAGCGGC TGCTGGGAAGT TGGGCGAAGT TCCAAGAGAT TCCAAGAGAT TCCAAGAGAT TCCAAGAGAT TCCAAGAGAT TCACTATAGCT CGTCCACT GCAAATGTGG AAGTCTCCAC AACTTTGCCAC GAAATGTGG AAGTCTCCA AACTTTGCCAC GAAATGTGG AAGTCTCCA TGTCCACT GCAAATGTGG AAGTCTCCA TTTTACTCG GGAAATGTG GGAAATGTT GCAGTGAAT TCAGGCACC TTTTATCTGG TTCAGGCACC AGGTAGAAC AAGACAACCT AAGACAACCT TTTATCTGG TTCAGGCACC AGGTAAGAC AGGCTAAGAC AGGCTAAGAC TTTTACCTGG TTCAGGCAGC TTTTATCTGG TTCAGGCAGC AGGCTAAGAC TTTTACCTGG TTCAGGCAGC AGGCTAAGAC TTTTACCGAT TCAGGCAGC TTTTACCACC TTTTCCCACC TTTTCCCACC TTTTCCCACC TTTTCCCACC TCCCCC TTTCCCACC TCCCCCC TTTCCCACC TCCCCCC TCCCCCC TCCCCCC TCCCCCCC TCCCCCC   | GACCGGGCCC GGGGAGCAGA GCTCAGGGGG CAACTTCCGC CAGGGCACG CAGTTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GTCTCACT CCCAAAGGAG CCGGCATT GACACACACA GTATGAATGC TGAAGACTGC TGAAGACTGC TGAAGACTGC CTCCAATGCAT CAGCACTTGC TGAAGACTGT CTGCCTGCC CTTCCAATGCA CATCTTATGT ATGTCCTCATC ATGTCCTCATC ATGTCCACC GCCAGCCAAA AGTCAAAGAA TCTGGAACAGA TTGTGTTAAAG TTGTGTAAAAGA TTGTGGAACAG TTGTGAAAAGA TTGTGAAAAGA TTGTGAACAG TGGAACAGT TGGAACAG TTGTAAAAGAA TTGTGAAAAGA TTGTGAAAAGA TTGTGAAAAGA  | 120<br>180<br>360<br>420<br>540<br>600<br>660<br>720<br>780<br>840<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1320<br>1430<br>1500<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600<br>1600 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | TTTCAGCAGA GGGGCCCCG GGGGCCCCG CGCTGGAGC AGCGAGCCAC AGCGAGCCAC TCCTACCGAG CTTCATGCTA GGGGGAGACC TTTGGCATAT TGGCATAT TGTGATGAAG GGCCATTTTG GCCTTCTACGCAG ATTCCATGTC GCTGCCAGC ATTCCAGAGC CTTACCCAAGC CTTACCCAAGC CTACCCAAGC ACAGGAAACA TTTCAGATGC CTACCCAAGC ACAGGAAACA TTTCAGATGC CTACCCAAGC ACAGGAAACA ATGCTGAGAG ACAGGAAACA TTTCAGATGC CAAGGAAACA ATGCTGAGAG AGGTTACCAAGA ATGCTGAGAT ACGTGAGAA ATGCTGAGAT AGGTTATCGGAGAA AGGTTATCGGAGAA AGGTTATCTGAGATC GCTATCCTAAT AAGGTTATTC   | TGTCCCGTTC GGAGTATCCC TGGGCCAGGC TTGTCTTCGTCG TCGTGGCGCAGCC TGGGCGCCA GGGGCAGCC GGAGAAACTC GCAAGGCAA ACTGCTACA ACTGCTACA ACTGCATCA ACTGCATCA CCAAGGAACTG TCCGATGAAAA AGGGAAACTG CCGAAAACTG CCGAAGGAACTG TCCGATGTCA GCTATGCATCA GCTATGCATCA GCTATGCATCA GCTATGCATCA GCTATGCATCA GCTATGCATCA GCTATGCATCA CCGAAACATGC CCGAAACATGC CCGAAACATGC CCGAAACATGC CCCAAAGATGT TCTGCTATGT GTACCACTTC CCCCCAATGCA ACGCACAC ACGCACAC AGGTTCATCA ACGTTCATCC ACACGGCAAC AGGTTCATCC ACACGGCAAC AGGTTCATCC ACACGGCAAC AGGTACATCC AGGTACACAC AGGTACATCC AGGTACACAC AGGTACACCAC AGGTACACCAC AGGTACACCAC AGGTACACCC AGGGACACAC AGGTACACCC AGGTACACCAC AGGTACACCC AGGCACCACC AGGTACACCC AGGTACACC AGGTACACCC AGGCACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGCACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGCACC AGGTACACCC AGGCACC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGCACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGTACACCC AGGCACC AGGTACACCC AGGTACACCC AGGTACACC AGGTACACCC AGGTACACC AGGTACACCC AGGTACACC AGGC | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTATT CTGTGACCGA TTACACCTCT GGCATCTTGGA TTACATTTATC CCCTGGATTT CAGTTCAGAG TTACTTTATC CCCTGGATTT CGGTCAGAG TGAAAAGGT TGACACTCT TGACCATCAGC TGAAGGTTAC TGACATCAGC TGAAGATTCCCT TGAAAATGG CAACTTTCCC TGAAAATGG CAACTTTCCCC TGAAAATGG CAACTTTCCCC TGAAAATGG CAACTTTCCCC TGAAAATGG CAACTTTCCCC TGAAAATGG CAACTTTCCCC TGAACATTCCCT CTGCCAGATT CTGCCAGAT CTGCCATACC CGCAAGCTTGCCT CACCTCCATA   | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG TCCGACTTCC GCGCTTCCC GGCGCTTCC GGCGCTTCC GGCGCTTCC GGAGTTTC TGAATGACA GAATTTGAGGA CAAGATTTAGAGA CAAGACCTGG AGCTTCT GATCTTCTAAACACT GATCTTCTAAACACT CAAAACACT CAACACCT GATCTTCTCACA AGCTCACACACC CCACACCT CCACCTTACC GCCACCCC GCCACACCT CCACCTTACC GCCACCCC GCCACCC GCCACC GCCACCC GCCACC GCCACCC GCCACC GCCC GCCC GCCC GCCC GCCCC GCCC G | TCTTCCCGA ACGAAGCGGC TGCTGGGAAGT TGGGCGAAGT TGGGCGAGT TCCAAGAGAGCGC TCCAAGAGAGCGC TCCAAGAGAT AGCAAGCGC TCTTAGCTCG GCAATGTGG GCAATGTGG GCAATGTGG GCAATGTGG GCAATGTGG GAATGTGCACA AGGTAGAGAACACA AGGAGAGAAT TGGAGCGCA TTTTATCTGG TTCAGGCAGCA AGGAAGACC TTTTATCTGG AGGAAGACC TTTTATCTGG TTCAGGCAGC AGGAAGACC TTTTATCTGG TTCAGGCAGC TGGCAAGCA CAGGAGAAGT TTTTATCTGG TTCAGGCAGC TGGCAGCAGC TGGCAGCAGC TGGCAGCAGC TTTTATCTGG TTCAGGCAGC TTCCCAATGC CAGTTCCCACT CCAGTTCCCACT CCAGTTCCACT CCAGTT | GACCGGGCCC GGGGAGCAGA GCTCAGGGGC CACGGCCACG CACGTCACC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGACTACAC GTATGATGT GACACACA GTATGATGT TGAAGACTGT TGAAGACTGT CTGCATGC CTTCAATGCA CATCTTATGT ATATTATGATGC CTTCAATGCA CATCTTATGT ATATACACAC CATCTTATGT ATATACACAC CTTCTATGCA CTTCTATGT TGTGCCTGCC TGCCTGCC TTCAATGCA CTTCTATGT TTTGCATGCA TGTTCACC GCCAGCCAAA TGTTGTGTAAA TGTTGTGAAAGA TTGTGTGAAAGG TTGTGTGAAAGG TTGTGTAAAAG TTGTGTGAAAGG TTGGAAAAGT TTGTGTAAAGG TTGGAAAGG TTGGAAAAGG TTGGAAAAGG TTGGAAAAGG TTGGAAAAGG TTGGAAAGGA TTGTGTAAAAGG TTGGAAAAGG TTGGAAAAGG TTGGAAAAGG TTGGAAAAGG TTGCACTCAGGG CAACTCAGGG  | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>960<br>1020<br>1080<br>1140<br>1260<br>1380<br>1440<br>1560<br>1560<br>1740<br>1680<br>1740<br>1680<br>1740<br>1860<br>1980<br>2040  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | TTTCAGCAGA GGGGCCCCG GTGGAGC CGCTGGAGC CGCTGGAGC AGCGAGCTCA AGCGAGCTCA TCCACCGGC TCCTACCGAG CTTCATGCTA GGGGAGACC TTTGGCATAT CATGAAGATC ATTCATGTA GCCATTTTG ACTGACAGAG CTTCATGCTA CTGTATGAAG GCCATTTTG ACTGACAGAG CTTCCATGTC GCCTGTGGGG CTACCCAATG CTTCGCCAGG ACATGTTTGG ACAGAAACA TTTCAGATGG ACATGTTTGG CAAGAATCA TTTCGGACGG GAAGATTCTG GCTGTAGGGG GAAGATTCTG GCTATCGTATT AGGTTATTG GCTATCGTAT AAGGTTATTG GCTCTCAGAGG GCTATCGTAT AAGGTTATTG GCTCAGAGGAGAACA GTTTCTCGGAGGG GCTATCGTAT AAGGTTATTG GCTCAGAGGAGAG GCTGAATTGGGAGGG GCTATCGTAT AGGTTATTGG GCTGAATTGGGAGGAGAG GCTGAATTGGGAGGAGAG GCTGAATTGGGAGGAGAG GCTGAATTGGGAGGAGAG GCTGAATTGGGAGGAGAG GCTGAATTGGGAGAG GCTGAATTGGGAGGAGAG GCTGAATTGGGAGGAGAG CCTACTCATAT AGGTTATTGG  | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCT TGTTCGTCCG TGGGCCAGCCA GGGAGAAACTTC GCCAGGCAA GCCAGGCAA ACCTCCTACA ACCTCTCACA ACTGCATCT CATCGGGAA ACGTCATCA GCAAAATGTA GCCAATGTCA GCCAAGAACATC GCAAAGATCT CGAAAACATCA CCCAAAGATCT CCCAATGTCA CCCAAAGATCT CCCATCGAAA CCCAAAGATCT CCCAATGTCA CCCACAC ACGTCAAC ACGTCAAC ACGTCAAC ACGTCAAC CCAATGTCA CCCACAC CCCACAC CCCACAC CCCACAC CCCCCACAC CCCCCACAC CCCCCC   | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTTT TGCAGCGTCA CATTCGAGAG GCATTTGAA GAGTTTTATT CTGTGACCGA TGAAAAGGGT TTACATCACC GCCATCTGGC TTACTTTATC CCCTGGATTT CGCATCTGGC TGAAGGGTA CATCATCACC TGGAAATTGC AAGTTTCCC TGGCAGATT CGGCAGATT CACCTGTCCT AGCTTCACC TGGCAGATT CACCTGTCCT CGCAGATT CACCTGTCCT CACCTGCAGATT CACCTGTCCT CACCTGCAGATT CACCTGTCATA CACCTGTCATA CACCTGTCATA CACCTGTCATA CACCTGTCATA CACCTGTCATA   | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG TCCGACTTCC ACTTCCAACTGG GCGCTTCCGGCGCTTCC GGCGCTTCC GGCGCTTCC GGCGCTTCC GTATTTCTCA GAATTGACA GAATTTGAGG CAAGAAGCT TATTACGGAAGCT CAAGAACACTTG GATCTTGTGG AGCTACAC CCCCCGGTGTC CCCCCACACT CAAGACAGCTA AGACAGCTA CCACCTGGAA CCCCCGTGGAA CCCCCCGTGGAA CCCCCCCGTGGAA CCCCCCGTGGAA CCCCCCCGTGGAA CCCCCCGTGGAA CCCCCCGTGGAA CCCCCCGTGGAA CCCCCCGTGGAA CCCACCTTACC CCACACTCC CCACACGCTC CCACACTC CCACACTGGAGAC CCACCTTACC GGCAACAGCT CCACCTTACC GGCAACAGCG GATGGGCCC CAAGGGACC CAAGGGAAC CCAACGTGGAGC CCAAGGGAAC CCAACGGAGAC CCAACGGAGAC CCAACGGAGAC CCAACGGAGAC CCAACGAGAAC CCAACGAGAAC CCAACCTTACC CCACCTTACC CCACACAGC CAAGGAGAC CCAACGAGAAC CAAGGAGAC CCAACGAGAAC CCAACCTTACC CAAGGAGAC CCAACAGCAGAAC CAACAGCAGAAC CCAACAGCAGAAC CCAACAGCAAC CAACAGCAGAAC CAACAGAAC CAACAGCAGAAC CAACAGCAGAAC CAACAGCAGAAC CAACAGCAAC CAACAGCAAC CAACAGCAAC CAACAGCAAC CAACAGCAAC CAACAACAAC CAACAGCAAC CAACAGCAAC CAACAGCAAC CAACAAC CAACAACAAC CAACAACAAC CAACAA   | TCTTCCCGA ACGAAGCGGC TGCTGGTGCC TGCTGGTGCC TGCCGGAAGT TCCAAGAGAG AGGAAGCGC TCACTGATGG CAGGAGTGAA TGGCTCACC TGCTGCACC TGCTGTTCCAC CAGGAGTGAA TGGCTCACC CAGAGTCAC AAGTTCTCCA CAGAGAGAAT TGGACACC GCAACAACCA GAGCAAT TGGACGCA TTTTATCTCG TTTTACTCG AAGCACCC ACGTAAGAC TTTTATCTCAC TTTTACTCAC TTTCACCAC AGGCAAGCA TTCACCCCC ACTCCCCC ACTCCCCC ACTCCCCC ACTCCCCC ACTCCCCC ACTCCCCCC TTTTCCCCCCC ACTCCCCCC ACTCCCCCC ACTCCCCCC TTTTCCCCCC ACTCCCCCC ACTCCCCCC TTTTCCCCCCC ACTCCCCCC TTTTCCCCCCC TTTTCCCCCCC TTTTCCCCCC   | GACCGGGCCC GGGGACAGA GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT CCCAAAGGAG CTCATATCTT GACACACACA GTATGAATGC TGAAGACTGT CTGAAGCTGC CATTAGATGC ACACTTAGT ATATACACT ATATACACT CATTAGATGC CATTAGATGC CATTAGATGC CATTAGATGCA CATCTTTGT ATATAGACA ACTCTACTTGT CTGCACCACACACAC GCTACACACAC TTGTACTTGT TTCCACC GCCAGCCAAA AGTCAAAGAA TTGTGTTAAA TTGTGTAAAGA TTGTGTAAAG TTGTGTAAAGA TTGTGTAAAGA TTGTGAAAGA TTGCATTCCAGGG AGGGGAGACT  | 120<br>180<br>360<br>420<br>540<br>600<br>660<br>720<br>780<br>840<br>960<br>1020<br>1080<br>1140<br>1200<br>1320<br>1320<br>1340<br>1440<br>1500<br>1680<br>1740<br>1860<br>1920<br>1980<br>1980<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>20  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | TTTCAGCAGA GGGGCCCCCG GTGGAGCGC CGCCTGGAGC AGCGAGCTCA ACCGAGC TCCTACCGAG CTTCATCCTA GAGCACTGTTATCTA GAGCACTGTT CATGAAGAT CATGAGAACC TTTGGCATAT GAGCACTGTT CATGAAGAT CTTCATGAAG GTCTGCAGAG CTTCCATGTC GTCTGCAGAG CTTCCATGTC GTCTGCAGAG CTTACCCAATG CTACCCAATG CAAGATTCTC GTCTCAGCAGA CAAGATTCTC GTCTCCGCAGA CAAGATTATTC GTCTCCGCAGAG CTACTTCATAT CTCCCGAGAG CTCAATTTCCGAGAG CTCACTGAATTCCCGAGAG CTCAATTTCCGAGAG ATACTCCGAGAG CTCAATTTCCGAGAG ATACTCCGAGAG CTCAATTTCCGAGAGA CTCTCCGAGAG CTCAATTTCCGAGAG ATAGTACAGT CTCACGACAG CTCAATTTCCGAGAGA CTCTCCGAGAGA CTCTCCGAGAGA CTCTCCGAGAG CTCAATTTCCGAGAGA CTCTCCGAGAGA CTCTCTCGAGAGA CTCTCCGAGAGA CTCTCTCCGAGAGA CTCTCTCCGAGAGA CTCTCCGAGAGA CTCTCCTCCGACAA CTCTCTCCGACAA CTCTCTCCGACAA CTCTCTCCGACAA CTCTCTCCGACAA CTCTCTCCGACAA CTCTCTCCGACAA CTCTCTCCACAC CTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCTCCCACAC CTCTCCCACAC CTCCCCACAC CTCTCCCACAC CTCTCCCACAC CTCTCCCACACAC CTCTCCCACACAC CTCT | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCT TGTTCGTCG TGGGCGGCCA GGGAGCGCA GGGAGGGAA ACCTGCTACA TACCTTCTG GCAGGGAA ACCTGCTACA TACCTTCTGG GCAGGGAA ACCTGCTACA TACCTTCTGG GCAGGAATGA TCGTATACA TCGGGAA AGGGATCA GTTTCTGGT CGAAAATGG TCGATGCA TTGCCTGTAC TTGCCTGTAC TTGCCTGTAC TGTCCTGTAC CCAAAGATGT TCTCCTCTAAAT CGAATGTTACAC CACAGGGAA ACGGGAAC ATGCAGCAA ATGCAGCAA ATGCAGCAA ATGCAGCAA ATGCAGCAA TGTACTACCC TTCTTCAAAT CACAGGGAAC ATGCAGCAA ATGCAGCAA ATGCAGCAA ATGCAGCAAC ATGCAGCACC ATGCA | GCGCAATTTC CGCGCCGCCC GTTCCGGCGC GTTCCGGCGCA GGTGGATGAT CAAGCTGCTC GCACCAAG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG GAGTTTTATT CTGTGACCGA TGAAAAGCT TTACTTTATT CCCTCTGGATTT CCGTTCAGAG CAATTACT CCCTCGAATT CCGTTCAGAG CACATCAGC TGAAAGGTATC CCCTGGAATT CGGTTCAGAG CACTTCACG TGGCAGAT CACCTCT CGGCAGATT CCGCTCAGAG CACTTCACC TGGCAGATT CCGCTCAGAG CACTTCACC TGGCAGATT CCGCTCATACC TGCCAGATT CCGCTCATACC TGCCAGATT CCGCTCATACC TGCCAGATT CCGCAGATT CCGCAGAT CCCCCTCA   | AGCTTCCGCC GCTCCTGGGG CTCCTGGGG TCCGACTTCC AACTACGTGG GCGCTCCC GGGGCCTTCC GGGGCCTTCC GTATTTCTCA GGATTTCTAGG CAAGATGTA ATGGGAAGCT TATTACGGA CAAGATGTTA ATGGGAAGCT TATTACGGA AGCTCTGC CAACATCTGAACCTT GATCTTGTGG AGCTACTGCA CCCCCGGAAC CCCCCGGAAC CCCCCACACCT CCCCACACCT CCACCTACC GGCAACACGG GACTGGGA GGCACCTGGAA CCACCTTACC CAACGGTTCA CCACCTTACC CCACCTACC CCACCTACC CCACCTACC CCACCTACC CCACACTC CCACCTACC CCACACT CCACCTACC CCACACG CCACCTACC CCACGGGAACC CCACGGGAACC CCACGGGAACC CCACGGGAACC CCACGGGAACC CCACGGGAACC CCACGACT CCACGGGAACC CCACGACT CCACGGAACC CCACGACT C | TCTTCCCGA ACGAAGCGGC TGCGGGAAGT TGGGGGAAGT TGCGGGAAGT TGCAGAGGGAAGT AGCAAGCGGC TCACTGATGG TGGCTCCAC TGGTCCACT GGAAGTGCA TGGTCCACT GGAACACCA ACTTGTCCA GGAACACCA GAACACCA GAGAGAAT TTTACTGG TGGCAGG AGGTTGAAGA TGGAGGACA TTTTACTGG AGGTTAAGAC AGGTTAAGAC AGGTTAAGAC TTTTACTGG AGGCACC AGGTTAAGAC AGGCTGAAGAC TTTTACTGG AGGCACC AGGTTAAGAC AGGCTGCACC AGGTTAAGAC AGGCTGCACC AGGTTAAGAC AGGCTAAGAC AGGCTAAGAC AGGCTAAGAC AGGCTAAGAC TTTTCCCCACC AGTTCCCACC AGTTCCCACC AGTTCCCACC AGTTCCCACC AGTTCCCACC AGTTTCCCACC AGTTTCCCACC TTTTCCCTCACC TTTTCCCTCACC AGTTTCCCACC AGTTTCCCACC AGTTTCCCACC AGTTTCCCCACC TTTTCCCTCACC AGTTTCCCACC TTTTCCCTCACC AGTTTCCCACC TTTTCCCTCACC TTTTCCCTCACC TTTTCCCTCACC TTTTCCCTCACC TTTTCCCTCACC TTTTCCCTCACC TTTTTCCCTCACC TTTTCCCTCACC TTTTTCCCTCACC TTTTTCCCTCACC TTTTTCCTCTCACC TTTTTCCTCTCACC TTTTTCCTCTCACC TTTTTCCTCTCACC TTTTCCTCACC TTTTTCCTCTCACC TTTTCCTCTCACC TTTTTCCTCTCACC TTTTTCCTCTCACC TTTTCCTCACC TTTTCCTCACC TTTTCCTCACC TTTTCCTCTCACC TTTTCCTCACC T | GACCGOGCCC GGGGACCAG GCTCAGCGAG GCTCAGCGAG CCACTTCCGC CACGCCACC CGATTACATC CCCTGCCATC GCAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CCGGGCATTG CTCATATCTT GACACACACA GTATGAATGC CAGCAGTTGC TGAAGAGTTGC TGACCTGCC CTTCAATGCA ATATACTTATTGT ATATACACAC GCTTACTTGT ATATACACAC GCTTACTTGT CTGTCCACC GCCAGCCAAA AGTCAAAGAA TGTGTAAAAG TTGTGAACAG TTGCATCATC TTCCCATCCAG CAACTCAGGG AGGGGAGCT AGGGGGAGCT  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1560<br>1680<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2160   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | TTTCAGCAGA GGGGCCCCG GGGGCCCCG GGGGGCCAG AGCAGGCCAC AGCAGGCAC TCCACCGGCC TCCTACCGAG CTTCATGCTA GGGGABACC TTTGGCATAT TGGCATAT TGTGATGAAG ACACTTTTG GCCATTTTG GCCATTTTG GCCATTTTG GCCATTTTG GCCATTTTG GCCATTTTG GCCATTTTG GCCATTTTG GCCTGCAGAG ATCCCAATG CTCGCCAGC ACATGTTTGG CAGGAAACA TTTCAGATGC CTTTGGGACGA ATGCTGAGAG ATGCTGAGAG ATGCTGAGAT GCCATGAGAT ACGTTAGAGAT GCCATGCAGA ATGCTGAGAT GCCATGCAGA ATGCTGAGAT GCCATGCAGA ATGCTGAGAT GCCATGCAGA ATGCTGAGAT GCCATGCAGA ATGCTGAGAT GCCAGCAGAAAAAAAAAA  | TGTCCCGTTC GGAGTATCCC TGGGCCAGGC TTGTCTTCGTCGG GGAGAAACTC CTGAGCCAT GGCGCGCA GGGCAGGCA GGCAAGGCA ACCTGCTACC CTAGACCAT AGTGCATCT GCAAGGAAC CTGATGAAAA ACCTGCATCA AGTGCATCTA AGTGCATCTA CGAAGGATCA CGAAAACTG CCGAAGGATCA GCATGTCA GTTTCTGGTC CGAAGACTC CGAAAGATGT CTGCTGTCA GCAAGACT CCGAAGTC CCCAAAGATC CCCAAGGAC CCCAAGGAC AGTCCAC ACCACGCAAC AGGTCATCA AGGTCATCA AGGTCATCA AGGTCATCC ACACGCAAC AGGTACATCC ATTCACCAC ATTCACCAC ATTCACCAC GTTCTCCCTC ATTTACCAC ATTCACCAC ATTCACCAC GTTCTCCCTC ATTTACCAC ATTCACCAC ATTCACCAC GTTCTCCCTC ATTCCCAC ATTCACCAC | GCGCAATTTC CGGCCGCCC GTTCCGGCG GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG CAGTTTTGAA GAGTTTTATT CTGTGACCGA ATACAACTT TCACACCTCT GGCATCTGGC TTACTTTATC CCTGGATTTTAGA CATCATAGA CATCATAGC TGAAAAGGT TGACGATTTAGA CATCATAGC TGACATCAGC TGAAAATGG CAACTTTCCG CAACTCTCG CAACTCTCGC AAGTTTCCGC AAGTTCCCT CTGCAGATT CTGCAGATTC CTGCAGATT CTGCAGATTC CTGCAGATT CTGCAGATTC CTGCAGACTTC CTGCAGCTC CTGAAAATTC CTGAAATTC CTGAA | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG TCCGACTTCC GCGCTTCC GGCGCTTCC GGCGCTTCC GGCGCTTCC GGCGCTTCC GGCGCTTCC GGCGCTTCC GGCGCTTCC GGCGTTCC GGAATTACGCA GAATTACGCA CAAGATATA ATGGGAAGCT CAACACTGTGA AGCTTGTG AGCTATTCACCA AGACTATCA AGACTATGAC CCCCGGTGTG CCCCACACT AATGCGAACAC CCAACACGCA AAGGCATACGC CCACACGCA AAGGCATCC CCACACGCA CCACACGCACACC CCACACCT CCACACGCACACC CCACACGCACACC CCACACCT CCACACGCACACC CCACACCT CCACACCAC CCACACCAC CCACACCAC CCACACCAC  | TCTTCCCGA ACGAAGCGGC TGCGGGAAGT TGGGCGAAGT TGGGCGAGT TCCAAGAGAGCGC TCCAAGAGAGCGC TCCCAAGAGAGCGC TCACTGATGG CAGGAGTGAA TGGCTCCAC GCAAATGTGG CAAATGTGG CAAGAGCAC GCAACACCA GAAGCACCA GGAACACCA GGAACACCC TTTTATCTGG TTCAGGCAGCA TTTTATCTGG TTCAGGCAGCA AGGTAGAAC TTTTATCTGG TTCAGGCAGCA TTTTATCTGG TTCAGGCAGCA CGGCAAGACAC CGGCAAGACAC CGGCAAGAC TTTTATCTGG TTCAGGCAGC TTTTACTCG TTCAGGCAGC TTTTCCCCAT CGACTCCAC CAGCTGCAAC CAGCTCCAC CAGCTCCAC CAGCTCCAC CGGCCCAC CGGCACCAC CGGCCCCAC CGGCCCCAC CGGCCCCC CGGCCCC CGGCCC CGGCCCC CGGCCC CGGCCCC CGGCCC CGGCC CGGCCC CGCC CGCCC CGCC C | GACCGGGCCC GGGGAGCAGA GCTCAGGGGG CAACTTCCGC CAGGGCACG CAACTTCCGC CAGGCCACG CGATTACATC CCCAAAGGAG CCGGCATTC CCCAAAGGAG CCGGCATTC CCCAAAGGAG CCGGCATTG GCAAAGCACA GTATGAATGC TGAAGACTGT TGAAGACTGT CTGCCTTGCC CTTCAATGCA CATCTTATGT ATATACACAC CATCTTATGT ATATACACAC CTTCTATGT TGTTCCACC GCTACATGCA CTTTCATGT TTTTCAATGCA TGTTTCCACC CTTCAATGCA CTTCTGT TTTTCAATGCA TTTTCAATGCA CTTCTCTTT TTTCAATGCA CTTCCACC CTTCAATGCA CTTCTCATT TTTCAATGCA CTTCCACC CTTCCAGCAAAA TTTTCAATATT TTTTCAATTC CTCCCGTCCAG CAACTCAGGG AGGGGAGACT TTTCCATTT TTTTCAATTC TTTTCAATTC TTTTCAATTC TTTTCAATTC TTTTCAATTC TTTTCAATTC TTTTTAATTC  | 120<br>180<br>360<br>420<br>440<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1680<br>1740<br>1860<br>1980<br>2040<br>2160<br>2160<br>2220  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | TTTCAGCAGA GGGGCCCCG GTGGAGC CGCTGGAGC AGCGAGCTCA AGCGAGCTCA AGCGAGCACA TCCACCGGC TCCTACCGAG CTTCATGCTA GGGGAGACC TTTGGCATAT CATGAAGATC ATTCATGTA GCCATTTG ACTGACAGAG CTTCATGCTA CTGTATGAAG GCCATTTTG ACTGAAGATC GCCTGTGGGG CTACCCAATG CTCGCCAGG ACATGTTTGGACGAGA ACATGTTTGGACGAGA ACATGTTTGGACGAGA GCTGGAGGAGATCTG GCTGTGAGGAGATCTTGGAGAGATCAGATACAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA  | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCT TGTTCGTCCG TGGGCCAGCC TGGGCGCCA GGGAAAACT GGCAAGGGAA ACCTGCTACA ACCTGCTACA ACTGCTACA ACTGCACT ATACCTCTGG CAAAGAACT GCAAAAATGT TCTGTGGG CCAAAGAACT TCTGTGGAC CCAAAGAACT CCAAAGAACT CCAAAGAACT CCAAAGAACT CCAAAGAACT CCAAAGAACT CCAAAGAACT CCAATGTCA CCAAAGAACT CCAAAGAACT CCAATGTCA CCAAAGAACT CCAAAGAACT CCAAAGAACT CCAATGTCA CCAAAGAACT CCAATGTCA CCAATGTCA CCAATGTCA CCAATGTCA CCAATGTCA CCAATGTCA CCAATGTCA CCAATGTCAC CCAATGTCA CCACTCC CCCCCAAAGACC CCAATGTCAC CCACTCC CCCCCAAAGACC CCAATGTCAC CCCCCCAAAGACC CCAATGTCAC CCACTCC CCCCCCAACC CCCCCCC CCCCCCC CCCCCCCC   | GCGCAATTTC CGCGCCGCCC GTTCCGGCAG GTTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTTT TGCAGCGTCA CATTCGAGAG GCATTTGAA GAGTTTTATT CTGTGACCGA TGAAAAGGG ATACAAACTT CCCTGGATTTCACCGA TGAAAAGGG TTACTTTATC CCCTGGATTT CCCTGGATTT CGGTTCAGAG CACATCAGC TGAAGGGTAC TGGGCCAGAAT CACACTGTCCT TGGCCAGATT CGGTCATACC TGGAAATTGCC ACTGTCATACC TGGAAATTGCC ACTGTCATACC ACTGTCATACC ACTGTCATACC ACTGTCATACC ACTGTCATACC ACTGTCATACC ACTGTCATACC ACTGTCATACC ACTGTCATACC ACGTTCATACC ACGTT | AGCTTCCGCC GCTCCTGGGG CTCCTGGGG TCCGACTTCC ACTTCCAACTGG GCGCTCCCGGGGCTTCC GGGGCCTTCC GGGGCCTTCC GGATTTCTCAACTGGG CAAGATGATA ATGGGAAGCT TATTACGGA CAAGAAGCTTAC CAACTGGGAACCTCAC CACCACACC CCCCGGTGTG CCCCCACAACT CCACCTGGAA AGACACTTCC CAACAGCTTAC CAACAGCTTAC CAACAGCTTAC CAACAGCTTAC CAACAGCTTAC CAACAGCTCAC CCACCACAC CCACCACAC CCACCACAC CCACCA   | TCTTCCCGA ACGAAGCGGC TGCTGGTGCC TGCTGGTGCC TGCCGGAAGT TCCAAGAGAGCGC TCACTGATGG CAGGAGTGAA TGGCTCACC TGCTGCTCCAC CAGGAGTGAA TGGCTCACC CAGGAGTGAA TGGCTCACC CAGGAGGAAT TGCACACG CAAATGTGC AACTTGTCCA CGCAACAACCA CAGGAGAAT TGGACGGCA GGCAAGAGAA TGGACGCA TTTTATCTCG AAGCACTCC AACTTGTCCAC AAGCACCC AAGCACCC AAGCACCC AAGCACCC AAGCACCC AGGCAAGCA TTTACTGC AGGCAAGCA TTTACTGC AGGCAAGCA TTTACCTCAC AGGCTAAGAC CAGCTCCACC AGTTCCACC AGTTCCACC AGTTCCACC AGTTCCACC AGTTCCACC TTTTCCCACC AGTTCCCACC AGTTCCCACC AGTTCCCACC AGTTCCCACC AGGCATGGGCT TTTTCCCCCC TTTTCCCACC AGTTCCCACC AGTTCCCACC AGTTCCCACC AGTTCCCACC AGGCATGGGCT TTAGAGGGCT TTTACCTCC TGAGGGCT TTTCCCCCC TGAGAGCGCT TTTTCCCACC TTTTCCACC TTTTCACC TTTTCCACC TTTCCACC TTTCCACC TTTTCCACC TTTTCCACC TTTCCACC TTTCACC TTTCCACC TTT | GACCGGGCCC GGGGACAGA GCTCAGCGAG CAACTTCCGC CACGGCCACG CGATTACATC CCCTGCCATC GCAAATCCTT ATATTCCAAT CCCAAAGGAG CTCATACTCT GACACACACA GTATGAATGCT CTGAAAGGAG CTGAGCTTGC CTGAAGCACT ATATCTT ATATCATT GACACACACA GTATGAATGC CAGCAGTTGC CTTCAATGCA ATTTCAATGCA ATTTCATTCT ATATAAGACA GCTTACTTGT ATATAAGACA TGGGTACACAC TTGGTACACC GCCAGCCAAA AGTCAAAGAA TTGTGTTAAT TTTCCATATC TTCCATATC TTCCATATC TTCCATATC TTCCATATC TTCCATATC TTTCCATATC TTCCATATC TTTTCATATC AGGGGAGACT AGGGGAGACT TTTTCCATATT TTTTTATATGC TGCATCACGGG AGGGGAGACT TTTTCCATATT TTTTTTATATGC TTGTTCACATTT TTTTTTATATGC TTGTTCACATTT TTTTTTATATGC TTGATTCACATTT TTTTTTATATGC TTGATTCACATTT TTTTTTATATGC TTGATTCACATTT TTTTTTATATGC TTGATTCACATTT TTTTTTATATGC TTGATTCACATTT TTTTTTATATGC TTGATTTCACATTT TTTTTATATGC TTGATTTATATGC TTGATTTATTATGC TTGATTTATATGC TTGATTTATTATGC TTGATTATTATGC TTGATTATTATGC TTGATTATTATGC TTGATTATATGC TTGATTATTATGC TTGATTATTATTATGC TTGATTATTATGC TTGATTATTATTATGC TTGATTATTATTATGC TTGATTATTATTATGC TTGATTATTATTATGC TTGATTATTATTATGC TTGATTATTATTATGC TTGATTATTATTATGC TTGATTATTATT | 120<br>180<br>360<br>360<br>420<br>440<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1080<br>1140<br>1250<br>1320<br>1320<br>1440<br>1500<br>1680<br>1740<br>1860<br>1920<br>1980<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>2040<br>2040<br>2022<br>2022<br>2028  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | TTTCAGCAGA GGGGCCCCGG GTGGAGGGC CGCCTGGAGC AGCGAGGCCCA AGCGAGCCCA TCCACCAGG TCCTACCGAG CTTCATGCTA GAGCACTGTT CATGAAGAT CATGAAGAT CATGAAGAT ATCCAAGT GTCATCATGTA ACACTTGCAAGA CTTGCAAGAGCT CTGAAGCCTC GCCTGTCGGAG CTACCCAATG CTAGCAGAACA TTTCAGATGA ATCTCAGATGA ATCTTGAGATG CAAGATTCTC GTCTCAGAAG ATCTCAGATG CAAGATTCTC GTCTCAGAAG ATCTCAGATG CTCAGAAGATCT GTCTCAGAAG ATCTCAGATG GTCAAGATT AAGGTTATTC GTCTCAGAAT ACTTCCAGATA ACTTCCAGATA AAGGTTATTC GTCTCAGAAT CTCAGAATT CGCTCAGAAT CGCTCAAAAAG ATCTCAGAAT AAGGTTATTC GTCTCAGAAT AAGGTTATTC GTCATAAAAAG ACTCCAAGAT ACACGTCCAGAGA ACTCCAGATT GTCATCAAAAAA ACTCCAGATA ACACGTCCAGAAA ACTCCAGATT GAAGGGTCTA   | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TTGTCTTCT TGTTCGTCG TGGGCGGCCC GGGGGGCCC GGGGGGCCC GGGAGGGAA ACCTGCTACA TACCTTCTG GCAAGGGAA ACCTGCTACA TACCTTCTGG GCAAGGACTG AGGGATCA AGGGATCA AGGGATCA TCGTGTACA TTGCCTGTACA TTGCTGTCG CCAAAGATGT CCAAAGATGT CTCCTCAAAT CGAACATCA AGGGAACCG ATGCCACAC AGGGCAA ATGCACCCC AGGGCAA ATGCACCCC AGGCAAC TTGCTCTCAAT TCTCCTCAAT TCTCCTCAAT TCTCCTCAAAT TCTCCTCAAAT TCTCCTCAAAT TCTCCTCAAAT TCTCCTCAAAT TCTCTCATCGC TTCCTCAAAT TCTCCTCAAAT TCTCCTCAAAT TCTCCTCAAAT TCTCCTCAAAT TCTCCTCAAAT TCTCCTCCAAAT TCTCCTCCAAAT TCTCCTCCAAAT TCTCCTCCAAAT TCTCCTCCAAAT TCTCCTCCAAAT TCTCCTCCCAAAT TCTCTCCCCC TCTCTCCCCC TCTCTCCCCC TCTCTCCCCC TCTCTCCCCC TCTCTCCCCC TCTCTCCCCC TCTCTCCCCC TCTCTCCCCC TCTCTCCCCCC   | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG GAGTTTTGAA GAGTTTTATT CTGTCACCGA TGAAAAGGGT TTACTACCTCT GGCATCTGGC TTACTTTATC CCCTGGATTTCACCGA TGAAAAGGGT TGACCGATCAGC TGACCTCT CCGTTCAGAG CACATCAGC TGACAGCTCAGAG CACATCAGC TGACAGCTCAGAG CACATCAGC TGACAGCTCC AGGTTCAGAG CACATCAGC TGACAGTTCCC CTGGCAGATT CGGTTCAGAG CACTTCACC TGACACTTCCC TGACAGTTCCC TGACAGTTCCC TGACACTTCCC TGACACTTCCC TGACATTCCC TGACACTTCCC TGACACTTCCC TGACACTTCCC TGACACTTCCC TGACACTTCCC TGACACTTCCC TGACACTTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TTACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCC TGACACTCCCC TTATTGTCCC TTATTGTCCC TTATTGTCCC TTATTGTCCC TTATTGTCCC TTATTGTCCT TTATTGTCCCT TTATTGTCCCT TTATTGTCCC TTATTCCTCCCCCCCC TTATTTCTCCCT TTATTTGTCCT TTATTTGTCCT TTATTTGTCCT TTATTTGTCCCCCCCAAG TTATTTCTCCCCCCCAAG TTATTTTTCCCT TTATTTTCCCT TTATTTTCCCT TTATTTTCCCT TTATTTTCCCT TTATTTTCCCT TTATTTCCCT TTATTCCCT TTATTTCCCT TTATTTCCCT TTATTTCCCT TTATTCCCT TTATTTCCCT TTATTCCCT TTATTTCCCT TTATTCCCT TTATTCCCCT TTATTCCCCT TTATTCCCCT TTATTCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCT TTATTCCCCCC TTATTCCCCCCC TTATTCC | AGCTTCCGCC GCTCCTGGGG CTCCTGGGG TCCGACTTCC AACTACTTGG GGGCCTTCC GGGCCTTCC GGGGCCTTCC GTATTTCTCA GAATTTGAGG CAAGATGTA ATGGGAAGCT TATTACGGA AGACCTGG AGCTACTGG AGCTACTGG AGCTACTGG AGCTACTGGACTGG  | TCTTCCCGA ACGAAGCGGC TGCGGGAAGT TGGGGGAAGT TGCGGGAAGT TCCAAGAGGAT AGCAAGCGGC TCCACTGATGG CAGGAGTGAA TGGCTCCACT GGCAACT TGGTCCACT GGAAGAGAC AGGATCAA AGGTCACAC AACTTGTCCA GGAAATGTG GAAATGTGG AACTTGTCCA GGAACAACCA TTTTACTGG TTCAGGAGGAT TTTATCTGG AGGCTAAGAC AGGCTAAGAC AGGCTAAGAC CAGGAAACT TTTTACCTCAC CAGCTCCACC CAGTCCCACC CAGCTCCCACC CAGTTCCCACC CAGCTCCCACC CAGTTCCCACC CAGCTCCCACC CACCTCCCACC CACCTCCACC CACCTCCCACC CACCTCCACC CACCTCCCACC CACCTCCACC C | GACCGOGCCC GGGGACCAGA GCTCAGCGAG GCTCAGCGAG CCACTTCCGC CACGCCACG CGATTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT CCCAAAGGAG CCGGGCATTG CCGAAAGGAG CCGGCATTGC GCAACACACA GTATGAATGC CAGCACTTGC CTTCAATGCC CTTCAATGCA GTATGATTCT ATATACTCAT ATATAAGACA GCTATCTTGT CTGCTCATC CTGCTCATCTTG TGTGAACAG TGTGTAAAG TCTGTGTAAA TCTGGACAG TGTGTAAAGA TCTGGACAG CAACTCAGGG CAACTCAGGG CAACTCAGGG CAACTCAGGG CAACTCAGGG CAACTCAGGG CAACTCAGGG CAGCCATAT TTTTTATATGC TGTGTACATTT TTTTTTATATGC TGTGTACATTT TTTTTTATATGC TGTGTACATTT TTTTTTATATGC TGTGTACATTT TTTTTTATATGC TGTGTACATTT TTTTTTTATATGC TGTGTACATTT TTTTTTTATATGC TGTGTACATTT TTTTTTTTATATGC TGTGTACATTT TTTTTTTATATGC TGTGTACATTT TTTTTTTTTT  | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1220<br>1320<br>1380<br>1440<br>1560<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2160<br>2210<br>2220<br>2280<br>2340   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | TTTCAGCAGA GGGGCCCCG GTGGAGCGC CGCTGGAGC CGCTGGAGC AGCAGCACCACCACCACCACCACCACCACCACCACCACCA  | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TGGGCCAGGC TGGTCTTCT TGTTCGTCG GCGCGCCA GGGAAAACT GCCAGGCA GGCAGGCA GGCAGGCA GGCAGGCA GGCAGGCA   | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG ACAAAAGTT TGCAGCGTCA CATTCGAGAG ATTCGAGAG ATACAAACCT TTCACACCTCT GGCATCTGGC TTACTTTATC CCCTGGATCT CCCTGGATCT CCCTGGATCT CCCTGGATTT CGGTTCAGAG CATCATATCC TGACACACTCT TGCACATT CTGCAGATT CTGCAGATT CTGCAGATT CTGCACCTCT TGCACCTCT TGCACCTCT TGCACCTCT TGCACCTCT CTGCACGTT CTGCACCTCT ACCTTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC CACTTGTACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGCCAAAAAAA TTGTTGTCCT TGCCAAAAAAA  | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG GCGCTTCC GCAGATT CTGAATGACA ATGGGAAGCT TATTACGGAA CCACCTGGCA AGCCTGGC AGCTCC CCACCTGGA AGCCTCC CCCCCACACT CCACCTGGAA AAGCCTTC CCACACACGCT AAGGACC CCACCTGGAA AGGCTCAC CACACGCT CCACACGCT CCACACGCT CCACACGCT CAAGGAGAC CCACCTGGAA AGGCTCAC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCT CAAGGCTC CAAGGCT CAAGGCTC CACAGCT CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCT CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCT CAAGCT CACCT CAAGCT CA | TCTTCCCGA ACGAAGCGGC TGCTGGGAA TGGGCGAAGT TGGGCGAAGT TCCAAGAGAGC TCACTGATGG TCCACTGATGG TCACTGATGG TCACTGATGG TGGCCACTG TGGTCCACTG TGGTCCACTG TGGTCCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGAGGAAT TGAGAGGAAT TGAGAGGAAT TGAGAGGCCA TGGCAGGCCA TTTTTATCCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTCCCACTG TTTTCCCACTG TTTTCCCCCCTG TGAGCACTCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTCCCCC TTTTCCCCCCC TTTTCCCCCCC TTTTCCCCCC   | GACCGCGCCC GGGGACAGA GCTCAGCGAG CAACTTCCGC CACGGCCACC CGGTTACATC CCCTGCCATC GCAAATTCTT ATATTCCAAT GATCTTCACT CCCAAAGGAG CTCAATACT GACACACAC GTATGAATGC TGAAGACTGT CAGCACCACA GTATGAATGC CAGCACTGC CAGCACTGC CAGCACTGC CAGCACTGC CAGCACTGC CAGCACTGC CTCATTGATGCA CATCTTTATGT ATATAAGACA CTTACTTGT ATATAAGACA TTTGGAACAC TTTGGAACAC TTGGGACACA TTTTCACTC CCCGTCCAG CAGCCAAA TTTTCAATGC TCGGACAGA TTTTCAATGC TCGGACAGAAG TTGGGAACAG TTGGGAACAG TTGGGAACAG TTGGGAACAG TTGGGAACAG TAGCACACATATT TTTTTATATGC TCGATCCAC TTTTTATATGC TTGAATCCTTT CAGTTCCACA ACCAACATATT CAGTTCCTTT CAGTTCCTCAG TTGTTTATATGC TTGTTTAAA   | 120<br>180<br>240<br>360<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1080<br>1140<br>1260<br>1320<br>1320<br>1440<br>1500<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2160<br>2280<br>2280<br>2340<br>2460   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | TTTCAGCAGA GGGGCCCCG GTGGAGCGC CGCTGGAGC CGCTGGAGC AGCAGCACCACCACCACCACCACCACCACCACCACCACCA  | TGTCCCGTE GGAGTATCCC TGGGCCAGGC TGGGCCAGGC TGGTCTTCT TGTTCGTCG GCGCGCCA GGGAAAACT GCCAGGCA GGCAGGCA GGCAGGCA GGCAGGCA GGCAGGCA   | GCGCAATTTC CGCGCCGCCC GTTCCGGCGA GGTGGATGAT CAAGCTGCTG GCACAAGTGC CTACACCAAG AACAAAGTT TGCAGCGTCA CATTCGAGAG ACAAAAGTT TGCAGCGTCA CATTCGAGAG ATTCGAGAG ATACAAACCT TTCACACCTCT GGCATCTGGC TTACTTTATC CCCTGGATCT CCCTGGATCT CCCTGGATCT CCCTGGATTT CGGTTCAGAG CATCATATCC TGACACACTCT TGCACATT CTGCAGATT CTGCAGATT CTGCAGATT CTGCACCTCT TGCACCTCT TGCACCTCT TGCACCTCT TGCACCTCT CTGCACGTT CTGCACCTCT ACCTTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC CACTTGTACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGACCTTCACC TGCCAAAAAAA TTGTTGTCCT TGCCAAAAAAA  | AGCTTCCGCC GCTCCTGGCG GCTCCTGGCG GCGCTTCC GCAGATT CTGAATGACA ATGGGAAGCT TATTACGGAA CCACCTGGCA AGCCTGGC AGCTCC CCACCTGGA AGCCTCC CCCCCACACT CCACCTGGAA AAGCCTTC CCACACACGCT AAGGACC CCACCTGGAA AGGCTCAC CACACGCT CCACACGCT CCACACGCT CCACACGCT CAAGGAGAC CCACCTGGAA AGGCTCAC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCT CAAGGCTC CAAGGCT CAAGGCTC CACAGCT CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCT CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCTC CAAGGCT CAAGCT CACCT CAAGCT CA | TCTTCCCGA ACGAAGCGGC TGCTGGGAA TGGGCGAAGT TGGGCGAAGT TCCAAGAGAGC TCACTGATGG TCCACTGATGG TCACTGATGG TCACTGATGG TGGCCACTG TGGTCCACTG TGGTCCACTG TGGTCCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGTCACTG TGGAGGAAT TGAGAGGAAT TGAGAGGAAT TGAGAGGCCA TGGCAGGCCA TTTTTATCCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTATGCCACTG TTTTCCCACTG TTTTCCCACTG TTTTCCCCCCTG TGAGCACTCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTGCACTG TTTTCCCCCCC TGGCTCCCCC TTTTCCCCCCC TTTTCCCCCCC TTTTCCCCCC   | GACCGGGCCC GGGGAGCAGA GCTCAGGGGG CAACTTCCGC CAGGGCACG CAACTTCCGC CAGGCCACG CGATTACATC CCCAAAGGAG CCGGCATC GCAAATTCTT ATATTCCAAT GCACACACA GTATGAATGC TGAAGACTGT CTGCCTTGCC TGAAGACTGT ATATCAATGCA CATCTTATGT ATATACAATGCA CATCTTATGT ATATACACAC CATCTTATGT ATATCCACT CTTCAATGCA CATCTTATGT ATATACACAC CTTCCATCCAC CGCCAGAA ATTCTCAT TTTTCAATGCA TGGGAAAGA TTGGGAAAGA TTGGGAAAGA TTGGGAAAGA TTGGAAAGA TTGGAAAGA TTGGAAAGA TTTTCATTC TTTCCATCAC CAACTCAGG AGGGGAGACT TTTTCATTC TTTTCATTC TTTTCATTC TTTTCATTC TTTTTATATGC TGAATCATATT TTTTTATATGC TGAATCATT TTTTTATATGC TCAACCTTT TTTTATATGC TCAACCTTT CAAGTCCTTT CAAGTCCTT CAAGTCCTT CAAGTCCTT CAAGTCCTT CAAGTCCTT CAAGTCCTT CAAGTCCTT CAAGTCCTT CAAGTCCTT CAAGTCCT CAACTCT CCCTCCAC CAACTCT CAACTC CAACT CAACTC CAACTC CAACT | 120<br>180<br>240<br>360<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1080<br>1140<br>1260<br>1320<br>1320<br>1440<br>1500<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2160<br>2280<br>2280<br>2340<br>2460   |

|     | GACTGCAGAC | TCC20CC20        | CCTCACCAAA  | AAATATTCCC  | TACAATATAA | TTATCACTAT                   | 2580 |
|-----|------------|------------------|-------------|-------------|------------|------------------------------|------|
|     | GAAAATGGCT |                  |             |             |            |                              | 2640 |
|     | TACGATGACT | TOCARITOG        | TCTCCDAGA   | ACAGCCACAA  | GCATCGCAA  | TGCCAAGTCC                   | 2700 |
|     | TCACGGATTA | NA A CA A CONCAC | TOTOCAMON   | CACTATABAA  | TTARCTTART | TTTTAACATC                   | 2760 |
| 5   | ACAGCTAGTG |                  |             |             |            |                              | 2820 |
| ,   | CGACTCCTTC |                  |             |             |            |                              | 2880 |
|     | CCCATGTATT |                  |             |             |            |                              | 2940 |
|     | ACAAAAAAGG |                  |             |             |            |                              | 3000 |
|     | AATTGCCCTT |                  |             |             |            |                              | 3060 |
| 10  |            |                  |             |             |            |                              | 3120 |
| 10  | GGATCCTATC |                  |             |             |            |                              |      |
|     | ACGGAATATA |                  |             |             |            |                              | 3180 |
|     | TACTCATACA |                  |             |             |            |                              | 3240 |
|     | TTTGGTTCCC |                  |             |             |            |                              | 3300 |
| 1.5 | GTGAACATTT |                  |             |             |            |                              | 3360 |
| 15  | ATGCCCTGTC |                  |             |             |            |                              | 3420 |
|     | CTGGCCTGTC | CCTTTTATGG       | AACTACCCCA  | TTCGCTGGTT  | CCAGATCCAT | CACAGAATGT                   | 3480 |
|     | TCAACTTCAG | TTCTGAATAT       | TACTATTTTC  | GGTGGATTTG  | GGCATCTGGA | GTTGTTAAAT                   | 3540 |
|     | TGTCCTTCTG | AGGTTTTCCA       | TGAATGCTTC  | TTTAACCCTT  | GCCACAATAG | TGGAACCTGC                   | 3600 |
| 00  |            |                  |             | TGTCCACTTG  |            |                              | 3660 |
| 20  |            |                  |             | CCTTGCCTCA  |            |                              | 3720 |
|     |            |                  |             | TCAGGTTACA  |            |                              | 3780 |
|     | AATATAAATG | AGTGTAGCTC       | CAGTCCTTGT  | TTAAATAAAG  | GAATCTGTGT | TGATGGTGTG                   | 3840 |
|     |            |                  |             | TTTGTAGGCC  |            |                              | 3900 |
|     |            |                  |             | AATGCAGTCT  |            |                              | 3960 |
| 25  |            |                  |             | GGTACCCGAT  |            |                              | 4020 |
|     | TGTCTCAGTC | AGCCATGCAA       | AAATGGAGCT  | ACCTGTAAAG  | ACGGTGCCAA | TAGCTTCAGA                   | 4080 |
|     | TGCCTGTGTG | CAGCTGGCTT       | CACAGGATCA  | CACTGTGAAT  | TGAACATCAA | TGAATGTCAG                   | 4140 |
|     | TCTAATCCAT | GTAGAAATCA       | GGCCACCTGT  | GTGGATGAAT  | TAAATTCATA | CAGTTGTAAA                   | 4200 |
|     |            |                  |             | GAAACAGAAC  |            |                              | 4260 |
| 30  |            |                  |             | GTCATGCTAG  |            |                              | 4320 |
|     |            |                  |             |             |            | TGGAACACCA                   | 4380 |
|     | ATCTCCTATG | CAGTTGATAA       | CGGCAGCGAC  | AATACCTTGC  | TCCTGACTGA | TTATAACGGC                   | 4440 |
|     |            |                  |             | ATAACAAACT  |            |                              | 4500 |
|     |            |                  |             |             |            | AGTCTATATC                   | 4560 |
| 35  |            |                  |             |             |            | ACCTGGTGGT                   | 4620 |
| 55  |            |                  |             |             |            | CCCAGCTGAG                   | 4680 |
|     | GGIGCGIIAG | CCTCCATAAG       | CONCERCANC  | CHARGEGRACE | ATCTCCTCTC | TCCACAGCAG                   | 4740 |
|     |            |                  |             |             |            | GTTAGCATGG                   | 4800 |
|     |            |                  |             |             |            | CATATTTTGT                   | 4860 |
| 40  |            |                  |             |             |            |                              | 4920 |
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         CTCCTGCTTT TCTTTCCCCA TAGAAAGTAC CTTGAAGTAG CACAGTCCGT CCTTGCATGT
                                                                                         1380
         GCACGAGCTA TCATTTGAGT AAAAGTATAC ATGGAGTAAA AATCATATTA AGCATCAGAT
                                                                                         1440
         TCAACTIATA TITICIATIT CATCITCTTC CITTCCCTTC TCCACCTTC TACTCGGCAT
AATTATATCT TAATCATATA TGGAAATGTG CAACATATGG TATTTGTTAA ATACGTTTGT
                                                                                         1500
                                                                                         1560
         TTTTATTGCA GAGCAAAAAT AAATCAAATT AGAAGCAATA AAAAAAAAA AAAAAAAAA
                                                                                         1619
```

| •  | Nucleic Aci | C148 DNA Se<br>d Accession   | #: NM_0020  | 91.1            |              |                          |              |
|----|-------------|------------------------------|-------------|-----------------|--------------|--------------------------|--------------|
| 5  | 1           | 11                           | 21          | 31              | 41           | 51                       |              |
|    | î           | î                            | Ī           | Ĭ               | Ĩ            | Ĭ.                       |              |
|    |             | CTTCCCAGCC                   |             |                 |              |                          | 60           |
| 10 |             | CTCCCGCTGG                   |             |                 |              |                          | 120          |
| 10 |             | CTGCCTGCGG<br>GTGGGGGCACT    |             |                 |              |                          | 180<br>240   |
|    |             | AGCCTGAAGC                   |             |                 |              |                          | 300          |
|    |             | GGTCTCATAG                   |             |                 |              |                          | 360          |
| 15 |             | AATCAGCAGC                   |             |                 |              |                          | 420          |
| 13 |             | GGCAAAGTTG<br>AACCAGCAAT     |             |                 |              |                          | 480<br>540   |
|    |             | AGTTCTGCAA                   |             |                 |              |                          | 600          |
|    | AAATATTTGA  | CTATTCTGTA                   | TCTTTCATCC  | TTGACTAAAT      | TCGTGATTTT   | CAAGCAGCAT               | 660          |
| 20 |             | AAACTTGTTT                   |             |                 |              |                          | 720          |
| 20 | TAAAAGCTTA  | TAGGCTACCT<br>AACACAT        | GTTGGTTAGA  | TTCAAGGCCC      | CGAGCTGTTA   | CCATTCACAA               | 780<br>797   |
| 25 | Nucleic Ac  | C149 DNA Seld Accession      | #: NM_0122  | 261.1           |              |                          |              |
|    | 1           | 11                           | 21<br>      | 31              | 41           | 51<br>1                  |              |
|    | GATTTGCTCT  | GCCAGCAGCT                   |             | CGCTCGACAC      | CGAGTCCTAG   | CTAGGCGCTC               | 60           |
| 30 | ACAGAATACG  | CGCTCCCTCC                   | CTCCCCCTTC  | TCTGTCCCCC      | GCCTCTCGCT   | CACCCCGGCC               | 120          |
|    |             | GCGACTTTGA<br>GGCACTGCGA     |             |                 |              |                          | 180          |
|    |             | CTCCTGATGT                   |             |                 |              |                          | 240<br>300   |
| 25 | GGAAAATCTC  | TCAGGCCTTT                   | CCACTAACCC  | TGAAAAAGAT      | ATATTTGTGG   | TGCGGGAAAA               | 360          |
| 35 |             | TGTCTCATGG                   |             |                 |              |                          | 420          |
|    |             | TACGTAGATC                   |             |                 |              |                          | 480<br>540   |
|    |             | CTCAAAATGC                   |             |                 |              |                          | 600          |
| 40 |             | AGGCTGAGCA                   |             |                 |              |                          | 660          |
| 40 |             | GTCAGTGCTG<br>GGGAAGTCCT     |             |                 |              |                          | 720<br>780   |
|    |             | AAGACGGTCA                   |             |                 |              |                          | 840          |
|    |             | TTTGTCTTCA                   |             |                 |              |                          | 900          |
| 45 |             | TTGCCCCTGA                   |             |                 |              |                          | 960<br>1020  |
|    |             | AAGCACATGG                   |             |                 |              |                          | 1080         |
|    |             | CAGGTAGAAC                   |             |                 |              |                          | 1140         |
|    |             | ATCAAACAGG<br>AGGGGGAGAC     |             |                 |              |                          | 1200<br>1260 |
| 50 |             | GGAGGGGAGG                   |             |                 |              |                          | 1320         |
|    | TGACTCTCCA  | AAGAGCAATA                   | AATGCCACTT  | GGAGCTGTAT      | CTGGCCCCAA   | AGTTTAGGGA               | 1380         |
|    |             | GCTTCTTTGA                   |             |                 |              | TGGGGTGCTT<br>GAATACAACC | 1440         |
|    |             |                              |             |                 |              | CATTCTGCAT               | 1500<br>1560 |
| 55 |             |                              |             |                 |              | GCAGCACCAG               | 1620         |
|    |             |                              |             |                 |              | GGTCCAAGTC               | 1680         |
|    | TTCTCTGGC   | AAGAATCAAI                   | CIGIGIGAGI  | CIGITITICA      | . AAATGAAATA | AAACACACTA               | 1740<br>1749 |
| 60 |             |                              |             |                 |              |                          |              |
| 00 |             | C150 DNA S<br>id Accessio    |             | 226.1           |              |                          |              |
|    |             | puence: 22                   |             |                 |              |                          |              |
|    | 1           | 11                           | 21          | 31              | 41           | 51                       |              |
| 65 | î           | î .                          | î*          | í               | Ĩ.           | Ĩ                        |              |
|    |             |                              |             |                 |              | ACGTGGGCCT               | 60           |
|    |             |                              |             |                 |              | ACCCCCATGT<br>CTGGAGTGCC | 120<br>180   |
|    |             |                              |             |                 |              | CCTCCAGCTG               | 240          |
| 70 | CCCCTGGGAT  | GCAGGCTGAG                   | CACCCTTGCC  | CGGCTGTGAT      | TGCTGCCAGG   | CACTGTTCAT               | 300          |
|    |             | CTGTCCCTTT AACGAATAA         |             |                 | TGAAAGTTCA   | TATCTGGAGC               | 360<br>398   |
|    | CIGNIGICII  | AACGAATAA                    | GGICCCAIGC  | . ICCACCCG      |              |                          | 390          |
| 75 |             |                              |             |                 | ,            |                          |              |
| 13 |             | : C151 DNA S<br>cid Accessio |             | 1 200           |              |                          |              |
|    |             | nuence: 64.                  |             | .,,,,,,         |              |                          |              |
|    |             |                              |             |                 |              |                          |              |
| 80 | 1           | 11                           | 21<br>1     | 31              | 41<br>1      | 51<br>!                  |              |
| 00 | GGCACGAGC   | AGTCTCCGC                    | CCTCCACCC   | I<br>CCTCAGGAAG | CCGCGAACCC   | TCTCTTGACC               | 60           |
|    | ACTATGAGC   | TCCCGTCCAC                   | CCGCGCGCGC  | CGTGTCCCG       | GTCCTTCGGC   | CTCCTTGTGC               | 120          |
|    |             |                              |             |                 |              | COCTOGTCCT               | 180<br>240   |
|    | GICICIGCIA  | a TOCTONCHO                  | a actacatag | . ACTIGITIAN    |              | CAGAGTAAAC               | 240          |
|    |             |                              |             |                 | 4            | 202                      |              |

```
CCCAAAACGA TTGGTAAACT GCAGGTGTTC CCCGCAGGCC CGCAGTGCTC CAAGGTGGAA
       GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA
       AAGAAAGTCA TCCAGAAAAT TTTGGACAGT GGAAACAAGA AAAACTGAGT AACAAAAAAG
ACCATGCATC ATAAAATTGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC
                                                                                     420
                                                                                     480
 5
       CAGTAAGAAT AAGAAGGAAG GGTTGGTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT
                                                                                     540
        GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA
                                                                                     600
        CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCTTTGG
                                                                                     660
       CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT
TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG
                                                                                     720
                                                                                     780
10
        ATTTCGTATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTTGTTCTT
        ACTCACTCTT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTTCTTGGGG AATATGTTAC
                                                                                     900
        TCTTTACCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTCATACCG
                                                                                     960
        TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG
                                                                                     1020
        CTAATATATT CTCTTCCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT
15
        CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA
                                                                                     1140
       ATTCTGGTCA CTARATATAC ACTITAGATA GATGAAGAAG CCCARAAACA GATARATTCC TGATTGCTAA TTTACATAGA AATGTATTCT CTTGGTTTTT TARATARAAG CARAATTAAC
                                                                                     1200
                                                                                     1260
        AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT
                                                                                     1320
        CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT
                                                                                     1380
20
        TTTAAAGGTT TTGACCATTT TGTTATGAGG AATTATACAT GTATCACATT CACTATATTA
                                                                                     1440
        AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT
                                                                                     1500
        TGGAGAAACA ATAAAAGATT TCTAAACCAA AAAAAAAAA AAAAAAA
25
        Seq ID NO: C152 DNA Sequence
        Nucleic Acid Accession #: NM_005242.2
        Coding sequence: 148..1341
30
        CGGCCCGCCC TGGGGAGGCG CGCAGCAGAG GCTCCGATTC GGGGCAGGTG AGAGGCTGAC
        TTTCTCTCGG TGCGTCCAGT GGAGCTCTGA GTTTCGAATC GGTGGCGGCG GATTCCCCGC
        GCGCCCGGCG TCGGGGCTTC CAGGAGGATG CGGAGCCCCA GCGCGGCGTG GCTGCTGGGG
        GCCGCCATCC TGCTAGCAGC CTCTCTCTC TGCAGTGGCA CCATCCAAGG AACCAATAGA
                                                                                     240
35
        TCCTCTAAAG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCCACGT CACTGGAAAA
                                                                                     300
        GGAGTTACAG TTGAAACAGT CTTTTCTGTG GATGAGTTTT CTGCATCTGT CCTCACTGGA
                                                                                     360
        AAACTGACCA CGGTCTTCCT TCCAATTGTC TACACAATTG TGTTTGTGGT GGGTTTGCCA
                                                                                     420
        AGTAACGGCA TGGCCCTGTG GGTCTTTCTT TTCCGAACTA AGAAGAAGCA CCCTGCTGTG
                                                                                     480
        ATTTACATGG CCAATCTGGC CTTGGCTGAC CTCCTCTCTG TCATCTGGTT CCCCTTGAAG
                                                                                     540
40
        ATTGCCTATC ACATACATGC CAACAACTGG ATTTATGGGG AAGCTCTTTG TAATGTGCTT
        ATTGGCTTTT TCTATGGCAA CATGTACTGT TCCATTCTCT TCATGACCTG CCTCAGTGTG
CAGAGGTATT GGGTCATCGT GAACCCCATG GGGCACTCCA GGAAGAAGGC AAACATTGCC
                                                                                     660
                                                                                     720
        ATTGGCATCT CCCTGGCAAT ATGGCTGCTG ATTCTGCTGG TCACCATCCC TTTGTATGTC
                                                                                     780
        GTGAAGCAGA CCATCTTCAT TCCTGCCCTG AACATCACGA CCTGTCATGA TGTTTTGCCT
45
        GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCCTCT CTCTGGCCAT TGGGGTCTTT
                                                                                     900
        CTGTTCCCAG CCTTCCTCAC AGCCTCTGCC TATGTGCTGA TGATCAGAAT GCTGCGATCT
                                                                                     960
        TCTGCCATGG ATGAAAACTC AGAGAAGAAA AGGAAGAGGG CCATCAAACT CATTGTCACT
                                                                                     1020
        GTCCTGGCCA TGTACCTGAT CTGCTTCACT CCTAGTAACC TTCTGCTTGT GGTGCATTAT
                                                                                      1080
        TITCTGATTA AGAGCCAGGG CCAGAGCCAT GTCTATGCCC TGTACATTGT AGCCCTCTGC
CTCTCTACCC TTAACAGCTG CATCGACCCC TTTGTCTATT ACTTTGTTTC ACATGATTTC
                                                                                     1140
50
                                                                                     1200
        AGGGATCATG CAAAGAACGC TCTCCTTTGC CGAAGTGTCC GCACTGTAAA GCAGATGCAA
                                                                                     1260
        GTATCCCTCA CCTCAAAGAA ACACTCCAGG AAATCCAGCT CTTACTCTTC AAGTTCAACC
                                                                                     1320
        ACTGTTAAGA CCTCCTATTG AGTTTTCCAG GTCCTCAGAT GGGAATTGCA CAGTAGGATG
                                                                                     1380
        TGGAACCTGT TTAATGTTAT GAGGACGTGT CTGTTATTTC CTAATCAAAA AGGTCTCACC
                                                                                     1440
55
        ACATACCACC G
        Seq ID NO: C153 DNA Sequence
        Nucleic Acid Accession #: NM_003469.2
         Coding sequence: 92..1945
60
         GAAACGGCCC GAGAAGCTCG CCCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC
        CATATAAACA AAAAGAGGAA ATCTITCAAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG
                                                                                     120
65
         AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT
                                                                                      180
         TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAAAATG TCCAAAAGTT
        TCCCAGTCCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAGCTCA
TAAGGAAGAA AGCAGCCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA
                                                                                      300
                                                                                      360
         AAAAGAAAAT GGCGATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG
70
         GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA
         AGAAAATAAG CCCTATGCCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA
TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA
                                                                                      600
         TGAAGAGAAT TCCAGGGATA ACCCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA
                                                                                      660
         TACTCCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG
 75
         ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACTTTATA CGGATGATGA
                                                                                      780
         AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG
                                                                                      840
         GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAAGA
         GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT
                                                                                      960
         CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT
                                                                                      1020
 80
         AATTGCCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA
                                                                                      1080
         AAATGGGGAA AGGGCCACCA GGCTTTTTGA GAAACCTCTT GATTCTCAGT CTATTTATCA
         GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCCAGAA GACTTAATTG AGATGCTCAA AACTGGGGAG AAGCCGAATG GATCAGTGGA ACCGGAGCGG GAGCTTGACC TTCCTGTTGA
                                                                                      1200
                                                                                      1260
         CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT
```

|      | CTCCAAGAGT    | GGCTACCCTA     | AAACACCTGG     | TCGTGCTGGG            | ACTGAGGCCC                            | TACCAGACGG   | 1380 |
|------|---------------|----------------|----------------|-----------------------|---------------------------------------|--------------|------|
|      |               | GAGGATATTT     |                |                       |                                       |              | 1440 |
|      |               | CCCAATCCAT     |                |                       |                                       |              |      |
|      |               |                |                |                       |                                       |              | 1500 |
| _    |               | AGATCGAACC     |                |                       |                                       |              | 1560 |
| 5    | ACAGATGGCA    | TATGAAAACC     | TGAACGACAA     | GGATCAAGAA            | TTAGGTGAGT                            | ACTTGGCCAG   | 1620 |
|      | GATGCTAGTT    | AAATACCCTG     | AGATCATTAA     | TTCAAACCAA            | DANCORAGITE                           | TTCCTCCTCA   | 1680 |
|      | AGGCTCATCT    | GAAGATGACC     | TCCACCAACA     | CCDACAAATT            | CACCACCCCA                            | TCA A ACACCA | 1740 |
|      | TTTCARTORA    | OCCUPATION CC  | 10CAGGAAGA     | CONTONACT             | GAGCAGGCCA                            | ICAMAGAGCA   |      |
|      | TTTGAATCAA    | GGCAGCTCTC     | AGGAGACTGA     | CAAGCTGGCC            | CCGGTGAGCA                            | AAAGGTTCCC   | 1800 |
| 10   |               | CCGAAGAATG     |                |                       |                                       |              | 1860 |
| 10   | AATGAAAGTG    | CTGGAATACC     | TCAATCAAGA     | AAAGGCAGAA            | AAGGGAAGGG                            | AGCATATTGC   | 1920 |
|      |               | ATGGAAAATA     |                |                       |                                       |              | 1980 |
|      |               | AAATCCCAAC     |                |                       |                                       |              |      |
|      |               |                |                |                       |                                       |              | 2040 |
|      |               | AAATGATGTA     |                |                       |                                       |              | 2100 |
| 1.5  |               | TGTTATCTTG     |                |                       |                                       |              | 2160 |
| 15   |               | TCCATTATTC     |                |                       |                                       |              | 2220 |
|      | GGCTGTGGCA    | TTGTTGATGC     | TCACATATGA     | TAAAAAAGTG            | TCCTATAATT                            | CTATTGAAAG   | 2280 |
|      | TTTTTAATAT    | TTATTGAATT     | ATTTTTTAC      | TGTCTGTAGC            | CTTTTTCTCCA                           | CTACTCCACC   | 2340 |
|      | ΔΑΤΑΔΑΚΚΑ     | AGCATTATAA     | ΔΤΑΤΑ          |                       |                                       |              | 2365 |
|      |               |                | *******        |                       |                                       |              | 2303 |
| 20   | Com ID NO.    | C154 DNA Se    |                |                       |                                       |              |      |
|      |               |                |                |                       |                                       |              |      |
|      |               | ld Accession   |                | 755                   |                                       |              |      |
|      | cograd sed    | ience: 327.    | .5108          |                       |                                       |              |      |
|      |               |                |                |                       |                                       |              |      |
| ~~   | 1             | 11             | 21             | 31                    | 41                                    | 51           |      |
| 25   | ]             |                | 1              |                       |                                       | 1            |      |
|      | GAATTCCCGG    | AGCGGGCGGG     | CTRCCRACRCC    | COCCCCATC             | CCCCACCCCC                            | ACCCCTCCCA   | 60   |
|      |               | GCGCCCATTC     |                |                       |                                       |              |      |
|      | CCGGGIGGCI    | GCGCCCATTC     | CALACCEGEE     | GAMAGCGGAC            | ACTUTCAGCT                            | GAATCACTCC   | 120  |
|      | CCLITTAGGA    | GGAGGGAGGG     | GGAAAAGGTG     | TCTAGCTAAT            | TTCTGCTTAA                            | AAAAGCACAG   | 180  |
| 20   |               | GTCAGCTTTG     |                |                       |                                       |              | 240  |
| 30   | CTTCCTGCTG    | GGCACAGGCG     | AGCGCTTTAT     | TTCTGGAGCT            | GAGGGCTAAA                            | ACTITITICA   | 300  |
|      |               | CCTCAACATC     |                |                       |                                       |              | 360  |
|      |               | GGCTCAGCTC     |                |                       |                                       |              | 420  |
|      |               | TCGCTTCCCG     |                |                       |                                       |              | 480  |
|      |               |                |                |                       |                                       |              |      |
| 35   |               | GGGTCCAGTC     |                |                       |                                       |              | 540  |
| 33   |               | CACGAGCAGC     |                |                       |                                       |              | 600  |
|      | ACTACAGAAT    | TTCTCACGAG     | GAGAAGGACC     | TGTTTTTTAA            | CTTGACGGTC                            | AATCAAGGAT   | 660  |
|      | TTCTTTCCAA    | TAGCTACATC     | ATGGAGAAGA     | GATATGGGAA            | CCTCTCCCAT                            | GTTAAGATGA   | 720  |
|      |               | TGCCCCCCTC     |                |                       |                                       |              | 780  |
|      |               | AGCCCTCAGT     |                |                       |                                       |              | 840  |
| 40   |               | CATTGAACCC     |                |                       |                                       |              |      |
| -10  |               |                |                |                       |                                       |              | 900  |
|      |               | CAGGAGGCAG     |                |                       |                                       |              | 960  |
|      | ACAGTGTTAA    | CATCTCCCAG     | AAGCAAGAGC     | TATGGCGGGA            | GAAGTGGGAG                            | AGGCACAACT   | 1020 |
|      | TGCCAAGCAG    | AAGCCTCTCT     | CGGCGTTCCA     | TCAGCAAGGA            | GAGATGGGTG                            | GAGACACTGG   | 1080 |
|      | TGGTGGCCGA    | CACAAAGATG     | ATTGAATACC     | ATGGGAGTGA            | GAATGTGGAG                            | TCCTACATCC   | 1140 |
| 45   |               | GAACATGGTC     |                |                       |                                       |              | 1200 |
|      |               | GGTTCGGCTC     |                |                       |                                       |              |      |
|      |               |                |                |                       |                                       |              | 1260 |
|      |               | AAAGACACTG     |                |                       |                                       |              | 1320 |
|      |               | TCCTGTTCAT     |                |                       |                                       |              | 1380 |
| 50   | CIGGITICAA    | TCGCCCCTGC     | GAGACCCTGG     | GCCTGTCTCA            | CCTTTCAGGA                            | ATGTGTCAGC   | 1440 |
| 50   | CTCACCGCAG    | TTGTAACATC     | AATGAAGATT     | CGGGACTCCC            | TCTGGCTTTC                            | ACAATTGCCC   | 1500 |
|      | ATGAGCTAGG    | ACACAGCTTC     | GGCATCCAGC     | ATGATGGGAA            | AGAAAATGAC                            | TGTGAGCCTG   | 1560 |
|      |               | TCCGTACATC     |                |                       |                                       |              | 1620 |
|      |               | CAGCGAGGAG     |                |                       |                                       |              |      |
|      |               | ACCTAAAAAG     |                |                       |                                       |              | 1680 |
| 55   |               |                |                |                       |                                       |              | 1740 |
| 55   |               | CCACCAGTGC     |                |                       |                                       |              | 1800 |
|      |               | CTGCCAGACA     |                |                       |                                       |              | 1860 |
|      |               | AGATGGAACT     |                |                       |                                       |              | 1920 |
|      | TCACAGTGGG    | GAAGAAACCA     | GAGAGCATTC     | CTGGAGGCTG            | GGGCCGCTGG                            | TCACCCTGGT   | 1980 |
|      | CCCACTGTTC    | CAGGACCTGT     | GGGGCTGGAG     | TCCAGAGCGC            | AGAGAGGCTC                            | TGCAACAACC   | 2040 |
| 60   |               | GTTTGGAGGG     |                |                       |                                       |              | 2100 |
|      |               | CTGTCGCTCA     |                |                       |                                       |              | 2160 |
|      | y Ly Catalana | CTACAAGAAT     | Caronion       | Manusca<br>Curring Ch | ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ | WIGHTIIG     |      |
|      | ACACIGITCO    | CIACAAGAAI     | GAACICIACC     | ACIGGITICC            | CATTTTTAAC                            | CCAGCACATC   | 2220 |
|      | CITGIGAGCT    | CTACTGCCGA     | CCCATAGATG     | GCCAGTTTTC            | IGAGAAAATG                            | CIGGATGCTG   | 2280 |
| 65   | TCATTGATGG    | TACCCCTTGC     | TTTGAAGGCG     | GCAACAGCAG            | AAATGTCTGT                            | ATTAATGGCA   | 2340 |
| 05   | TATGTAAGAT    | GGTTGGCTGT     | GACTATGAGA     | TOGATTCCAA            | TGCCACCGAG                            | GATCGCTGCG   | 2400 |
|      | GTGTGTGCCT    | GGGAGATGGC     | TCTTCCTGCC     | AGACTGTGAG            | AAAGATGTTT                            | AAGCAGAAGG   | 2460 |
|      | AAGGATCTGG    | TTATGTTGAC     | ATTGGGCTCA     | TTCCAAAAGG            | AGCAAGGGAC                            | ATAAGAGTGA   | 2520 |
|      | TGGAAATTCA    | GGGAGCTGGA     | AACTTYCTTC     | CCATCAGGAG            | TCAACATCOT                            | GAAAAATATT   | 2580 |
|      | ACCTUANTOC    | VCCCdataly and | Tarana and a   | Access a cons         | TRACCIOCACE                           | GGGACTGTCT   | 2000 |
| 70   | TOTAL CONTROL | CACCALLATT     | ATCCM010GA     | ACCOUNTACTA           | INNOCIGULA                            | GGGACIGICI   | 2640 |
| 70   |               |                |                |                       |                                       | ACCAATGAGT   |      |
|      |               |                |                |                       |                                       | GAGTACACAA   |      |
|      |               |                |                |                       |                                       | TACGGCCACT   | 2820 |
|      | GGACAGAGTG    | CAGTGTGACC     | TGCGGGACAG     | · GTATCCGCCG          | CCAAACTGCC                            | CATTGCATAA   | 2880 |
|      | AGAAGGGCCG    | CGGGATGGTG     | AAAGCTACAT     | TCTGTGACCC            | AGAAACACAG                            | CCCAATGGGA   | 2940 |
| · 75 | GACAGAAGAA    | GTGCCATGAA     | AAGGCTTGTC     | CACCCACCOC            | GTCCCCACCC                            | GAGTGGGAAG   | 2000 |
|      | CATCOTOGO     | CACAMOOCC      | COCCE COCCE    | ACARCA SCIT           | O LOUGUAGGG                           | DAGLGGGAAG   | 3000 |
|      | CALGUICGGC    | GACATGCGGG     | CCCCACGGGG     | MUMAGAAGCG            | AACCGTGCTG                            | TGCATCCAGA   | 3060 |
|      | CCATGGTCTC    | TGACGAGCAG     | GCTCTCCCGC     | CCACAGACTG            | CCAGCACCTG                            | CTGAAGCCCA   | 3120 |
|      | AGACCCTCCT    | TTCCTGCAAC     | AGAGACATCC     | TGTGCCCCTC            | GGACTGGACA                            | GTGGGCAACT   | 3180 |
| 0.0  | GGAGTGAGTG    | TTCTGTTTCC     | TGTGGTGGTG     | GAGTGCGGAT            | TCGCAGTGTC                            | ACATGTGCCA   | 3240 |
| 80   | AGAACCATGA    | TGAACCTTGC     | GATGTGACAA     | GGAAACCCAA            | CAGCCGAGCT                            | CTGTGTGGCC   | 3300 |
|      | TCCAGCAATC    | CCCTTCTACC     | CGGAGAGTTC     | TGADACCAAA            | - TITOCOMOCI                          | ATTTCCAATG   | 3350 |
|      | GAAAAAA       | ACCENCACA      | V VCCCCCCCCCCC |                       | A DOOR OFFI                           | AGAATGCTGA   | 3400 |
|      | CANCACACA     | ACCCCCCCC      | montecorie     | CARCUTAC              | ATCCAGGCCC                            | AGAATGCTGA   | 3420 |
|      | CONCACCOAC    | AGGCCTGAG      | ICIAIGAGCA     | CHAGCACTCC            | AGCAATCAGC                            | AGCCCTAGTC   | 3480 |
|      | CTACCACAGO    | CTCCAAAGAA     | GGAGACCTGG     | GTGGGAAACA            | GTGGCAAGAT                            | AGCTCAACCC   | 3540 |
|      |               |                |                |                       |                                       | 20.4         |      |

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         TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC
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                                                                                             780
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         Nucleic Acid Accession #: NM_004591
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                                                                                             540
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         TAATTITCCA TAAGCTATTT TGGTTTAGTG CAAAGTATAA AATTATATTT GGGGGGGAAT AAGATTATAT GGACTTTCTT GCAAGCAACA AGCTATTTT TAAAAAAACT ATTTAACATT CTTTTGTTTA TATTGTTTTG TCTCCTAAAT TGTTGTAATT GCATTATAAA ATAAGAAAAA
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          Seq ID NO: C157 DNA Sequence
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Nucleic Acid Accession #: NM 013271.1

|     | Coding sequ  | ence: 278                    | 09         |            |  |                              |              |
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| 3   | TCCGGAGCCA   |                              |            |            |  |                              | 60<br>120    |
|     |              | GCCGGTAAAG                   |            |            |  |                              | 180          |
|     | AGACTGGCGC   | TCCTCGCCGC                   | TTCCGGCGGT | CAGTGCCCCG | AGGTGAGGCG                             | GCGGGGGGG                    | 240          |
| 10  |              | GCCCCGGGCG                   |            |            |  |                              | 300          |
| 10  |              | GCAGGAGGCT<br>CCCCCGCAAC     |            |            |  |                              | 360<br>420   |
|     |              | GCTCGCTCGC                   |            |            |  |                              | 480          |
|     | CCCAGCTTGT   | CCCCGCGCCC                   | GTCCCCGCCG | CGGCGCTCCG | ACCCCGGCCC                             | CCGGTCTACG                   | 540          |
| 15  |              | CGCGGGCCCG                   |            |            |  |                              | 600          |
| 13  |              | GAGGTACTTG                   |            |            |  |                              | 660<br>720   |
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|     |              | CCGCCTCTTG                   |            |            |  |                              | 840          |
| 20  |              | CCCGCCATCC                   |            |            |  |                              | 900          |
| 20  | GATCTGAGC    | CAGCCAGCCC                   | TUTCACCUGA | GGATCCCTAC | CCCTGGCCC                              | ACAATAACAT                   | 960<br>969   |
|     | Cittoronoc   |                              |            |            |  |                              | 202          |
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| 25  |              | ld Accession<br>Lence: 183.  |            | 245.2      |  |                              |              |
|     | couring sequ | icinco. 105                  |            |            |  |                              |              |
|     | 1            | 11                           | 21         | 31         | 41                                     | 51                           |              |
|     | GCGCAGGAAG   | ACCOCCTOC                    | CCCCACCACC | GGGGGGGGGG | GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | <br>  GGAGCGGGCG             | 60           |
| 30  |              |                              |            |            |  | GCCGCCGGC                    | 120          |
|     |              |                              |            |            |  | GCGGTGGAGA                   | 180          |
|     |              |                              |            |            |  | CACCGCTCGG<br>GGCGCAGTGG     | 240<br>300   |
|     |              |                              |            |            |  | CGCAAGCTGA                   | 360          |
| 35  | AGCGACGCTT   | CTTGGAGGAG                   | CACGAGTGCC | TGTCTGAGCA | GCAGCTGGAG                             | CAGTTCCTGG                   | 420          |
|     |              |                              |            |            |  | TCGGGCAACT                   | 480          |
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| 40  |              |                              |            |            |  | ACCGTGCACG                   | 660          |
| 40  |              |                              |            |            |  | CAGGTGGTGG                   | 720          |
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|     |              |                              |            |            |  | TACAATCAAA                   | 900          |
| A.E |              |                              |            |            |  | CTTATTGCCA                   | 960          |
| 45  |              |                              |            |            |  | GACCAACTGT                   | 1020<br>1080 |
|     |              |                              |            |            |  | CAAAATGAGC                   | 1140         |
|     | CTTTTGTGGC   | CACCCAGTCA                   | TCTGCCTGCG | TGGATGGCCC | TGCAAACCAT                             | TGAGCGTAGG                   | 1200         |
| 50  |              |                              |            |            |  | TAAGTATGTT                   | 1260         |
| 30  |              |                              |            |            |  | TACTGTTTGC                   | 1320<br>1380 |
|     | AGGATGTCTA   | ATATGTGAGG                   | AAATGAGATG | TCCACCTAAA | ATTCATATGT                             | GACAAAATTA                   | 1440         |
|     |              |                              |            |            |  | TAGAAGCAGA                   | 1500         |
| 55  |              |                              |            |            |  | TGATGGCTAA                   | 1560<br>1620 |
|     | GTTTATGTGT   | ACTGGTTTGC                   | ATGTACCCAC | CCAAAATGAT | TATTTTTGGA                             | GAATCTAAGT                   | 1680         |
|     |              |                              |            |            |  | AGTATAAATA                   | 1740         |
|     |              |                              |            |            |  | TGAAACTAAG<br>AGTTGCTACA     | 1800<br>1860 |
| 60  |              | GGGAATAATA                   |            |            |  |                              | 1901         |
|     | Cog ID NO.   | C159 DNA S                   |            |            |  |                              |              |
|     |              | id Accessio                  |            | 472.1      |  | •                            |              |
| 65  |              | ruence: 93                   |            |            |  |                              |              |
| 65  | 1            | 11                           | 21         | 31         | 41                                     | 51                           |              |
|     | i            | i                            | 1          | î          | ì                                      | 1                            |              |
|     | AAAGGGACTC   |                              |            |            |  | TGAGCTTCTA                   | 60           |
| 70  |              |                              |            |            |  | ACGGAGACCT                   | 120          |
| , 0 |              |                              |            |            |  | C AGCAATTTGC<br>G CGGGCCAGCC | 180<br>240   |
|     |              |                              |            |            |  | CTATTTGCTG                   | 300          |
|     |              |                              |            |            |  | AAGCGTAGTG                   | 360          |
| 75  |              |                              |            |            |  | AGGGCTGGGA<br>TGCTGTGGAC     | 420<br>480   |
|     | TGCATCAGGT   |                              |            |            |  |                              | 492          |
|     |              |                              |            |            |  |                              |              |
|     |              | : C160 DNA S<br>cid Accessio |            | 5245.1     |  |                              |              |
| 80  |              | quence: 187                  |            |            |  |                              |              |
|     |              |                              |            | . ,        |  |                              |              |
|     | 1            | 11<br>                       | 21<br>     | 31<br>     | 41<br>!                                | 51<br>I                      |              |
|     | CTGGGCGGC    | c GGGCGCGGG                  | AGAGGGCGC  | GGAGCGGCT  | C GTGCGGCAG                            | G TACCATGCGG                 | 60           |
|     |              |                              |            |            |  |                              |              |

|    | ACGCGCGAGC               | CCCCCCACCC | CCCCCACCC    | CCCTCCCTCC  | TOCCCCCCCC  | CCTGAGACGG   | 120          |
|----|--------------------------|------------|--------------|-------------|-------------|--------------|--------------|
|    | CGGGTGAGCT               |            |              |             |             |              | 180          |
|    |                          |            |              |             |             |              |              |
|    | TAAGCAATGG               |            |              |             |             |              | 240          |
| 5  | GGAGACAGTG               |            |              |             |             |              | 300          |
| ,  | TACAACGTCA               |            |              |             |             |              | 360          |
|    | ATGGGTGTTT               |            |              |             |             |              | 420          |
|    | AGTGAAAACC               |            |              |             |             |              | 480          |
|    | AGGACCAAAG               |            |              |             |             |              | 540          |
| 10 | ATAGTGAAAG               |            |              |             |             |              | 600          |
| 10 | GTGCTGGATA               |            |              |             |             |              | 660          |
|    | CCTGAAAACA               |            |              |             |             |              | 720          |
|    | GGAACCAACG               |            |              |             |             |              | 780          |
|    | CCAACCAGTG<br>GAGATGGAAA |            |              |             |             |              | 840          |
| 15 |                          |            |              |             |             |              | 900          |
| 13 | AGCATGGCCA               |            |              |             |             |              | 960          |
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|    |                          |            |              |             |             | TAAAGTCAAA   | 1140         |
|    |                          |            |              |             |             | ACTACAGGCT   | 1200         |
| 20 |                          |            |              |             |             | GACTTCTCCA   | 1260         |
| 20 |                          |            |              |             |             | AATAAGTGAA   | 1320         |
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|    |                          |            |              |             |             | CAACACTGGT   | 1440         |
|    |                          |            |              |             |             | ACTTGAAGTA   | 1500         |
| 25 |                          |            |              |             |             | TGCAAATAGC   | 1560         |
|    |                          |            |              |             |             | CGTGCCCATT   | 1620         |
|    |                          |            |              |             |             | TGGGTACGTG   | 1680         |
|    |                          |            |              |             |             | CACTGGTGCC   | 1740         |
|    |                          |            |              |             |             | TCTGAGGATT   | 1800         |
| 30 |                          |            |              |             |             | TACAATTACT   | 1860         |
|    |                          |            |              |             |             | AGGGACAATT   | 1920         |
|    | CCCAGAGATC               | TAGGCGTGGG | AGAGCAAATA   | ACCACTGTTT  | CTGCTATTGA  | TGCAGATGAA   | 1980         |
|    | CTTCAGTTGG               | TACAGTATCA | GATTGAAGCT   | GGAAATGAAC  | TGGATTTGTT  | TAGTTTAAAC   | 2040         |
|    | CCCAACTCGG               | GGGTATTGTC | ATTAAAGCGA   | TOGCTAATGG  | ATGGCTTAGG  | TGCAAAGGTG   | 2100         |
| 35 | TCTTTCCACA               | GTCTGAGAAT | CACAGCTACA   | GATGGAGAAA  | ATTTTGCCAC  | ACCATTATAT   | 2160         |
|    | ATCAACATAA               | CAGTGGCTGC | CAGTCACAAG   | CTGGTAAACT  | TGCAGTGTGA  | AGAGACTGGT   | 2220         |
|    |                          |            |              |             |             | CCAGGGAGAG   | 2280         |
|    | GTGGAGGATA               | TTTTCTTCGA | TTCTCACTCT   | GTCAATGCTC  | ACATACCGCA  | GTTTAGAAGC   | 2340         |
| 40 | ACTCTTCCGA               | CTGGTATTCA | GGTAAAGGAA   | AACCAGCCTG  | TGGGTTCCAG  | TGTAATTTTC   | 2400         |
| 40 |                          |            |              |             |             | TGTTTCTGGA   | 2460         |
|    |                          |            |              |             |             | AATTTTATCT   | 2520         |
|    |                          |            |              |             |             | TGACCTTGGG   | 2580         |
|    |                          |            |              |             |             | CAATGATAAT   | 2640         |
| 15 |                          |            |              |             |             | GGAGGTACAT   | 2700         |
| 45 |                          |            |              |             |             | ACACGTGACG   | 2760         |
|    |                          |            |              |             |             | TGTTGTTAAC   | 2820         |
|    |                          |            |              |             |             | TGAGGCCAGG   | 2880         |
|    |                          |            |              |             |             | ATCACTAGAA   | 2940         |
| 50 |                          |            |              |             |             | AGTCCGAGAG   | 3000         |
| 50 |                          |            |              |             |             | TTTAGGTCAG   | 3060         |
|    |                          |            |              |             |             | TGTGGATAAA   | 3120         |
|    |                          |            |              |             |             | AGTGTATAAT   | 3180         |
|    |                          |            |              |             |             | CAGCTTTGTG   | 3240<br>3300 |
| 55 |                          |            |              |             |             | GGTGTCGGCT   | 3360         |
| 55 |                          |            |              |             |             | TGGCTCTGGC   | 3420         |
|    |                          |            |              |             |             | TCGACTGGAC   | 3480         |
|    |                          |            |              |             |             | TGTCGTGCCT   | 3540         |
|    |                          |            |              |             |             | TGCACCACAG   | 3600         |
| 60 |                          |            |              |             |             | TGTATCTGTG   | 3660         |
|    |                          |            |              |             |             | GTACAAAATT   | 3720         |
|    |                          |            |              |             |             | CATCACAACT   | 3780         |
|    |                          |            |              |             |             | TACTGTGACA   | 3840         |
|    |                          |            |              |             |             | CCTTGATGAA   | 3900         |
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|    |                          |            |              |             |             | r agccaccgac | 4020         |
|    | AAGGATGAGG               | GCCCCAATG  | AGAAATCTCC   | TACAGCATCO  | AAGACGGGA   | A TGAGCATGGC | 4080         |
|    | AAATTTTTCA               | TCGAACCGA  | AACTGGAGTG   | GTTTCGTCC   | AGAGGTTTT   | CAGCAGCTGGA  | 4140         |
| ~~ |                          |            |              |             |             | A GTCATCAACC | 4200         |
| 70 | ACCAGACTCC               | ATATTGAATC | GATCTCCAAC   | CCCAAACAGT  | CCCTGGAGC   | C CATTTCATTT | 4260         |
|    |                          |            |              |             |             | A CATGATTGGA | 4320         |
|    | GTAATATCTC               | TGGAGCCTC  | TGGCATACCO   | CITTGGTTY   | ACATCACTG   | G TGGCAACTAC | 4380         |
|    |                          |            |              |             |             | A ACCTCTTGAT | 4440         |
| 75 |                          |            |              |             |             | C CACCACTATC | 4500         |
| 75 |                          |            |              |             |             | A GTTTTCTACA |              |
|    |                          |            |              |             |             | T TTTGCAAATC | 4620         |
|    |                          |            |              |             |             | G CAGTAGAGAT | 4680         |
|    |                          |            |              |             |             | A TACTTCTGAG | 4740         |
| 00 |                          |            |              |             |             | G AGATCAAGAT | 4800         |
| 80 |                          |            |              |             |             | C GAATGACCAC |              |
|    |                          |            |              |             |             | C AGCCGTTGGC | 4920         |
|    |                          |            |              |             |             | C TGAAGTGCTG | 4980         |
| •  |                          |            |              |             |             | T TGATCCTGTC |              |
|    | TTGGGCTCT                | TTAAAACTG  | C CAAAGAATT. | A GATCGAAGT | A ACCAAGCGG | A GTATGATTTA | 5100         |
|    |                          |            |              |             |             | 1007         |              |

|            | ATGGTAAAAG | CTACAGATAA  | GGGCAGTCCA  | CCAATGAGTG   | AAATAACTTC  | TGTGCGTATC   | 5160  |
|------------|------------|-------------|-------------|--------------|-------------|--------------|-------|
|            | TTTGTCACAA | TTGCTGACAA  | CGCCTCTCCG  | AAGTTTACAT   | CAAAAGAATA  | TTCTGTTGAA   | 5220  |
|            | CTTAGTGAAA | CTGTCAGCAT  | TGGGAGTTTC  | GTTGGGATGG   | TTACAGCCCA  | TAGTCAATCA   | 5280  |
| _          | TCAGTGGTGT | ATGAAATAAA  | AGATGGAAAT  | ACAGGTGATG   | CTTTTGATAT  | TAATCCACAT   | 5340  |
| 5          |            |             |             | GACTTTGAAA   |             |              | 5400  |
|            |            |             |             | TCCACTAATA   |             |              | 5460  |
|            |            |             |             | ATGCAGGCAG   |             |              | 5520  |
|            |            |             |             | ACAGACAGGA   |             |              | 5580  |
|            |            |             |             | TTGCTTGTAT   |             |              | 5640  |
| 10         |            |             |             | ACTGGTGCTA   |             |              | 5700  |
| 10         |            |             |             | ACCGTCCAAG   |             |              | 5760  |
|            |            |             |             | ACAGTACATG   |             |              | 5820  |
|            |            |             |             | GCATCTCTTT   |             |              | 5880  |
|            |            |             |             | GCTGATTCAA   |             |              | 5940  |
| 15         |            |             |             | AAGTITTCTA   |             |              | 6000  |
| 13         |            |             |             | AGCCGCTACG   |             |              | 6060  |
|            |            |             |             | AAAATTAATG   |             |              | 6120  |
|            |            |             |             |              |             |              | 6180  |
|            |            |             |             | GCGGTAGTGA   |             |              | 6240  |
| 20         |            |             |             | AGTCCAATCA   |             |              | 6300  |
| 20         |            |             |             | AGCCGCACTT   |             |              |       |
|            |            |             |             | GCGTTTGATG   |             |              | 6360  |
|            | GAACATAAGC | CTTCTGCAGT  | GGCCCACGTT  | GTCGTGAAGG   | TCATTGTAGA  | AGACCAAAAT   | 6420  |
|            |            |             |             | TACTACGCCG   |             |              | 6480  |
| 25         |            |             |             |              |             | AAACGGGGAA   | 6540  |
| 23         |            |             |             | CACTTTCAAA   |             |              | 6600  |
|            |            |             |             | TTAAATAAAG   |             |              | 6660  |
|            |            |             |             | GCGGAAGTTA   |             |              | 6720  |
|            |            |             |             | TTCTACAGTG   |             |              | 6780  |
| 20         |            |             |             | GCTAACAGCC   |             |              | 6840  |
| 30         |            |             |             | CAGTTCACTA   |             |              | 6900  |
|            |            |             |             | GCCCACCCGG   |             |              | 6960  |
|            |            |             |             | GAAGTATTTG   |             |              | 7020  |
|            |            |             |             |              |             | GTCTGAGGCA   | 7080  |
| 25         |            |             |             |              |             | AGAACCAAAT   | 7140  |
| 35         |            |             |             |              |             | TTTTCATGTA   | 7200  |
|            |            |             |             |              |             | GTCCCGGCAG   | 7260  |
|            |            |             |             |              |             | TGATGTGATT   | 7320  |
|            |            |             |             |              |             | ACAGATTTAT   | 7380  |
| 40         |            |             |             |              |             | AAAAGCCTAT   | 7440  |
| 40         |            |             |             |              |             | CAATGATCAT   | 7500  |
|            |            |             |             |              |             | GCACCGGCAC   | 7560  |
|            | GCCCTGAAGC | CATTITACAG  | TCTTAACCTG  | TCAGTGTCTG   | ATGGAGTTTT  | TAGAAGTTCC   | 7620  |
|            |            |             |             |              |             | CCTTCAGAAC   | 7680  |
|            | GAATATGAAG | TGGAACTAGC  | TGAAAACGCT  | CCCCTACATA   | CCCTGGTGAT  | GGAGGTGAAA   | 7740  |
| 45         |            |             |             |              |             | AAATGACTTT   | 7800  |
|            | GCCAAAGACA | GATTTTACAT  | AAATGAGAGA  | GGACAGATAT   | TTACTTŢGGĀ  | AAAACTTGAT   | 7860  |
|            | CGAGAAACCC | CGGCGGAGAA  | AGTGATCTCA  | GTCCGTTTAA   | TGGCTAAGGA  | TGCTGGAGGA   | 7920  |
|            |            |             |             |              |             | TGCACCACAA   | 7980  |
| ~^         |            |             |             |              |             | GACTTCAGTC   | 8040  |
| 50         |            |             |             |              |             | TGCCATTGAA   | 8100  |
|            |            |             |             |              |             | CGTAATCACT   | 8160  |
|            |            |             |             |              |             | TAGAGCTGTG   | 8220  |
|            |            |             |             |              |             | CCTTCCACCG   | 8280  |
| E E        |            |             |             |              |             | AGAGGACGTG   | 8340  |
| 55         |            |             |             |              |             | TCTTTACAGC   | 8400  |
|            |            |             |             |              |             | TGACAGACAG   | 8460  |
|            |            |             |             |              |             | GTATCAGITT   | 8520  |
|            |            |             |             |              |             | AGATGTTAGT   | 8580  |
| 60         |            |             |             |              |             | ATATGAGGCA   | 8640  |
| 60         |            |             |             |              |             | ATCTGATGCT   | 8700  |
|            |            |             |             |              |             | TGTGGAAGTC   | 8760  |
|            |            |             |             |              |             | GGAACTTGAC   | 8820  |
|            |            |             |             |              |             | TGAAAAGATC   | 8880  |
| <b>C</b> E |            |             |             |              |             | TAGTCCACCA   | 8940  |
| 65         |            |             |             |              |             | AGGTGGGGTG   | 9000  |
|            |            |             |             |              |             | AGTTACATAT   | 9060  |
|            |            |             |             |              |             | A GAATGAATGG | 9120  |
|            |            |             |             |              |             | TCTTACTATC   | 9180  |
| 70         |            |             |             |              |             | r TCTGGATGCA | 9240  |
| 70         |            |             |             |              |             | C TGAAGACGTC | 9300  |
|            | CTTCCTGGA  | AATTGATCA   | r GCAGATCTC | r gctacagaco | CAGACATCO   | G CTCTAACGCT | 9360  |
|            |            |             |             |              |             | A TCCAGACACA | 9420  |
|            |            |             |             |              |             | A TCATCTTCTC | 9480  |
| 7.         |            |             |             |              |             | T CACGCTAGAA | 9540  |
| 75         |            |             |             |              |             | C CGTGTTTGAA | 9600  |
|            |            |             |             |              |             | A CGCAGGATTA | 9660  |
|            |            |             |             |              |             | C CATTAACGAA | 9720  |
|            |            |             |             |              |             | C AGTATACACC | 9780  |
| 00         |            |             |             |              |             | C TGGCACTGTG | 9840  |
| 80         |            |             |             |              |             |              | 9900  |
|            |            |             |             |              |             | A TGCAGCAAGT | 9960  |
|            |            |             |             |              |             | A TGAACATGGG |       |
|            |            |             |             |              |             | T GGATTATGAG |       |
|            | AGCTCTCAT  | G AGTATTACC | T AACAGTAGA | G GCCACTGAT  | G GAGGCACGC | C TTCACTGAGC | 10140 |
|            |            |             |             |              |             |              |       |

|     |            | CTGTGAACGT                   |              |             |              |                              | 10200          |
|-----|------------|------------------------------|--------------|-------------|--------------|------------------------------|----------------|
|     |            | ACACGACAGT                   |              |             |              |                              | 10260          |
|     |            | ATGATGCCGA<br>GAAGCTCGTT     |              |             |              |                              | 10320<br>10380 |
| 5   |            | GAGAAACGAT                   |              |             |              |                              | 10440          |
|     | AGTCCACCCA | GAGTCAACAC                   | GACGACCGTG   | AACATCGATG  | TGTCCGATGT   | CAATGACAAC                   | 10500          |
|     |            | TCTCCAGGGG<br>TGCAGCTGGT     |              |             |              |                              | 10560<br>10620 |
|     |            | TTGTAACTGG                   |              |             |              |                              | 10680          |
| 10  | CTCCTGACAT | CATCTGCCAT                   | CAAGAGGAAG   | GAGAAAGATC  | ATTACTTACT   | GCAGGTGAAG                   | 10740          |
|     | GTGGCAGATA | ATGGAAAGCC<br>TCTATCCGCC     | TCAGTTGTCA   | TCTTTGACAT  | ACATTGACAT   | TAGGGTAATT                   | 10800<br>10860 |
|     |            | CAGGTGGCGT                   |              |             |              |                              | 10920          |
| 1.5 | ACTCTAACCT | ACAGTCTCGA                   | CCCTCAGATG   | GACAACCTGT  | TCTCTGTTTC   | CAGCACAGGG                   | 10980          |
| 15  |            | TAGCACACAA                   |              |             |              |                              | 11040<br>11100 |
|     |            | ACCACACCAT                   |              |             |              |                              | 11160          |
|     | GGTGACTACT | GGCGCAACTT                   | CCAGCGAGCT   | TTACGGAACA  | TCCTGGGTGT   | GAGGAGGAAC                   | 11220          |
| 20  |            | TTGTTAGTTT                   |              |             |              |                              | 11280          |
| 20  |            | AACCAGGTAG<br>CTGACATTGA     |              |             |              |                              | 11340<br>11400 |
|     |            | GACTGGACTG                   |              |             |              |                              | 11460          |
|     | AGTGTGATGT | CAACACACAG                   | CACAGCCAGA   | CTGAGTTTTG  | TGACTCCCCG   | CCACCACAGG                   | 11520          |
| 25  |            | GTCTCTGCAA<br>CTGAGGGATC     |              |             |              |                              | 11580<br>11640 |
| 23  |            | GCGGCAGGTT                   |              |             |              |                              | 11700          |
|     | AACAGCTACG | TGAAATACCG                   | TCTGACGGAA   | AATGAAAACA  | AATTAGAGAT   | GAAACTGACC                   | 11760          |
|     |            | GAACATATTC<br>AGATTCATCA     |              |             |              |                              | 11820<br>11880 |
| 30  |            | CTGTTCAGAG                   |              |             |              |                              | 11940          |
|     | GAAGTGAATG | GAAACTATGC                   | TCGCTTGGTT   | CTAGACCAAG  | TTCATACTGC   | ATCGGGCACA                   | 12000          |
|     |            | CTCTGAAAAC<br>GAACAAGGCA     |              |             |              |                              | 12060<br>12120 |
|     |            | TTTATTTGAA                   |              |             |              |                              | 12180          |
| 35  | GCACACATCG | AAGAGTCGGT                   | GGATGTATCT   | CCAGGCTGCT  | TCCTGACGGC   | CACGGAAGAC                   | 12240          |
|     |            | ACCCTTGCCA                   |              |             |              |                              | 12300<br>12360 |
|     | TACTGCAAAT | GCAGTGCCTT<br>CATGCCTCTA     | TGGGGGCACG   | TGTGTTGTCG  | ACAACGGAGG   | CTTTGTTTGC                   | 12420          |
| 40  | CAGTGTAGAG | GATTATATAC                   | TGGTCAGAGG   | TGTCAGCTTA  | GTCCATACTG   | CAAAGATGAA                   | 12480          |
| 40  | CCCTGTAAGA | ATGGCGGAAC                   | ATGCTTTGAC   | AGTTTGGATG  | GCGCCGTTTG   | TCAGTGTGAT                   | 12540<br>12600 |
|     |            | GGGGAGAAAG<br>CCCTCTGTGA     |              |             |              |                              | 12660          |
|     |            | GTCACTGCGA                   |              |             |              |                              | 12720          |
| 45  |            | CGGAAGGAAT                   |              |             |              |                              | 12780<br>12840 |
| 43  |            | TTCTCTGCCG                   |              |             |              |                              | 12900          |
|     |            | ACATTACTO                    |              |             |              |                              | 12960          |
|     |            | TTCCAAGTGA                   |              |             |              |                              | 13020<br>13080 |
| 50  | AAAGCAGTG  | G AGCATCCCGA<br>G CGGTCTGCAG | CTTCAGCACT   | AACCTGCCTC  | CCCCACCCC    | CGGGCACCGA                   | 13140          |
| •   | CCTTCTGAC  | GCGACTCCAT                   | CCAGAAGCCT   | AGCTGGGACT  | TTGACTATGA   | CACAAAAGTG                   | 13200          |
|     |            | ATCCCTGTCT                   |              |             |              |                              | 13260          |
|     |            | G AAAGCCTGTC<br>G GGTATCACTG |              |             |              |                              | 13320<br>13380 |
| 55  |            | TCCCCAACTA                   |              |             |              |                              | 13440          |
|     |            | A TOGATACGGA                 |              |             |              |                              | 13500          |
|     | AATCACTCTT | 3 AAGACTTCCC<br>3 AATCCATCCA | CCCTCCTAGE   | GAGCTACCAC  | CCGCGGGTAG   | CGAATTCAGC                   | 13560<br>13620 |
|     | TCATCAAGA  | A ACCGGCAGAG                 | GTTCAACTTC   | AATCAGTATI  | TGCCCAATTI   | TTATCCCCTC                   | 13680          |
| 60  | GATATGTCT  | G AACCTCAAAC                 | AAAAGGCAC    | GGTGAGAATA  | GTACTTGTAG   | AGAACCCCAT                   | 13740          |
|     |            |                              |              |             |              | GAGCATGCCC<br>CGAAGTGGAG     | 13800<br>13860 |
|     | TCCGAGGTC  | A TGATGAGTGA                 | CTATGAGAGG   | GGGGACGACG  | GCCACTTCGA   | AGAGGTGACG                   | 13920          |
| 65  |            |                              |              |             |              | CCCCAAAGTG                   | 13980          |
| U.J |            |                              |              |             |              | CGCCTCTGGA                   | 14040<br>14100 |
|     |            |                              |              |             |              | CGGCTGTGCC                   | 14160          |
|     |            |                              |              |             |              | ACGAAAAATC                   | 14220          |
| 70  |            |                              |              |             |              | TAATTTTCCT AACTAGATTT        | 14280<br>14340 |
| ,,  |            |                              |              |             |              | CATTATCTAG                   | 14400          |
|     |            |                              |              |             |              | TCCACTGAAG                   | 14460          |
|     |            |                              |              |             |              | A CATAGGATGA<br>A ATTATAAACA | 14520<br>14580 |
| 75  |            |                              |              |             |              | ACCAAAACCA                   |                |
|     | CCATGACAC  | A GITTTTATA                  | G TGTCTGTAT. | A TTTGTGATG | C AATGGTCTTY | TAAAGGTTTT                   | 14700          |
|     | TAATGAAAA  | C TACCATTAG                  | C CAGTCTTTC  | T TACTGACAA | AAATTATTA    | A TAAAAT                     | 14756          |
| 80  |            | : C161 DNA                   |              | 4220 1      |              |                              |                |
|     |            | quence: 102                  |              |             |              |                              |                |
|     | 1          | 11                           | 21           | 31          | 41           | 51                           |                |
|     | 1          | 11<br>                       | 1            | Ĩ.          | 41<br>       | 1                            |                |
|     | •          | •                            | •            | '           | ,            | •                            |                |
|     |            |                              |              |             |              | 1299                         |                |

|            | GTGGTGTTTG   |  |   |  |   |   | 60   |
|------------|--|--|---|--|---|---|--|
|            | CTGAAGACAA   | AGAGAAGGGG   | GAGAAAACCT  | AGCAGACCAC   | CATGTGCTAT  | GGGAAGTGTG  | 120  |
|            | CACGATGCAT   | CGGACATTCT   | CTGGTGGGGC  | TCGCCCTCCT   | GTGCATCGCG  | GCTAATATTT  | 180  |
|            | TGCTTTACTT   |  |   |  |   |   | 240  |
| 5          |  |  |   |  |   |   |  |
| J          | TGTGGTTCTT   |  |   |  |   |   | 300  |
|            | TCATTGGGCT   | GGAACAGGAT   | GACTGCTGTG  | GCTGCTGTGG   | CCATGAAAAC  | TGTGGCAAAC  | 360  |
|            | GATGTGCGAT   | GCTTTCTTCT   | GTATTGGCTG  | CTCTCATTGG   | AATTGCAGGA  | TCTGGCTACT  | 420  |
|            | GTGTCATTGT   |  |   |  |   |   | 480  |
|            |  |  |   |  |   |   |  |
| 10         | AGTGGAACTA   | CACCTTTGCC   | AGCACCGAGG  | GCCAGTACCT   | TCTGGATACC  | TCCACATGGT  | 540  |
| 10         | CCGAGTGCAC   | TGAACCCAAG   | CACATTGTGG  | AATGGAATGT   | ATCTCTGTTT  | TCTATCCTCT  | 600  |
|            | TGGCTCTTGG   |  |   |  |   |   | 660  |
|            |  |  |   |  |   |   |  |
|            | GAGGCATATG   |  |   |  |   |   | 720  |
|            | CCAGGACAGA   | GCCACAATCT   | TCCTCTATTT  | CATTGTAATT   | TATATATTTC  | ACTTGTATTC  | 780  |
|            | ATTTCTAAAA   | CTTTGTATTA   | GTGTAACATA  | CTCCCCACAG   | מדידדים מידים א   | CANACTOCTIC   | 840  |
| 15         |  |  |   |  |   |   |  |
| 13         |  |  |   | GTTTAAATTT   |   |   | 900  |
|            | GTTTATTTGT   | TTTTGTTTTT   | TTTTAAGGAA  | TGAGGAAACA   | AACCACCCTC  | TGGGGGTAGT  | 960  |
|            | TTACAGACTG   | AGTGACAGTA   | CTCAGTATAT  | CTGAGATAAA   | CTCTATAATG  | TTTTGGATAA  | 1020   |
|            |  |  |   | GTGCATGTAT   |   |   | 1080   |
|            |  |  |   |  |   |   |  |
| 20         |  |  |   | AATCCGACAA   |   |   | 1140   |
| 20         | CACTGCTTGT   | ATGATGTTTC   | CCATTCATAC  | ACCTATAAAT   | CTCTAACAAG  | AGGCCCTTTG  | 1200   |
|            |  |  |   | TTTACTTAGA   |   |   | 1260   |
|            |  |  |   |  |   |   |  |
|            |  |  |   | TACAATGCTG   |   |   | 1320   |
|            | GAGATTCAAA   | TTTTTCTAAC   | ATATGGAAAG  | CCTTTTGTCC   | TCCAAAGATG  | AGTACTAGGG  | 1380   |
|            | ATCATGTGTT   | TAAAAAAAGA   | AAGGCTACGA  | TGACTGGGCA   | AGAAGAAAGA  | TGGGAAACTG  | 1440   |
| 25         |  |  |   | ATGGGGACGA   |   |   |  |
| 25         |  |  |   |  |   |   | 1500   |
|            | AGGAAATACC   | CTCAAAACTA   | ACTTGTTTAC  | AACAAAATAA   | AGTATTCACT  | ACGAAAAAA   | 1560   |
|            | AAAAAAAAA  | AAAAAAAAA  | AAA   |  |   |   | 1583   |
|            |  |  |   |  |   |   |  |
|            | a  |  |   |  |   |   |  |
| 20         | seq ID NO:   | C162 DNA Se  | equence   |  |   |   |  |
| 30         | Nucleic Aci  | ld Accession   | 1 #: NM 003   | 759.1  |   |   |  |
|            |  | ence: 150  |   |  |   |   |  |
|            | couring negl   | ACACC. 250   |   |  |   |   |  |
|            |  |  |   |  |   |   |  |
|            | 1  | 11   | 21  | 31   | 41  | 51  |  |
|            | 1  | 1  | 1   | 1  | 1   | 1   |  |
| 35         |  | NON CROWCE CA  | CACAAMMOOGA   | GTGCTGTCCT   | TOTOTO A CAROLI   | COMCONONNO  | 60   |
| 55         |  |  |   |  |   |   |  |
|            |  |  |   | GAAGGGCTTT   |   |   | 120  |
|            | TTGGGGATTT   | GGGAGGCTTA   | GCAGGAAAGA  | TGTCCACTGA   | AAATGTGGAA  | GGGAAGCCCA  | 180  |
|            | GTAACCTTGG   | GGAGAGAGGA   | AGAGCCCCGGA   | GCTCCACTTT   | CCTCAGGGTT  | GTCCAGCCAA  | 240  |
|            |  |  |   |  |   |   |  |
| 40         |  |  |   | TCTCTCCTGC   |   |   | 300  |
| 40         | TCTTGGGAGA   | GGAGGATGAC   | AGCCCAGCTC  | CCCCTCAGCT   | CTTCACGGAA  | CTGGATGAGC  | 360  |
|            | TECTECCCET   | GGATGGGCAG   | GAGATGGAGT  | GGAAGGAAAC   | AGCCAGGTGG  | ATCAACTTTC  | 420  |
|            |  |  |   |  |   |   |  |
|            |  |  |   | GGAGCAAGCC   |   |   | 480  |
|            | TTCATAGTTT   | ATTTGAGCTG   | AGGACATGTA  | TGGAGAAAGG   | ATCCATCATG  | CTTGATCGGG  | 540  |
|            | AGGCTTCTTC   | TCTCCCACAG   | TTGGTGGAGA  | TGATTGTTGA   | CCATCAGATT  | GAGACAGGCC  | 600  |
| 45         |  |  |   | CCTATACTTT   |   |   |  |
| 73         |  |  |   |  |   |   | 660  |
|            | AAACCAAGAA   | ATCCAACCTT   | CGGTCCCTGG  | CTGACATTGG   | GAAGACAGTC  | TCCAGTGCAA  | 720  |
|            | GTAGGATGTT   | TACCAACCCT   | GATAATGGTA  | GCCCAGCCAT   | GACCCATAGG  | AATCTGACTT  | 780  |
|            |  |  |   |  |   | AATAAGTTCA  | 840  |
|            |  |  |   |  |   |   |  |
| 50         |  |  |   | CCAACGTGCT   |   |   | 900  |
| 50         | TGGATACTCC   | TTTCATTGCC   | TTTGTTAGGC  | TACAGCAGGC   | TGTCATGCTG  | GGTGCCCTGA  | 960  |
|            | CTGAAGTTCC   | TETECCCACA   | <b>PCCホルヘルルCホ</b>   | TCATTCTCTT   | ACCTOTANG   | CCCDDACCCD  | 1020   |
|            |  |  |   |  |   |   |  |
|            |  |  |   |  |   | GTGTTCCATG  | 1080   |
|            | ACATTGCTTA   | TAAAGCAAAA   | GACAGGCACG  | ACCTGATTGC   | TGGTATTGAT  | GAGTTCCTAG  | 1140   |
|            | ATGAAGTCAT   | CGTCCTTCCA   | CCTGGGGAAT  | GGGATCCAGC   | AATTAGGATA  | GAGCCTCCTA  | 1200   |
| 55         |  |  |   |  |   | AATGTTCAGA  | 1260   |
| -          |  |  |   |  |   |   |  |
|            |  |  |   |  |   | GATTGTGAAG  | 1320   |
|            | AATTGCAGCG   | AACTGGACGG   | TTCTGTGGTG  | GACTAATTAA   | AGACATAAAG  | AGGAAAGCGC  | 1380   |
|            | CATTTTTTGC   | CAGTGATTTT   | TATGATGCTT  | TARATATTCA   | AGCTCTTTCG  | GCAATTCTCT  | 1440   |
|            |  |  |   |  |   | GGGGATGCCA  | 1500   |
| 60         |  |  |   |  |   |   |  |
| 00         |  |  |   |  |   | GGAGCCATCT  | 1560   |
|            |  |  |   |  |   | GTCCTAGTTT  | 1620   |
|            | TTGAGAGGCT   | TCTATTTAAT   | TTCAGCAAGG  | ACAATAATTT   | TGACTATTTG  | GAGTTTCGCC  | 1680   |
|            | <b>ተተጥረር አ</b> ተጥረር  | COTOTOCOTO   | COOTTOTAL   | CITCH CATHER   | CCTACCCACT  | GATGCCAGCT  | 1740   |
|            |  |  |   |  |   | ATTAGCTTCA  |  |
| 65         | TCTTGGTTCA   | ATACTICACA   | CGTTTCACGG  |  | TTCCTCTCTG  |   | 1800   |
| 65         |  |  |   |  |   |   | 1860   |
|            |  | TGATGCTTTC   |   |  |   |   | 7000   |
|            |  | TGATGCTTTC   |   |  |   |   |  |
|            | CCAACTTCAA   | TGATGCTTTC   | AACACTCTCT  | TTTCCTGTAC   | CTGTGTGCCA  | CCTGACCCAG  | 1920   |
|            | CCAACTTCAA<br>CTAATATCTC   | TGATGCTTTC<br>AGTGGGCTAC<br>AATATCTAAT   | AACACTCTCT GACACCACAC   | TTTCCTGTAC   | CTGTGTGCCA<br>GTATTTGCCA  | CCTGACCCAG<br>ACTATGTCTT  | 1920<br>1980   |
|            | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACAT   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT  | AACACTCTCT GACACCACAC ACTACCTTTG  | TTTCCTGTAC<br>TGGCCCCAGA<br>ACTGGGCATT   | CTGTGTGCCA<br>GTATTTGCCA<br>TTTGTCGAAG  | CCTGACCCAG<br>ACTATGTCTT<br>AAGGAGTGTT  | 1920<br>1980<br>2040   |
| <b>~</b> ^ | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACAT   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT  | AACACTCTCT GACACCACAC ACTACCTTTG  | TTTCCTGTAC<br>TGGCCCCAGA<br>ACTGGGCATT   | CTGTGTGCCA<br>GTATTTGCCA<br>TTTGTCGAAG  | CCTGACCCAG<br>ACTATGTCTT  | 1920<br>1980<br>2040   |
| 70         | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACAT<br>CAAAATACGG   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT AGGAAACCTT   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA   | TTTCCTGTAC<br>TGGCCCCAGA<br>ACTGGGCATT<br>ACTGTAATTT   | CTGTGTGCCA<br>GTATTTGCCA<br>TTTGTCGAAG<br>TGTTCCTGAT  | CCTGACCCAG<br>ACTATGTCTT<br>AAGGAGTGTT<br>ATCACACTCA  | 1920<br>1980<br>2040<br>2100   |
| 70         | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACAT<br>CAAAATACGG<br>TGTCTTTTAT   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT AGGAAACCTT CCTCTTCTTC  | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA  | TTTCCTGTAC<br>TGGCCCCAGA<br>ACTGGGCATT<br>ACTGTAATTT<br>CCTCTTCCAT   | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAA  | CCTGACCCAG<br>ACTATGTCTT<br>AAGGAGTGTT<br>ATCACACTCA<br>AAATTCAAAA  | 1920<br>1980<br>2040<br>2100<br>2160   |
| 70         | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACAT<br>CAAAATACGG<br>TGTCTTTTAT<br>CTAGTCCTTA   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT AGGAAACCTT CCTCTTCTTG TTTTCCAACC   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA  | TTTCCTGTAC TGGCCCCAGA ACTGGGCATT ACTGTAATTT CCTCTTCCAT AACTGATCAG  | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAA  | CCTGACCCAG ACTATGTCTT AAGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT   | 1920<br>1980<br>2040<br>2100<br>2160<br>2220   |
| 70         | CCAACTTCAA CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CTAGTCCTTA CCATTCTCAT   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT AGGAAACCTT CCTCTTCTTC TTTTCCAACC   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACAGCAAGAA ATAGATGCCC  | TTTCCTGTAC TGGCCCCAGA ACTGGGCATT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT   | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAA TGATTTTGCC   | CCTGACCCAG ACTATGTCTT AAGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTG  | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280   |
| 70         | CCAACTTCAA CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CTAGTCCTTA CCATTCTCAT   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT AGGAAACCTT CCTCTTCTTC TTTTCCAACC   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACAGCAAGAA ATAGATGCCC  | TTTCCTGTAC TGGCCCCAGA ACTGGGCATT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT   | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAA TGATTTTGCC   | CCTGACCCAG ACTATGTCTT AAGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT   | 1920<br>1980<br>2040<br>2100<br>2160<br>2220   |
|            | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACAT<br>CAAAATACGG<br>TGTCTTTTAT<br>CTAGTCCTTA<br>CCATTCTCAT<br>TGCCAAGTGA   | TGATGCTTTC AGTGGGCTAC AATATCTAAT GTACCATAAT AGGAAACCTT CCTCTTCTTC TTTTCCAACC CTTTTGTGTA GTTCAAGCCC   | ACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACAGCAAGAA ATAGATGCCAA  | TTTCCTGTAC TGGCCCCAGA ACTGGGCATT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT ACCGAGGTTG  | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAA TGATTTTGCC GGACACCCCA GTTCGTTCCA   | CCTGACCCAG ACTATGTCTT AAGGAGTGTT ATCACACTCA AAAATTCAAAA ATTATCTTGT AAACTAATTG   | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340   |
|            | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACAT<br>CAAAATACGG<br>TGTCTTTTAT<br>CTAGTCCTTA<br>CCATTCTCAT<br>TGCCAAGTGA<br>AAAACCCCTG   | TGATGCTTTC AGTGGGCTAC AGTAGCATAAT GTACCATAAT AGGAAACCTT CCTCTTCTTC ATTTTCCAACC CTTTTTGTAA AGTCAAGCCA GTCAAGCCA GTCGAGTGTGC   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACAGCAAGAA ACAGCACACA ACAGCACACA CTTGCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC  | TTTCCTGTAC TGGCCCAGA ACTGGGCATT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT ACCGAGGTTG CTATCCCGGC  | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAT TGATTTTGCC GGACACCCCA GTTCGTTCCA TTTGTTGTCC  | CCTGACCCAG ACTATGTCTT AAGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTG ACCTTTTGGAG ACTATACTGA   | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2400   |
| 70<br>75   | CCAACTTCAA<br>CTAATATCTC<br>CTACTGACTC<br>CAAATACGG<br>TGTCTTTTAT<br>CTAGTCCTTA<br>CCATTCTCAT<br>TGCCAAGTGA<br>AAACCCCTC<br>TTTTCATGGA   | TGATGCTTTC AGTGGGCTAC AGTAGCATAAA GGAAACCTT CCTCTTCTTC ATTTCCAACC CTTTTGTAGCCC GGTGGGTGTGG CCAACAAAT   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACAGCAGAA ATAGATGCCC ACAAGTCCAA CTTGCTGCTC ACAGCTGTGC  | TTTCCTGTAC TGGCCCCAGA ACTGGCCAT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT ACCGAGGTTG CTATCCCGGC  | CTGTGTGCCA GTATTTGCCA GTTTCCTGAT GGCTCTGAA TGATTTGCC GGACACCCCA GTTCGTTCCC TTTGTTGGTC GAAAGAACAT  | CCTGACCCAG ACTATGTCTT AAGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTG ACTATATGGGG CACTATACTGAGA AACTCAAGA  | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2400<br>2460   |
|            | CCAACTTCAA CTAATATCTC CTACTGACAI CAAAATACGG TGTCTTTTAT CTAGTCCTTA CCATTCTCAT TGCCAAGTGA AAAACCCCTT TTTTCATGGAAAACCCAAGTGAAAACCCAAGTGAAAACCCAAGAGAAAACCAAGAAAACCAAGAAAAACCAAGAAAAACCAAGAAAAACCAAGAAAAACAAAAAA   | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GTACCATAAT AGGAAACCTT CCTCTTCTTG TTTTCCAACC CTTTTGGTA GTTCAAGCCS GTGGGTGTGG CCAACAAAT GTATCACTTC   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGGACCTACA ACAGCAAGAA ATAGATCCAA CTTGCTGCTACA CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  | TTTCCTGTAC TGGCCCCAGA ACTGGCATT ACTGTAATTT ACTGTTACAGG TAGTAGGCGT ACCGAGGTTG CTTACCCGG TTGTAAACAG  | CTGTGTGCCA GTATTTGCCA GTATTTGCGAAG TGTTCCTGATA GGCTCTGAAA TGATTTTGCC GGACACCCCA GTTCGTTCCA TTGTTGGTTCCA GAAGAACAT CCTCATGGTT CCTCATGGTT   | CCTGACCCAG ACTATGTCTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTGG CCGTTTGGAG ACTATACTGA AAACTCAAGA ATATGCTCCC  | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2400   |
|            | CCAACTTCAA CTAATATCTC CTACTGACAI CAAAATACGG TGTCTTTTAT CTAGTCCTTA CCATTCTCAT TGCCAAGTGA AAAACCCCTT TTTTCATGGAAAACCCAAGTGAAAACCCAAGTGAAAACCCAAGAGAAAACCAAGAAAACCAAGAAAAACCAAGAAAAACCAAGAAAAACCAAGAAAAACAAAAAA   | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GTACCATAAT AGGAAACCTT CCTCTTCTTG TTTTCCAACC CTTTTGGTA GTTCAAGCCS GTGGGTGTGG CCAACAAAT GTATCACTTC   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGGACCTACA ACAGCAAGAA ATAGATCCAA CTTGCTGCTACA CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  | TTTCCTGTAC TGGCCCCAGA ACTGGCATT ACTGTAATTT ACTGTTACAGG TAGTAGGCGT ACCGAGGTTG CTTACCCGG TTGTAAACAG  | CTGTGTGCCA GTATTTGCCA GTATTTGCGAAG TGTTCCTGATA GGCTCTGAAA TGATTTTGCC GGACACCCCA GTTCGTTCCA TTGTTGGTTCCA GAAGAACAT CCTCATGGTT CCTCATGGTT   | CCTGACCCAG ACTATGTCTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTGG CCGTTTGGAG ACTATACTGA AAACTCAAGA ATATGCTCCC  | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2400<br>2460<br>2520   |
|            | CCAACTTCAA<br>CTAATATCTC<br>CAAAATACGG<br>TGTCTTTTAT<br>CTAGTCCTTA<br>TGCCAAGTGA<br>AAACCCCTC<br>TTTTCATGGA<br>AAGGAGCAG<br>TCATGGCTCT   | TGATGCTTTC AGTGGGCTAC AGTGGGCTAC GTACCATAAT GGAAACCTT CCTCTTCTAC TTTTCCAACC CTTTTGGTAC GTTCAAGCC GTGGGTGGAC CCAACAAATT TCCGTGCTAC TCCGTGGTAT   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACTAGATGACC ACTAGATGCCA ACTAGATGCCA ACTAGATGCTGTGT ACTAGATGTCTTTT GTTAGCTGCTTTTT GTTAGCTGCTTCTTTT  | TTTCCTGTAC TGGCCCAGA ACTGGGCATT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT ACCGAGGTTG CTATCCCGGC TTGTAAACAG GGGTGGCAT   | CTGTGTGCCA GTATTTGCCA GTATTTGCCGAAA TGTTCCTGAAA GGCTCTGAAA GGACACCCCA GGTCGTTCCA TTTGTTCGT GGAAGAACAT CCTCATGGTT CATTGCTCA  | CCTGACCCAG ACTATGTCTT AAGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTG CCGTTTGGAG ACTATACTGA AAACTCAAGA ATATGCTCCC ATGGACAGTT   | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2400<br>2460<br>2520<br>2580                                 |
|            | CCAACTTCAA CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CCATTCTCAT TGCCAAGTTAT AAAACCCCTC TTTTCATGGA AAGGAGCACC TCATGGCTCT TGATGGCTCT TGATGGCTCT TGATGGCTCT TGATGGCTCT TGATGGCTCT TGATGGCTCT TGATGGCTCT TGATGGCTCT TGATGGCTCT   | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GGAAACCTT CCTCTTCTGGTA AGTTCAAGCG CTTTTGGTA GGTCAACCACAAAT GGTATCAACCT TCCGTGGTAG CCAACAAAT GGTATCACCTT TCCGTGGTAA   | AACACTCTCT GACACCACAC ACTACCTTG GTCGGGAACA GGAACCTACG GCAAGAA ATAGATGCCA ACAGTCCAA ACAGCTGCTG ACAGCTGCTG TGCTGCTGCTG TGCTGCTGCTGCTG TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  | TTTCCTGTAC TGGCCCCAGG ACTGGGCATT ACTGTAATTT ACTGTAATTT ACTGTACGGG TAGTAGGCGT ACCGAGGTTG ACCGAGGTCAC ACTGTAAACAG ACGGGCCAT  | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAA TGATTTTGCC GGACCCCA GTTCGTTCCA TTTGTTGGTC GAAGAACAT CCTCATGGTT CATTGCTCA AAGTTTCTCA AAGTTTCTCA AAGTTTCTCA AAGTTTCTCA AAGTTTCTCA AAGTTTCTCA AAGTTTCTCAC AAAGTTTCTCAC AAAGTTTCTCAC  | CCTGACCCAG ACTATGTCTT ARGAGGTGTT ATCACACTCA ARATTCARAA ATTATCTGT ARACTARTTG CCCTTTGGAG ACTATACTGA ARACTCARGA ATATGCTCAC ATGACAGTT GGAGTGACGGG   | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2460<br>2520<br>2580<br>2640                                 |
| 75         | CCAACTTCAA CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CTAGTCCTTA CCAATTCTCAT TGCCAAGTGGA AAAACCCCTT TTTTCATGGA AAGGAGCAGC TCATGGCTCT TGAAGATGGCTCT TGAAGATGGA AACAAGAGT   | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GTACCATAAT AGGAAACCTT CCTCTTCTTGT CTTTTGTGTA GGTGGGTGTGC CCAACAAATT GTATCACTTC TCCGTGGTAT GGAACACAAC CCACGGAACC CACGGAACC CACTGGAACC   | AACACTCTCT GACACCACAC ACTACCTTG GTCGGGAACA GGAACCTACG GCAGACACA ACAGACCACA ACAGGTCCAA ACAGCTGCTGC ACAGCTGTGT GCACCTCTTTT GTAGCTGCTGC CTTGCTGCTCTTT TCTGCACCCC CTTGTGTTTT  | TTTCCTGTAC TGGCCCCAGE ACTGGGCATT ACTGTAATTT ACTGTTCCAT AACTGATCAG TAGTAAGCGTTG TATTACCAGE TTGTAAACAG GGGTGGCCAT ACGGTCATCCAG TGGTAAACAG GGGTAGACACCA TTGTAAACAG TGGTAAACAG TGGTAAACAG TGGTAAACAC   | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAA GGCTCTGAAA GGACCCCA GTTCGTTCCA GTTCGTTCCA TTTGTTGGTC GAAAGAACAT CCTCATGGTT CATTGCTCA AAAGTTTCAA  | CCTGACCCAG ACTATGTCTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTGG CCGTTTGGAG ACTATACTGA AAACTCAAGA ATATGCTCCC ATCGACAGT GGAGTGAGGG TTTATGGCCC  | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2400<br>2460<br>2520<br>2580                                 |
|            | CCAACTTCAA CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CTAGTCCTTA CCAATTCTCAT TGCCAAGTGGA AAAACCCCTT TTTTCATGGA AAGGAGCAGC TCATGGCTCT TGAAGATGGCTCT TGAAGATGGA AACAAGAGT   | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GTACCATAAT AGGAAACCTT CCTCTTCTTGT CTTTTGTGTA GGTGGGTGTGC CCAACAAATT GTATCACTTC TCCGTGGTAT GGAACACAAC CCACGGAACC CACGGAACC CACTGGAACC   | AACACTCTCT GACACCACAC ACTACCTTG GTCGGGAACA GGAACCTACG GCAGACACA ACAGACCACA ACAGGTCCAA ACAGCTGCTGC ACAGCTGTGT GCACCTCTTTT GTAGCTGCTGC CTTGCTGCTCTTT TCTGCACCCC CTTGTGTTTT  | TTTCCTGTAC TGGCCCCAGE ACTGGGCATT ACTGTAATTT ACTGTTCCAT AACTGATCAG TAGTAAGCGTTG TATTACCAGE TTGTAAACAG GGGTGGCCAT ACGGTCATCCAG TGGTAAACAG GGGTAGACACCA TTGTAAACAG TGGTAAACAG TGGTAAACAG TGGTAAACAC   | CTGTGTGCCA GTATTTGCCA TTTGTCGAAG TGTTCCTGAT GGCTCTGAAA GGCTCTGAAA GGACCCCA GTTCGTTCCA GTTCGTTCCA TTTGTTGGTC GAAAGAACAT CCTCATGGTT CATTGCTCA AAAGTTTCAA  | CCTGACCCAG ACTATGTCTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTGG CCGTTTGGAG ACTATACTGA AAACTCAAGA ATATGCTCCC ATCGACAGT GGAGTGAGGG TTTATGGCCC  | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2280<br>2340<br>2460<br>2520<br>2580<br>2640                                 |
| 75         | CCAACTTCAA CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CTAGTCCTTAT TGCCAAGTGF AAAACCCCTT TTTTCATGGG TAGGGGCAG TCATGGCTCT TCATGGCTCT TCATGGCTCT TCATGGCTCT CCATCTTGAA   | TGATGCTTTC AGTGGGCTAC AGTGGGCTAC GTACCATAAT GGAAACCTT TTTTCCAACC CTTTTGTGTA GGTGGGTGG CCACAAAAT GGTACAACAAAT TGATCAACCTC TCCGTGGTAA AGACAGAACCT CACGGAACACC CTCCGTGGTAA  | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACAGCAGGA ACAGGTGCA ACAGGTGCA ACAGCTGTGT GTTGCTGCT GTAGCTCTTTT GTAGCTGCTT TCTGCACCT ATGCTGTTTT ATGCCCTGTAGT ATGCCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ATGCCTGTAGT ACACCTCTT | TTTCCTGTAC TGGCCCAGA ACTGGCATT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT CTATCCGGC TTGTAAACA CGGCGCTTG CGGTCATCTC GGGTGGCCAT CGGTCATCTC CGGTCATCTC CGGTCATCTC CGGTCATCTC CGTCATCTGCC TTCTGAACACC TTCTGAACACC TTCTGATGGTGT  | CTGTGTGCCA GTATTTGCCA TTTGTCGAAA TGATTTGCCAA GGCTCTGAAA TGATTTTGCC GGACACCCCA GTTCGTTCCA TTTGTTGGTC GAAAGAACAC CATTGCTCAC CATTGCTCAC CATTGCTCAC AAAGTTCTC GTTCCTGTAC GTTCCTGTAC GTTCCTGTAC GTTCCTGTAC GTTCCTGTAC GTTCCTGTAC   | CCTGACCCAG ACTATGTCTT ARGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTG CCGTTTGGAG ACTATACTGA AAATTCAGA AAATTCAGA AAATTCAGA AAATTCAGA CGGTGAGGG GGGTGAGGG TTTATGGCTCC ATCGACAGTT GGAGTGAGGG TTATAGGTCTC TTATGGCTCC TTTATGGCTCC | 1920<br>1980<br>2040<br>2100<br>2220<br>2280<br>2340<br>2400<br>2520<br>2520<br>2580<br>2700<br>2760                         |
| 75         | CCAACTTCAA CTAATATCTC CTAATATCTC CAAAATACGG TGTCTTTTAT CTAGTCCTTAT TGCCAAGTGP AAAACCCCTC TTTTCATGG AAGGGCAGG ACGGAGTGP AGGAGCAGG ACCAAGGTGP CCATCTTGAA CCATCTTGAA CCATCTTGAACAACAC CCATCTTGAACAACAC CCATCTTGAACACCCTTAACACCCTTAACACCCTTAACCCTTAACCCTTAACCACC   | TGATGCTTTC AGTGGGCTAC AGTTGGGTA GTACCATAAT GTACCATAAT AGGAAACCTT CTTTTCTACC TTTTTGGTA GTTCAACCC GTGGGTGTG CCACCAAAAT GGAAACTT GGAACCAAAAT GGAACCAAAAT AGACAGAACC CTCCGTGGTAA AGACAGAACC CTCCGTGGTAA AGACAGAACC AGTTATACCC ATGGTGGCAA   | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACA ACAGCTGCTC ACAGCTGCTC ACAGCTGTGCT GTAGCTGCTC TCTGCTGCTC TCTGCTGCTC TCTGCTCTTTT TCTGCACCTC TTTGTGTTAC TTCTGTGTAC TTCTGTGTAC TTCTGTGTAC TTCTGTGTAC TTCTGTGTAC TTCTGTGTAC   | TTTCCTGTAC TGGCCCAGA ACTGGACATT ACTGTAATTT CCTCTTCCAT AACTGATCAG TAGTAGGCGT CTATCCCGGC TTGTAAACAG CGGTCGCCAT CGGTCATCTCC GAGAACAACC TTCTGACTGC CTCTTCGACTGC CTCTTGAAGCT CTCTTGAAGCT CTCTTGAAGCT CTCTTGAAGCT CTCTTAAGCT   | CTGTGTGCCA GTATTTGCCA TTTGTCGAAA TGTTCTGAAA TGATTTTGCC GGACACCCCA TTTGTTGGTC GAAAGAACAT CATTGTTGCT CATTGTTGCT CATTGTTGCT CATTGTTCT CATTGTTCT CATTGTTCT CATTGTTCT CATTGTTCT CATTGTTCT CATTGTTCT GGTTCTGTAGTT GGTTCTGTAGT GGTTCTGTAGT GGTTCTGTTAGT GGTTCTGTAGT GGTTCTGTAGT GGTTCTGTAGT  | CCTGACCCAG ACTATGTCTT ARGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTG CCGTTTGGAG ACTATACTGA ATTGCTCCC ATGGACAGTT GGAGTGAGGG TTTATGGCTC ATGGGAGTAG CCTCTGAAGC   | 1920<br>1980<br>2040<br>2100<br>2220<br>2280<br>2340<br>2400<br>2520<br>2580<br>2640<br>2700<br>2820                         |
| 75         | CCAACTTCAC CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CCATTCTCAT TGCCAAGTGG AAAACCCCTC TTTTCATGGCTCT AAGGAGGAGG AAGGAGGGAGG CCATCTTGAAGGTGG AACAAAGAGT CCATCTTGAAGGCCTT TGAAGGATGGAACAAAGGGCCTTATGACGCTCTTAAAAGAGGTCCCTTAAAAGAGGTCCCTTAAAAGAGGTCCATCCCTTTAAAAGGCCTGAACAAGGCCTGAACAAGGCCTGAACAAGGCCTTAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCCTGAAAAGGCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCAAAGGCAAAGGCAAAAGGCAAAAGGAAAGGCAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGCAAAAGGAAAAGGAAAAGGAAAAGAAAAGGAAAAGGAAAAGAAAA | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GTACCATAAT AGGAAACCTT TTTCCAACC CTTTTGTGTA GTTCAAGCCA GTTCAAGCAA GTACCATAAT GGAACAAATT GGAACAAATT CTCCGTGGTAC CACGAGAC CACTGGAAC AGTTTAACCC CACTGGAAC AGTTTAACCC CACTGGAAC AGTTTAACCC AGTTTAACC AGTTTAACCC AGTTTAACC AGTTTAACCC AGTTTAACC | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACG ACAGGTCGCC ACAGGTCCAC ACAGGTCCAC ACAGGTCCTCC ACAGCTGCTGCTCC ACAGCTGCTGCTCCCC CTTGCTGCTCCCCCCCCCC   | TTTCCTGTAC TGGCCCCAGE ACTGGCCAT ACTGTAATTT ACTGTAATTT ACTGTACAGE TAGTAGGCST ACCGAGGTTG CTTTACAGG TGGTAAACAG GGGTGGCCAT ACGGTCATTCC TTCTATAGTGT TTCTATGGTGT GTCTGAAGCT TTCTATGGTGT TTCTTTGACGG TTCTTAGGTGT TTCTTTGACGGG TTCTTAGGTGT TTCTTTTGCCGGT TTCTTTTGCCGGT TTCTTTTGCCG | CTGTGTGCCA GTATTTGCCA TTTGTCGAGG TGTTCCTGAT GGCTCTGAAA GGCTCTGAAA GGTTCTGCCA GTTCGTTCCA GTTCGTTCCA CTTTGTTGGTC CATTGTCGTC CATTGTCGTC CATTGTCTCA TCTCTCAGTC TCTGTCAGTC GTTCCTGTAG GCTTCTGATC GCTTCTGATC GCTTCTGATC GCTTCTGATC  | CCTGACCCAG ACTATGTCTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTGG CCGTTTGGAG ATATGCTCCC ATCGACAGT ATATGCTCCC ATTGACAGT TTTATGTCCC TTTGAGGGG TTTATGGCTCC ATGGACAGTT GGAGTGAGGG TTTATGGCTC ATGGAGTGAGGG CCTCTGAAGC CCTCTGAAGC        | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2340<br>2400<br>2520<br>2580<br>2640<br>2700<br>2760<br>2820<br>2880         |
| 75         | CCAACTTCAC CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CCATTCTCAT TGCCAAGTGG AAAACCCCTC TTTTCATGGCTCT AAGGAGGAGG AAGGAGGGAGG CCATCTTGAAGGTGG AACAAAGAGT CCATCTTGAAGGCCTT TGAAGGATGGAACAAAGGGCCTTATGACGCTCTTAAAAGAGGTCCCTTAAAAGAGGTCCCTTAAAAGAGGTCCATCCCTTTAAAAGGCCTGAACAAGGCCTGAACAAGGCCTGAACAAGGCCTTAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCTGAAAAGGCCCTGAAAAGGCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCCCTGAAAAGGCAAAGGCAAAGGCAAAAGGCAAAAGGAAAGGCAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGCAAAAGGAAAAGGAAAAGGAAAAGAAAAGGAAAAGGAAAAGAAAA | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GTACCATAAT AGGAAACCTT TTTCCAACC CTTTTGTGTA GTTCAAGCCA GTTCAAGCAA GTACCATAAT GGAACAAATT GGAACAAATT CTCCGTGGTAC CACGAGAC CACTGGAAC AGTTTAACCC CACTGGAAC AGTTTAACCC CACTGGAAC AGTTTAACCC AGTTTAACC AGTTTAACCC AGTTTAACC AGTTTAACCC AGTTTAACC | AACACTCTCT GACACCACAC ACTACCTTTG GTCGGGAACA GGAACCTACG ACAGGTCGCC ACAGGTCCAC ACAGGTCCAC ACAGGTCCTCC ACAGCTGCTGCTCC ACAGCTGCTGCTCCCC CTTGCTGCTCCCCCCCCCC   | TTTCCTGTAC TGGCCCCAGE ACTGGCCAT ACTGTAATTT ACTGTAATTT ACTGTACAGE TAGTAGGCST ACCGAGGTTG CTTTACAGG TGGTAAACAG GGGTGGCCAT ACGGTCATTCC TTCTATAGTGT TTCTATGGTGT GTCTGAAGCT TTCTATGGTGT TTCTTTGACGG TTCTTAGGTGT TTCTTTGACGGG TTCTTAGGTGT TTCTTTTGCCGGT TTCTTTTGCCGGT TTCTTTTGCCG | CTGTGTGCCA GTATTTGCCA TTTGTCGAGG TGTTCCTGAT GGCTCTGAAA GGCTCTGAAA GGTTCTGCCA GTTCGTTCCA GTTCGTTCCA CTTTGTTGGTC CATTGTCGTC CATTGTCGTC CATTGTCTCA TCTCTCAGTC TCTGTCAGTC GTTCCTGTAG GCTTCTGATC GCTTCTGATC GCTTCTGATC GCTTCTGATC  | CCTGACCCAG ACTATGTCTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTGG CCGTTTGGAG ATATGCTCCC ATCGACAGT ATATGCTCCC ATTGACAGT TTTATGTCCC TTTGAGGGG TTTATGGCTCC ATGGACAGTT GGAGTGAGGG TTTATGGCTC ATGGAGTGAGGG CCTCTGAAGC CCTCTGAAGC        | 1920<br>1980<br>2040<br>2100<br>2220<br>2280<br>2340<br>2400<br>2520<br>2580<br>2640<br>2700<br>2760<br>2820                 |
| 75         | CCAACTTCAA CTAATATCTC CTACTGACAT CAAAATACGG TGTCTTTTAT CCATTCTCAT TGCCAAGTGA AAAACCCCTTC TTTTCATGGG TCATGGGCTC TGAAGATGGC TCATGGCTC TGAAGATGGC TCATGGCTC TGAAGATGGC TCATGCCTTTAAAACCCCTTTAAAACCCCTTTAAAACCCCTTTAAAACCCCTTTAAACACCCTGCACCCTGCAGGGT TCCTGCAGGGT  | TGATGCTTTC AGTGGGTAC AGTGGGTAC GTACCATAAT GTACCATAAT GTACCATAAT GTACCATCATC CTTTTTGTAC GTTCAACC GTGGGTGTG CCAACAAAT GTATCACTTC TCCGTGGTAC CACTGGAACC AGTTATACCC ATGTGTGCAA CTTCATCTAC GTTCATCTAC GTTGTGTCAC GTTTCATCTAC GTTGTGTCAC GTTGTGTCAC GTTGTGTCAC GTTGTGTCAC GTTGTGTCAC GTTGTGTCAC GTTGTGTCAC GTTGTGTCAC  | AACACTCTCT GACACCACAC GACACCACAC GTCGGGAACA GGAACCTACA GGAACCTACA ACAGACAGAA ACAGACAGAA ACAGACTCCA ACAGCTGGTGCT GGTCGCTCTTTT GTAGCTGCTCT CTTGCGCTCTAC ATGCTTTT ATGCCTGTAC GTCGCGTCATC GCCCTGCTTCACAC GCCCTGCTTCACAC GCCCTGCTTCACAC GCCCTGCTTCACAC GCCCTGCTTCACC                                       | TTTCCTGTAC TGGCCCCAGA ACTGGCATT ACTGTAATT ACTGTTACAT ACTGATAG TAGTAGGCST ACCGAGGTTG CTATCCCGG TTGTAAACAG GGGTGGCCAT ACGGTCATCTC GGAGACAACAC TCTGACTGC TCTATGGTGT TCTTAGGTGT TCTTTGCC GGAGACCAC TCTTGCCGGG TTCTTAGGTGT TTCTCTCTCCC GGAGACCACC TTCTGCCG GGATCCTCAF           | CTGTGTGCCA GTATTTGCCA GTATTTGCAAG TGTTCCTGATA GGCTCTGAAA TGATTTTGCC GGACACCCCA GTTCGTTCCA GTTCGTTCCA CCTCATGGTT CATTGCTCAC CATTGCTCAC GTTCCAGTC GTTCCTGTAT GCTCTCTGATC GCTCCAGTCCAC GTCAGGTCCAC | CCTGACCCAG ACTATGTCTT ARGGAGTGTT ATCACACTCA AAATTCAAAA ATTATCTTGT AAACTAATTG CCGTTTGGAG ACTATACTGA ATTGCTCCC ATGGACAGTT GGAGTGAGGG TTTATGGCTC ATGGGAGTAG CCTCTGAAGC   | 1920<br>1980<br>2040<br>2100<br>2160<br>2220<br>2340<br>2400<br>2460<br>2520<br>2580<br>2640<br>2700<br>2760<br>2820<br>2880 |

|     |            | CCTCAGCTTC                   |               |            |              |                            | 3060         |
|-----|------------|------------------------------|---------------|------------|--------------|----------------------------|--------------|
|     |            | GAAAAAGAAA<br>CTCAGAAAAA     |               |            |              |                            | 3120<br>3180 |
|     |            | AAGCGATAGC                   |               |            |              |                            | 3240         |
| 5   |            | ATGCTGATAA                   |               |            |              |                            | 3300         |
|     |            | TAAAAGTTGC                   |               |            |              |                            | 3360         |
|     |            | AGCAAGGGAA                   |               |            |              |                            | 3420<br>3480 |
|     |            | TTAATGTCAT<br>TTTTTGGTCA     |               |            |              |                            | 3540         |
| 10  |            | TCAAGACAAT                   |               |            |              |                            | 3600         |
|     |            | AAACTTTCAG                   |               |            |              |                            | 3660         |
|     |            | GACCCTGTCC                   |               |            |              |                            | 3720         |
|     |            | TTTATGAAAA                   |               |            |              |                            | 3780         |
| 15  |            | CTTTGTCTGG                   |               |            |              |                            | 3840<br>3900 |
| 1.5 |            | GAGTTATCAA                   |               |            |              |                            | 3960         |
|     |            | TCATTGTAGC                   |               |            |              |                            | 4020         |
|     |            | ATGAACTTAT                   |               |            |              |                            | 4080         |
| 20  |            | TTATGGGGCC                   |               |            |              |                            | 4140         |
| 20  |            | GTAAAGAAAA<br>ATTTGTAGCT     |               |            |              |                            | 4200<br>4260 |
|     |            | ACATACACAC                   |               |            |              |                            | 4320         |
|     |            | CACCATGTTT                   |               |            |              |                            | 4380         |
| 25  |            | AGGAGATTGA                   |               |            |              |                            | 4440         |
| 25  |            | TAGTAGCATC                   |               |            |              |                            | 4500         |
|     |            | TTAGACATTT<br>GGTGTATATA     |               |            |              |                            | 4560<br>4620 |
|     |            | TTGAATCTCT                   |               |            |              |                            | 4680         |
| 20  | TCCATTAAGG | GTCCAAGAAG                   | TCTGTCCATA    | TGAAAATGAG | GGTAAATATA   | GTTTATTTCC                 | 4740         |
| 30  |            | TCATTATAAT                   |               |            |              |                            | 4800         |
|     |            | CCCATTTACA                   |               |            |              |                            | 4860<br>4920 |
|     |            | AGATATATTT                   |               |            |              |                            | 4980         |
|     |            | ACATTTATTA                   |               |            |              |                            | 5040         |
| 35  |            | CATATTGTGA                   |               |            |              |                            | 5100         |
|     |            | TATAACCACA                   |               |            |              |                            | 5160         |
|     |            | AGAATGAAAC<br>TGTTAATTAA     |               |            |              |                            | 5220<br>5280 |
|     |            | GAGTTAGCTG                   |               |            |              |                            | 5340         |
| 40  |            | GTCAATAATG                   |               |            |              |                            | 5400         |
|     |            | TAAAACCTCA                   |               |            |              |                            | 5460         |
| •   |            | TGAGTCTATA                   |               |            |              |                            | 5520         |
|     |            | GCTTAACCCG                   |               |            |              |                            | 5580<br>5640 |
| 45  |            | ACTITATION                   |               |            |              |                            | 5700         |
|     |            |                              |               |            |              | TGAGTAGAGG                 | 5760         |
|     |            | GTGTACTTCT                   |               |            |              |                            | 5820         |
|     |            | CATTTGCTAA                   |               |            |              |                            | 5880         |
| 50  |            | TTTTAAAAAT<br>CCTGAGGTTT     |               |            |              | AACCAAACTA                 | 5940<br>6000 |
| 30  |            | AAGAATGAAC                   |               |            |              |                            | 6060         |
|     |            | AGTAAATTTT                   |               |            |              |                            | 6120         |
|     |            | TTCAAAAGAT                   |               |            |              |                            | 6180         |
| 55  |            | GCAGAAACAC                   |               |            |              |                            | 6240         |
| 55  |            | CAAAAATGCC                   |               |            |              | AATTCTAATT                 | 6300<br>6360 |
|     |            |                              |               |            |              | TTGAGGAGTG                 | 6420         |
|     |            |                              |               |            |              | CTCTCCTCAG                 | 6480         |
| 60  |            |                              |               |            |              | CAGTTTGCGT                 | 6540         |
| 60  |            |                              |               |            |              | ATATACTGGT                 | 6600         |
|     |            | A GAATGATTGT<br>G TATTGACTGO |               |            |              |                            | 6660<br>6720 |
|     |            | TTGACATTGT                   |               |            |              |                            | 6780         |
| ~ ~ |            |                              |               |            |              | GATATTTCAC                 | 6840         |
| 65  |            |                              |               |            |              | GTACAATCAA                 | 6900         |
|     |            |                              |               |            |              | ATTTCATTGA                 | 6960<br>7020 |
|     |            |                              |               |            |              | TCAAGTIGTG CTCTATGGGT      | 7020         |
|     |            |                              |               |            |              | GCTAAAGTCA                 | 7140         |
| 70  | TCCAGTGAA  | A CTTTTAGAGO                 | CAGAAGTAA     | TTTGTCCCA  | 3 TCCTACAATC | TGAAAAGAGT                 | 7200         |
|     |            |                              |               |            |              | CATTACTTTT                 | 7260         |
|     |            |                              |               |            |              | TTOAATTATT 7               | 7320         |
|     |            |                              |               |            |              | COTGGAACAA<br>A ATATAAATCC | 7380<br>7440 |
| 75  |            |                              |               |            |              | GACTTTTATG                 | 7500         |
|     | GAATTAAGA  | G ATGAAGAAG                  | TGAGATATT     |            |              | A ATTATATGTA               | 7560         |
|     | TACTTAAAA  | A TAAAGTAACT                 | TTATGC        |            |              |                            | 7586         |
|     | Seq ID NO  | : C163 DNA S                 | Sequence      |            |              |                            |              |
| 80  | Nucleic A  | cid Accessio                 | 00_MM : # .IC | 0958       |              |                            |              |
|     | Coding se  | quence: 389                  | 1855          |            |              |                            |              |
|     | 1          | 11                           | 21            | 31         | 41           | 51                         |              |
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|     | -          | •                            |               | -          |              | •                          |              |
|     |            |                              |               | •          | J            | 301                        |              |

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                                                                                              780
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CAGCTCCTTC CTCATTCTCG CCACCGTCCT CTGCAACGTG CTTGTGTGCG GCGCGCTGCT
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                                                                                               1080
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          CCTCCAAACT TACTTGAGAA TTTAAGTCCA GAAGATTCTG TATTAGTTAG AAGAGCACAG
TTTACTTTCT TCAACAAAAC TGGACTTTC CAGGATGTAG GACCCCAAAG AAAAACTTTA
                                                                                                300
                                                                                                360
          GTGAGTTATG TGATGGCGTG CAGTATTGGA AACATTACTA TCCAGAATCT GAAGGATCCT
```

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GTTCAAATAA AAATCAAACA TACAAGAACT CAGGAAGTGC ATCATCCCAT CTGTGCCTTC
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       AGAGATTCAG ATGCAAGTGA GACAGTCTGC CTGTGTAACC ACTTCACACA CTTTGGAGTT
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        CTGATGGACC TTCCAAGAAG TGCCTCACAG TTAGATGCAA GAAACACTAA AGTCCTCACT
                                                                                   660
       TTCATCAGCT ATATTGGGTG TGGAATATCT GCTATTTTTT CAGCAGCAAC TCTCCTGACA
                                                                                   720
       TATGTTGCTT TTGAGAAATT GCGAAGGGAT TATCCCTCCA AAATCTTGAT GAACCTGAGC
        ACAGCCCTGC TGTTCCTGAA TCTCCTCTTC CTCCTAGATG GCTGGATCAC CTCCTTCAAT
                                                                                   840
       GTGGATGGAC TTTGCATTGC TGTTGCAGTC CTGTTGCATT TCTTCCTTCT GGCAACCTTT
ACCTGGATGG GGCTAGAAGC AATTCACATG TACATTGCTC TAGTTAAAGT ATTTAACACT
                                                                                   900
                                                                                   960
10
        TACATTCGCC GATACATTCT AAAATTCTGC ATCATTGGCT GGGGTTTGCC TGCCTTAGTG
        GTGTCAGTTG TTCTAGCGAG CAGAAACAAC AATGAAGTCT ATGGAAAAGA AAGTTATGGG
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        AAAGAAAAAG GTGATGAATT CTGTTGGATT CAAGATCCAG TCATATTTTA TGTGACCTGT
                                                                                   1140
        GCTGGGTATT TTGGAGTCAT GTTTTTTCTG AACATTGCCA TGTTCATTGT GGTAATGGTG
                                                                                   1200
        CAGATCTGTG GGAGGAATGG CAAGAGAAGC AACCGGACCC TGAGAGAAGA AGTGTTAAGG
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        AACCTGCGCA GTGTGGTTAG CTTGACCTTT CTGTTGGGCA TGACATGGGG TTTTGCATTC
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                                                                                   1380
                                                                                    1440
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        GCTACCAATA TCATCAAGAA AAGTTCTGAT AATCTAGGAA AATCTTTGTC TTCAAGCTCC
                                                                                   1560
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        ATTGGTTCCA ACTCAACCTA TCTTACATCC AAATCTAAAT CCAGCTCTAC CACCTATTTC
                                                                                   1620
        AAAAGGAATA GCCACACAGA TAATGTCTCC TATGAGCATT CCTTCAACAA AAGTGGATCA
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        CTCAGACAGT GCTTCCATGG ACAAGTCCTT GTCAAAACTG GCCCATGCTG ATGGAGATCA
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                                                                                    1860
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        TCTTAGATGA TGGAGTCCAT GCAGTTTCTT AGAAATCGGT CTCAGTGCAT GCTGTGCTTT
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                                                                                    2760
40
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                                                                                    2820
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                                                                                    2880
        GAGCTTTTAG GCTACACAGC AACCCAAGGG ACCTCTCACC TTTTGCTGAG CTTCAATCAG
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        GAAGCTATTT GCCTGGCTCC AGCAGATGAT GAGATAATGA GGTAGTGGGT TTTTTATTAC
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        TGTTCCATTT TGCAACATCC TGCAACACCA TCCTGGGAGA CAAGAGCATT ACCCAGCTTG
                                                                                    3060
45
        GCTTTCACGG GGGAGGGTTG TATTCAGT
                                                                                    3088
        Seq ID NO: C166 DNA Sequence
        Nucleic Acid Accession #: NM 000574.1
         Coding sequence: 66..1211
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         CCGCTGGGCG TAGCTGCGAC TCGGCGGAGT CCCGGCGGCG CGTCCTTGTT CTAACCCGGC
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                                                                                     180
         CCCCAGATGT ACCTAATGCC CAGCCAGCTT TGGAAGGCCG TACAAGTTTT CCCGAGGATA
         CTGTAATAAC GTACAAATGT GAAGAAAGCT TTGTGAAAAT TCCTGGCGAG AAGGACTCAG
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                                                                                     300
                                                                                     360
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         TTCCAGTCGG TACTGTTGTG GAATATGAGT GCCGTCCAGG TTACAGAAGA GAACCTTCTC
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         TATCACCAAA ACTAACTTGC CTTCAGAATT TAAAATGGTC CACAGCAGTC GAATTTTGTA
                                                                                     540
         AAAAGAAATC ATGCCCTAAT CCGGGAGAAA TACGAAATGG TCAGATTGAT GTACCAGGTG
GCATATTATT TGGTGCAACC ATCTCCTTCT CATGTAACAC AGGGTACAAA TTATTTGGCT
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         CGACTTCTAG TTTTTGTCTT ATTTCAGGCA GCTCTGTCCA GTGGAGTGAC CCGTTGCCAG
                                                                                     720
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         AGTGCAGAGA AATTTATTGT CCAGCACCAC CACAAATTGA CAATGGAATA ATTCAAGGGG
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         TGATTGGAGA GCACTCTATT TATTGTACTG TGAATAATGA TGAAGGAGAG TGGAGTGGCC
                                                                                     900
         CACCACCTGA ATGCAGAGGA AAATCTCTAA CTTCCAAGGT CCCACCAACA GTTCAGAAAC
                                                                                     960
         CTACCACAGT AAATGTTCCA ACTACAGAAG TCTCACCAAC TTCTCAGAAA ACCACCACAA
                                                                                     1020
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         AAACCACCAC ACCAAATGCT CAAGCAACAC GGAGTACACC TGTTTCCAGG ACAACCAAGC
                                                                                     1080
         ATTTTCATGA AACAACCCCA AATAAAGGAA GTGGAACCAC TTCAGGTACT ACCCGTCTTC
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         TATCTGGGCA CACGTGTTTC ACGTTGACAG GTTTGCTTGG GACGCTAGTA ACCATGGGCT
                                                                                     1200
         TGCTGACTTA GCCAAAGAAG AGTTAAGAAG AAAATACACA CAAGTATACA GACTGTTCCT
                                                                                     1260
         AGTITCITAG ACTIATCIGC ATATIGGATA AAATAAATGC AATIGTGCTC TICATTIAGG
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                                                                                     1380
         ATGCTTTCAT TGTCTTTAGG ATGTGTTAGG ANTOTCAGCA GAGCAGGGG ARAAMAGCA
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TGAGAGTGAT TCCTTTCCTA AAAGTGTAAG AAAGCATAGA GATTTGTTCG TATTTAGAAT
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                                                                                     1500
         GGGATCACGA GGAAAAGAGA AGGAAAGTGA TTTTTTTCCA CAAGATCTGT AATGTTATTT
                                                                                     1560
         CCACTTATAA AGGAAATAAA ARATGAAAAA CATTATTTGG ATATCAAAAG CAAATAAAAA CCCAATTCAG TCTCTTCTAA GCAAAATTGC TAAAGAGAGA TGAACCACAT TATAAAGTAA
                                                                                     1620
 80
                                                                                     1680
          TCTTTGGCTG TAAGGCATTT TCATCTTTCC TTCGGGTTGG CAAAATATTT TAAAGGTAAA
                                                                                     1740
         ACATGCTGGT GAACCAGGGG TGTTGATGGT GATAAGGGAG GAATATAGAA TGAAAGACTG
AATCTTCCTT TGTTGEACAA ATAGAGTTTG GAAAAAGCCT GTGAAAGGTG TCTTCTTTGA
                                                                                     1800
                                                                                     1860
          CTTAATGTCT TTAAAAGTAT CCAGAGATAC TACAATATTA ACATAAGAAA AGATTATATA
```

| 5  | ATTTATATTT  | ATCGAGATGT<br>ATTTATGACA<br>TGAAGAAAAA   | GTGAACATTC | TGATTTTACA | TGTAAAACAA | GAAAAGTTGA               | 1980<br>2040<br>2100<br>2102 |
|----|-------------|--|------------|------------|------------|--------------------------|------------------------------|
| J  | Nucleic Aci | C167 DNA Se<br>d Accession<br>lence:1265 | #: Eos sec | quence     |            |                          |                              |
| 10 | 1           | 11                                       | 21         | 31         | 41         | 51                       |                              |
|    | 1           |  | 1          |            | 1          | 1                        |                              |
|    |             | CCCGGCTCGG                               |            |            |            |                          | 60                           |
|    |             | CTCCCAGGTC<br>GCAGGATGTT                 |            |            |            |                          | 120<br>180                   |
| 15 |             | TCAGCGTCTT                               |            |            |            |                          | 240                          |
|    |             | ATCCCCTGCC                               |            |            |            |                          | 300                          |
|    |             | ACATTCCCAA                               |            |            |            |                          | 360                          |
|    |             | ATCAGCTAAG<br>GTCTGGATGC                 |            |            |            |                          | 420                          |
| 20 |             | TGAGGCACCT                               |            |            |            |                          | 480<br>540                   |
|    |             | GTTTATCGGC                               |            |            |            |                          | 600                          |
|    | ATACCAGACT  | ATGCCTTTGG                               | AAACCTCTCC | AGCTTGGTAG | TTCTACATCT | CCATAACAAT               | 660                          |
|    |             | CCCTGGGAAA                               |            |            |            |                          | 720                          |
| 25 |             | ATAACCTTGA<br>TCTATGACAA                 |            |            |            |                          | 780<br>840                   |
|    |             | GAACACTGAC                               |            |            |            |                          | 900                          |
|    | ACTGGAACTG  | CAAACCTGGA                               | GAGTCTGACT | TTAACTGGAG | CACAGATCTC | ATCTCTTCCT               | 960                          |
|    |             | GCAATCAGTT                               |            |            |            |                          | 1020                         |
| 30 |             | CCAGTTTTTC<br>AAATTAAAGT                 |            |            |            |                          | 1080<br>1140                 |
|    |             | ACAAAATTGC                               |            |            |            |                          | 1200                         |
|    | ATAAAGCTGG  | ACCTATCGTC                               | CAACCTCCTG | TCGTCTTTTC | CTATAACTGG | GTTACATGGT               | 1260                         |
|    |             | TAAAATTAAC                               |            |            |            |                          | 1320                         |
| 35 |             | TCAAGGTTAT<br>CCTATAAGAT                 |            |            |            |                          | 1380                         |
| 55 |             | AGAAAGATGC                               |            |            |            |                          | 1440<br>1500                 |
|    |             | ACTTTGAGGA                               |            |            |            |                          | 1560                         |
|    |             | TCAAACCCTG                               |            |            |            |                          | 1620                         |
| 40 |             | CAGTTCTGGC                               |            |            |            |                          | 1680<br>1740                 |
|    |             | TCTCCAGTGC                               |            |            |            |                          | 1800                         |
|    | GCACGACATG  | GTGCCTGGTG                               | GGAGAATGGG | GTTGGTTGCC | ATGTCATTGG | TTTTTTTTCC               | 1860                         |
|    |             | CAGAATCATC                               |            |            |            |                          | 1920                         |
| 45 |             | ATTCTGCAAA<br>GTGCCCTGCT                 |            |            |            |                          | 1980<br>2040                 |
|    | AAGTATGGCG  | CCTCCCCTCT                               | CTGCCTGCCT | TTGCCTTTTG | GGGAGCCCAG | CACCATGGGC               | 2100                         |
|    |             | CTCTCATCTT                               |            |            |            |                          | 2160                         |
|    |             | ACTGCAATTT<br>TTGCCCTGTT                 |            |            |            |                          | 2220<br>2280                 |
| 50 |             | CCTCTTTAAT                               |            |            |            |                          | 2340                         |
|    | CTTCTGGTGG  | TAGTCCCACT                               | TCCTGCATGT | CTCAATCCCC | TTCTCTACAT | CTTGTTCAAT               | 2400                         |
|    |             | AGGAGGATCT                               |            |            |            |                          | 2460                         |
|    | AGACACCCAA  | GCTTGATGTC<br>TGGTAACCTT                 | TACCAGCTCT | ACCATCACTT | AAAAACAGTC | TOTGACTCA                | 2520<br>2580                 |
| 55 | GTGCCATCAC  | CAGCTTATCC                               | AGTGACTGAG | AGCTGCCATC | TTTCCTCTGT | GGCATTTGTC               | 2640                         |
|    | CCATGTCTTA  |  |            |            |            |                          | 2651                         |
|    | Sec ID NO.  | C168 DNA S                               | omience    |            |            |                          |                              |
|    |             | id Accession                             |            | 667.2      |            |                          |                              |
| 60 |             | uence: 49                                |            |            |            |                          |                              |
|    | 1           | 11                                       | 21         | 31         | 41         | 51                       |                              |
|    | ī           | ī  | î.         | Ĩ.         | Ĩ.         | 1                        |                              |
| 65 |             | CGCCCGCGTC                               |            |            |            |                          | 60                           |
|    |             |  |            |            |            | GGGCAGCTCT               | 120                          |
|    |             |  |            |            |            | GCCCGACGGC<br>TTCCAACCTC | 180<br>240                   |
|    |             |  |            |            |            | GCTCCCGAAT               | 300                          |
| 70 | CCCCTGCCCA  | GTCTCCGCTT                               | CCTGGAGGAG | TTACGTCTTG | CGGGAAACGC | TCTGACATAC               | 360                          |
| 70 |             |  |            |            |            | GCAGAATAAT               | 420                          |
|    |             |  |            |            |            | ATCCCTGCGT<br>GCATTCCCTG | 480<br>540                   |
|    |             |  |            |            |            | TTTTAGAAGT               | 600                          |
| 75 | TTATCGGCAT  | TGCAAGCCAT                               | GACCTTGGCC | CTGAACAAAA | TACACCACAT | ACCAGACTAT               | 660                          |
| 75 | GCCTTTGGAA  | ACCTCTCCAG                               | CTIGGTAGTI | CTACATCTCC | ATAACAATAG | AATCCACTCC               | 720                          |
|    |             |  |            |            |            | AAATTACAAT               | 780                          |
|    |             |  |            |            |            | TTCTCTTATT               | 840<br>900                   |
| 90 | ACAATACATT  | TCTATGACAA                               | TCCCATCCAA | TTTGTTGGGA | GATCTGCTTT | TCAACATTTA               | 960                          |
| 80 | CCTGAACTAA  | GAACACTGAC                               | TCTGAATGGT | GCCTCACAAA | TAACTGAATT | TCCTGATTTA               | 1020                         |
|    | CAAACCCTCT  | , саласствва<br>, всявлевет              | ACCTAATCTC | TAACTGGAG  | CACAGATCTC | ATCTCTTCCT<br>CAACCTATTA | 1080<br>1140                 |
|    | GAAGATTTAC  | : CCAGTTTTTC                             | AGTCTGCCAA | AAGCTTCAGA | AAATTGACCT | AAGACATAAT               | 1200                         |
|    | GAAATCTACG  | AAATTAAAGT                               | TGACACTTTC | CAGCAGTTGC | TTAGCCTCCG | ATCCCTGAAT               | 1260                         |
|    |             |  |            |            |            | 004                      |                              |

|                |  |   |  | CCCAATGCAT   |  |  | 1320   |
|----------------|--|---|--|--|--|--|--|
|                | ATAAAGCTGG   | ACCTATCGTC  | CAACCTCCTG   | TCGTCTTTTC   | CTATAACTGG   | GTTACATGGT   | 1380   |
|                | TTAACTCACT   | TAAAATTAAC  | AGGAAATCAT   | GCCTTACAGA   | GCTTGATATC .   | ATCTGAAAAC   | 1440   |
|                |  |   |  | TATGCTTACC   |  |  | 1500   |
| 5              |  |   |  | TGGAATAAAG   |  |  | 1560   |
| 9              |  |   |  |  |  |  |  |
|                |  |   |  | CAGGCTCAAG   |  |  | 1620   |
|                | TTCCTGCTTG   | ACTTTGAGGA  | AGACCTGAAA   | GCCCTTCATT   | CAGTGCAGTG   | TTCACCTTCC   | 1680   |
|                | CCAGGCCCCT   | TCAAACCCTG  | TGAACACCTG   | CTTGATGGCT   | GGCTGATCAG   | AATTGGAGTG   | 1740   |
|                |  |   |  |  |  |  |  |
| 10             |  |   |  | AATGCTTTGG   |  |  | 1800   |
| 10             | TCCCCTCTGT   | ACATTTCCCC  | CATTAAACTG   | TTAATTGGGG   | TCATCGCAGC   | AGTGAACATG   | 1860   |
|                | CTCACGGGAG   | TCTCCAGTGC  | CGTGCTGGCT   | GGTGTGGATG   | CGTTCACTTT   | TGGCAGCTTT   | 1920   |
|                |  |   |  | GTTGGTTGCC   |  |  | 1980   |
|                |  |   |  |  |  |  |  |
|                |  |   |  | CTTACTCTGG   |  |  | 2040   |
| 1.5            | TCTGTGAAAT   | ATTCTGCAAA  | ATTTGAAACG   | AAAGCTCCAT   | TTTCTAGCCT   | GAAAGTAATC   | 2100   |
| 15             | ATTTTGCTCT   | GTGCCCTGCT  | GGCCTTGACC   | ATGGCCGCAG   | TTCCCCTGCT   | GGGTGGCAGC   | 2160   |
|                | AAGTATGGCG   | CCALCACALCAL  | CTGCCTGCCT   | TTGCCTTTTG   | GCGAGCCCAG   | CACCATGGGC   | 2220   |
|                |  |   |  |  |  |  |  |
|                |  |   |  | CTTTGCTTCC   |  |  | 2280   |
|                | ACCAAGCTCT   | ACTGCAATTT  | GGACAAGGGA   | GACCTGGAGA   | ATATTTGGGA   | CTGCTCTATG   | 2340   |
|                | GTAAAACACA   | TTGCCCTGTT  | GCTCTTCACC   | AACTGCATCC   | TAAACTGCCC   | TGTGGCTTTC   | 2400   |
| 20             |  |   |  | TTTATCAGTC   |  |  | 2460   |
| ~0             |  |   |  |  |  |  |  |
|                |  |   |  | CTCAATCCCC   |  |  | 2520   |
|                | CCTCACTTTA   | AGGAGGATCT  | GGTGAGCCTG   | AGAAAGCAAA   | CCTACGTCTG   | GACAAGATCA   | 2580   |
|                | AAACACCCAA   | GCTTGATGTC  | AATTAACTCT   | GATGATGTCG   | AAAAACAGTC   | CTGTGACTCA   | 2640   |
|                |  |   |  | AGCATCACTT   |  |  | 2700   |
| 25             |  |   |  |  |  |  |  |
| 25             |  |   |  | AGCTGCCATC   |  |  | 2760   |
|                |  |   |  | TGTTTTCAAA   |  |  | 2820   |
|                | GAGATTGAGT   | ATATCAGAGC  | AGTAATTAAT   | AAGAAGAGCT   | GAGGTGAAAC   | TCGGTTTAAA   | 2880   |
|                |  |   |  |  |  |  |  |
|                |  |   |  |  |  |  |  |
| 20             | seq ID NO:   | C169 DNA S  | edneuce  |  |  |  |  |
| 30             | Nucleic Act  | d Accession   | a #: NM 003  | 506.1  |  |  |  |
|                |  | ence: 259.  |  |  |  |  |  |
|                | couring ocd  | 1CHCC. 255.   | . 2317   |  |  |  |  |
|                |  |   |  |  |  |  |  |
|                | 1  | 11  | 21   | 31   | 41   | 51   |  |
|                | 1  | 1   | 1  |  | 1  | 1  |  |
| 35             | CCACCTCCAG   | TOTTCATC  | AACCCCCCCAC  | CCGTCTCAGG   | TOCOTOGGG  | CAACCCCTCCC  | 60   |
| -              |  |   |  |  |  |  |  |
|                |  |   |  | TCGACCGCCC   |  |  | 120  |
|                | CTCATTTTCA   | GGAAAGCCTG  | AAAATGAGTA   | AAATAGTGAA   | ATGAGGAATT   | TGAACATTTT   | 180  |
|                | ATCTTTGGAT   | GGGGATCTTC  | TGAGGATGCA   | AAGAGTGATT   | CATCCAAGCC   | ATGTGGTAAA   | 240  |
|                |  |   |  | ACATTTTTGT   |  |  | 300  |
| 40             |  |   |  |  |  |  |  |
| 40             |  |   |  | GAACCAATTA   |  |  | 360  |
|                | ATGGCCTACA   | ACATGACGTT  | TTTCCCTAAT   | CTGATGGGTC   | ATTATGACCA   | GAGTATTGCC   | 420  |
|                | GCGGTGGAAA   | TGGAGCATTT  | TCTTCCTCTC   | GCAAATCTGG   | AATGTTCACC   | AAACATTGAA   | 480  |
|                |  |   |  |  |  |  |  |
|                |  |   |  | TGCATAGAAC   |  |  | 540  |
|                | TGTCGTAAAC   | TTTGTGAGAA  | AGTATATTCT   | GATTGCAAAA   | AATTAATTGA   | CACTTTTGGG   | 600  |
| 45             | ATCCGATGGC   | CTGAGGAGCT  | TGAATGTGAC   | AGATTACAAT   | ACTGTGATGA   | GACTGTTCCT   | 660  |
|                |  |   |  | GGTCCTCAGA   |  |  | 720  |
|                |  |   |  |  |  |  |  |
|                |  |   |  | CTTAAGACTT   |  |  | 780  |
|                | TTTCTGGGAA   | TTGACCAGTG  | TGCGCCTCCA   | TGCCCCAACA   | TGTATTTTAA   | AAGTGATGAG   | 840  |
|                | CTAGAGTTTG   | CAAAAAGTTT  | TATTGGAACA   | GTTTCAATAT   | TTTGTCTTTG   | TGCAACTCTG   | 900  |
| 50             |  |   |  | AGAAGATTCA   |  |  | 960  |
| 50             |  |   |  |  |  |  |  |
|                |  |   |  | TCTCTTATGT   |  |  | 1020   |
|                | GGCGATAGCA   | CAGCCTGCAA  | TAAGGCAGAT   | GAGAAGCTAG   | AACTTGGTGA   | CACTGTTGTC   | 1080   |
|                | CTAGGCTCTC   | AAAATAAGGC  | TTCCACCCTT   | TTGTTCATGC   | TTTTTTTTATTT   | TTTCACAATG   | 1140   |
|                |  |   |  | ATTACTTGGT   |  |  | 1200   |
| 55             |  |   |  |  | ICIINGCIGC   |  |  |
| 33             |  | AAGCCATCGA  | . GCAAAAAGCA   |  |  |  |  |
|                | CARCETTACC   |   |  |  | ATGCTGTTGC   |  | 1260   |
|                |  |   |  | CTGAACAAAG   |  |  |  |
|                |  | TGACTGTTAT  | GCTTCTTGCT   | CTGAACAAAG   | TTGAAGGAGA   | CAACATTAGT   | 1260<br>1320   |
|                | GGAGTTTGCT   | TGACTGTTAT<br>TTGTTGGCCT  | GCTTCTTGCT<br>TTATGACCTG   | CTGAACAAAG<br>GATGCTTCTC   | TTGAAGGAGA<br>GCTACTTTGT   | CAACATTAGT<br>ACTCTTGCCA   | 1260<br>1320<br>1380   |
|                | GGAGTTTGCT<br>CTGTGCCTTT   | TGACTGTTAT<br>TTGTTGGCCT<br>GTGTGTTTGT  | GCTTCTTGCT<br>TTATGACCTG<br>TGGGCTCTCT   | CTGAACAAAG<br>GATGCTTCTC<br>CTTCTTTTAG   | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT   | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT   | 1260<br>1320<br>1380<br>1440   |
| 60             | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC   | TGACTGTTAT<br>TTGTTGGCCT<br>GTGTGTTTGT<br>AAGTCATACA  | GCTTCTTGCT<br>TTATGACCTG<br>TGGGCTCTCT<br>ACATGATGG  | CTGAACAAAG<br>GATGCTTCTC<br>CTTCTTTAG<br>CGGAACCAAG  | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA   | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG   | 1260<br>1320<br>1380<br>1440<br>1500   |
| 60             | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC<br>ATTCGAATTG   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG  | GCTTCTTGCT<br>TTATGACCTG<br>TGGGCTCTCT<br>ACATGATGGC<br>CGGCTTGTAT   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT   | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA<br>TAGTGACACT   | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT   | 1260<br>1320<br>1380<br>1440<br>1500   |
| 60             | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC<br>ATTCGAATTG<br>TACGTCTATG   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA   | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACC  | CTGAACAAG<br>GATGCTTCTC<br>CTTCTTTTAG<br>CGGAACCAAG<br>CTTGTGCCAT<br>TGGGAGATAA  | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA<br>TAGTGACACT<br>CTTGGGTCTC   | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT   | 1260<br>1320<br>1380<br>1440<br>1500   |
| 60             | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC<br>ATTCGAATTG<br>TACGTCTATG   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA   | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACC  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT   | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA<br>TAGTGACACT<br>CTTGGGTCTC   | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT   | 1260<br>1320<br>1380<br>1440<br>1500   |
| 60             | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC<br>ATTCGAATTG<br>TACGTCTATG<br>CGTCAGTACC   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG  | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACC  | CTGAACAAG<br>GATGCTTCTC<br>CTTCTTTTAG<br>CGGAACCAAG<br>CTTGTGCCAT<br>TGGGAGATAA<br>GCAAAAGCAA  | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA<br>TAGTGACACT<br>CTTGGGTCTC<br>AAGCTCGACC   | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680   |
| 60             | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC<br>ATTCGAATTG<br>TACGTCTATG<br>CGTCAGTACC<br>TTATTTATGA   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG  | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACC TCCTTATCAG GATGACATTA  | CTGAACAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA   | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA<br>TAGTGACACT<br>CTTGGGTCTC<br>AAGCTCGACC<br>TCTCTGCTGT   | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT<br>CTTCTGGGTT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740   |
|                | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC<br>ATTCGAATTG<br>TACGTCTATG<br>CGTCAGTACC<br>TTATTTATGA<br>GGAAGCAAAA   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACAG GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAC   | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACCG TCCTTATCAG GATGACATTA AGAATGGCCT  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAA TGGGAGATAA GGCAAAAGCAA ATTGTTGGCA GGGTTTTTTA  | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA<br>TAGTGACACT<br>CTTGGGTCTCC<br>AAGGTCGACC<br>TCTCTGCTGT<br>AACGAAATCG  | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT<br>CTTCTGGGTT<br>CAAGAGAGAT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740   |
| 60<br>65       | GGAGTTTGCT<br>CTGTGCCTTT<br>CATGTTCGAC<br>ATTCGAATTG<br>TACGTCTATG<br>CGTCAGTACC<br>TTATTTATGA<br>GGAAGCAAAA   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACAG GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAC   | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACCG TCCTTATCAG GATGACATTA AGAATGGCCT  | CTGAACAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA   | TTGAAGGAGA<br>GCTACTTTGT<br>CTGGCATTAT<br>AAAAACTAAA<br>TAGTGACACT<br>CTTGGGTCTCC<br>AAGGTCGACC<br>TCTCTGCTGT<br>AACGAAATCG  | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT<br>CTTCTGGGTT<br>CAAGAGAGAT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740   |
|                | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG TACGTCTATTC CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTC  | TGACTGTTAT TTGTTGGCCT GTGTGTTGG AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAA AGACATGCAA  | GCTTCTTGCT TTATGACCTG TGGGCTCTTG ACATGATGGG CGGCTTGTAT CAGGATTACCG TCCTTATCAG AGTAGACATG AGAATGGGGCT AGTACTACAG  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAA TGGGAGATAA GGCAAAAGCAA ATTGTTGGCA GGGTTTTTTA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACCAAATCG AGTTTTTCTT  | CAACATTAGT<br>ACTCTTCAAA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT<br>CTTCTGGGTT<br>CAAGAGACAT<br>AAAGCACAAT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740   |
|                | GGAGTTTGCT CTGTGCCTTTC CATGTTCGAATTG ATTCGAATTG TACGTCTATG CGTCAGTACC TTATTTTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAC AAAGTCCAAAA AACACAAAAAA  | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACCG TCCTTATCAG GATGACATTA AGAATGGCT AGTACTACAG AGAACTACAG GAAGCACTAT  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CTGGACCAAG CTGGGCGATAA GCAAAGCAA ATTGTTGGCA GGGTTTTTA GGAACCAAGTT AAACCAAGTT  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGTTTTTCTT CACACAAGCT   | CAACATTAGT<br>ACTCTTGCCA<br>TCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT<br>CTTCTGGGTT<br>CAAGAGAGAT<br>AAAGCACAAT<br>GAAGGTCATT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1680<br>1740<br>1800<br>1860   |
|                | GGAGTTTGCT CTGTGCCTTT CATGTTCGAATTG ATTCGAATTG TACGTCTATG CGTCAGTACC TTATTTATGA GGAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAC AAAGTCGAAA ATGCAAAAAA TGGGAACCAG   | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGAATGGGCT AGTACTACAG GATGACATTACAG GAGACACTA CACAGGAGCT CACAGGAGCT  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA ATTGTTGGCA ATTGTTGGCA ATTGTTGGCA AACCAAGTT AAACCAAGTT ACAGCAAATC   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGGTGT AACGAAATCG AGTTTTTCTT CACACAAGCT ATGGCACTTC  | CAACATTAGT<br>ACTCTTGCCA<br>TTCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGGT<br>CATCTGGGTT<br>CAAGAGAGAT<br>AAAGCACAAT<br>AAAGCACAAT<br>TGCAGTAGCA  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1800<br>1860<br>1920<br>1980   |
|                | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG TACGTCTATG CGTCAGTACC TTATTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTCT ATCAAATTCCA ATTACTAGCC   | TGACTGTTAT TTGTTGGCCT AGTCATACA GAGTCATACA GAGTCTTCAG AGCAAGTGAAA ATATCCCATA AGACATGCAA AGACATCAAA AAGACCAAAAA ATGGGAACCAG ATGGAACCAG ATGATTACCT  | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGAATGGCCI AGTACTACAG CAAGACACTAI CACAGGAGCC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CCGGAACCAAG CTTGTGCCAT TGGGAGATAA ACTGTTGGCA GGGTTTTTA GGAATCAAGTA AAACCAAGTT AAACCAAGTT ACAGCAAATC ACTTGACAA   | TTGAAGGAGA GCTACTTTGT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGGTGT AACGAAATCG AGTTTTCTT CACACAAGCT ATGGCACTTC  | CAACATTAGT ACTCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGAGAT AAAGCACAAT GAAGGTCATT TGCAGTAGCA CTCACCAGAA  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1800<br>1860<br>1920<br>1980<br>2040   |
| 65             | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG TACGTCTATG CGTCAGTACC TTATTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTCT ATCAAATTCCA ATTACTAGCC   | TGACTGTTAT TTGTTGGCCT AGTCATACA GAGTCATACA GAGTCTTCAG AGCAAGTGAAA ATATCCCATA AGACATGCAA AGACATCAAA AAGACCAAAAA ATGGGAACCAG ATGGAACCAG ATGATTACCT  | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGAATGGCCI AGTACTACAG CAAGACACTAI CACAGGAGCC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC AGGACAAGAAC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA ATTGTTGGCA ATTGTTGGCA ATTGTTGGCA AACCAAGTT AAACCAAGTT ACAGCAAATC   | TTGAAGGAGA GCTACTTTGT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGGTGT AACGAAATCG AGTTTTCTT CACACAAGCT ATGGCACTTC  | CAACATTAGT ACTCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGAGAT AAAGCACAAT GAAGGTCATT TGCAGTAGCA CTCACCAGAA  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1800<br>1980<br>1920<br>1980<br>2040<br>2100   |
|                | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTCG TACGTCATATCG TATTTATGAT GGAAGCAAAA CCAATCAGTC TCTAAAGTTA TCCAAATCCA ATTACTAGCC ACATCAATGA   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAA AAGTCGAAG AACACCAAG AACACAAAAA TGGGAACCAG ATGATTACCT GAGAGGTGAA  | GCTTCTTGCT TTATGACCTTTATTATACTTTATTATACTTTATACTTTATACTTATACACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATCACTTATACACTACACTTATACACTTATACACTTATACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACTACACACTACACACTAC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GGATAAAGCAA ATTGTTGGCA GGATTTTTA GGATCATGTG AAACCAAGTT ACAGCAATGT ACTAGACA ACTTAGACA   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACCAAATC AGTTTTTCTT CACACAAGCT ATGGCACTTC AAGCCAAACCT AAGCCAAACCT CACACAAGCT CACACAAGCT CACACAACCT CACACAACCT CACACAAACCT CACACAAACCT CACACAAACCT CACACAAACCT CACACAAACCT CACACAAACCT CACACAAACCT CCACGGTTAAAG   | CAACATTAGT<br>ACTCTTGCCA<br>TCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT<br>CTTCTGGGTT<br>CAAGAGAGAT<br>AAAGCACAAT<br>GAAGGTCATT<br>TCCAGTAGCA<br>ACTCACCAGAA<br>AGAACAGGAC   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1800<br>1860<br>1920<br>1980<br>2040   |
| 65             | GGAGTTTGCT CTGTGCCTTTT CATGTTCGAC ATTCGAATTG TACGTCTATTG CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGCC ACATCAATGA TGTGGTGAAC  | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAA AAAGTCGAAG AACACAAAAA TGGGAACCAG ATGATTACCT GGAGGTGTAA CTGGCTCGCC  | GCTTCTTGCT TTATGACCTG TGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGATGGGCT AGTACTACAG GAAGCACTAT CACAGGAGCT AGGACACTAT AGGGCACAG AGGACACTAT AGCAGGACCACT AGGACACTGC AGGACACTGC AGGACACTGC AGGACACTGC AGCACCGG   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GGAAAAGCAA ATTGTTGGCA ATTGTTGGCA AAACAAGTT AAACCAAGTT ACAGCAAATCA ACTTTGACAG ACTTTGACAG CGCTAGCACCC ATCTCCAGACC  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGTTTTTTCT CACACAAGCT ATGGCACTTC AAATCCAAAC CCAGGTTAAG CCAGGTTAAG   | CAACATTAGT<br>ACTCTTGCCA<br>TCCTTAAAT<br>GAAATTTATG<br>TCTCGGATGT<br>TGATCATTGT<br>AGAATTGGCT<br>CTTCTGGGTT<br>CAAGAGACAT<br>AAAGCACAAT<br>GAAGGTCATT<br>TGCAGCACAAT<br>GACACCAGAA<br>ACAACAGGAC<br>ACAGGTCGAC   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2100<br>2160   |
| 65             | GGAGTTTGCT CTGTGCCTTCT CATGTCTCTAC ATTCGAATTCG TACGTCTATTG CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGCC ACATCAATGG GGGAAGGGCC GGGAAGGGCC   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AGGCATGTAA AGACATGAA ATATCCCATG TAAAATACCT AGACATGCAA AGACATGCAA AGACATGCAC AAAGTCCAAA TGGGAACCAC ATGATTACCT GAGAGGTTAC CTGCCTCGCC AGGCAGGCAC  | GCTTCTTGCT TTATGACCTG TTGGGCTCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAC GATGACATTACAC GATGACATTACAC GATGACATTACAC GAAGCACTAA CACAGGAGCT AGGACACAA AGCGGACCGA AGCGGACCGA TGTATCTGAA   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGAGCAAA ATTGTTGGCA AATTGTTGGCA AAACAAGTT AAACAAGTT AACAAGTA ACTTGACAG ACTTGACAG AGTAGCACAA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGGTGT AACGAAATCG AGTTTTCTT CACACAAGCT ATGGCACTTC AAATCCAAAC CCAGGTTAAAC CCAGGTTAAAC TCTCTGGGGA GTGAAGGAAGG   | CAACATTAGT ACTCTTACAT TTCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT AAAGCACAAT TGCAGTAGCA TTCACCAGAA AGAACAGGAC ACAGGTCGAC GATTAGTCCA   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1680<br>1740<br>1800<br>1920<br>1980<br>2040<br>2100<br>2160<br>2220   |
| 65             | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTCG TACGTCATAC CGTCAGTACC GGAGCAAAA CCAATCAGTC TCTAAAGTTCA ATTACTAAGCC ACATCAATGA TGTGTGAC GGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AAGAGTGAT   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAA AACACCAAGAA TGGGAACCAG AACACCAAGAA TGGGAACCT GAGAGGTGAA CTGGCTCGCC CAGGCAGCAA TTACTGACAA   | GCTTCTTGCT TTATGACCTTTATTAGCT TTATGACTTTATTAGCT ACATGATGGC CGGCTTGTAT CAGGATTACCC TCCTTATCAG GATGACATTACAG GATGACATTACAG GAAGACACTAA AGAGAGACTA AGCAGAGACT AGGACAAGAA AGCGGACGGC AGCAGCATCC TGTATCTGAC TGGCCTGGCC  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA GGGTTTTTA GGATCATGTG AAACCAAGTT ACAGCAATC ACTTTGACAG AGTAGCACCC ATCTCCAGAC AGTGGCGCGA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGTTTTTCTT CACACAAGCT ATTGGCACTTC AAATCCAAAC CCAGGTTAAG CTCTCTGGGGA ATTTCGGGAAG ATTTGCAGGA   | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGAGAT AAAGGACAAT GAAGGTCAAT GAAGGTCAAT TGCAGTAGCA ACAGGTCGAC ACAGGTCGAC ACAGGTCGAC CCCCAGGTCT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1860<br>1920<br>1920<br>1920<br>2040<br>2100<br>2100<br>2220<br>2220   |
| 65             | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTCG TACGTCATAC CGTCAGTACC GGAGCAAAA CCAATCAGTC TCTAAAGTTCA ATTACTAAGCC ACATCAATGA TGTGTGAC GGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AGGGAAGGGCC AAGAGTGAT   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAA AACACCAAGAA TGGGAACCAG AACACCAAGAA TGGGAACCT GAGAGGTGAA CTGGCTCGCC CAGGCAGCAA TTACTGACAA   | GCTTCTTGCT TTATGACCTTTATTAGCT TTATGACTTTATTAGCT ACATGATGGC CGGCTTGTAT CAGGATTACCC TCCTTATCAG GATGACATTACAG GATGACATTACAG GAAGACACTAA AGAGAGACTA AGCAGAGACT AGGACAAGAA AGCGGACGGC AGCAGCATCC TGTATCTGAC TGGCCTGGCC  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA GGGTTTTTA GGATCATGTG AAACCAAGTT ACAGCAATC ACTTTGACAG AGTAGCACCC ATCTCCAGAC AGTGGCGCGA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGTTTTTCTT CACACAAGCT ATTGGCACTTC AAATCCAAAC CCAGGTTAAG CTCTCTGGGGA ATTTCGGGAAG ATTTGCAGGA   | CAACATTAGT ACTCTTACAT TTCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT AAAGCACAAT TGCAGTAGCA TTCACCAGAA AGAACAGGAC ACAGGTCGAC GATTAGTCCA   | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1680<br>1740<br>1800<br>1920<br>1980<br>2040<br>2100<br>2160<br>2220   |
| 65<br>70       | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG ATTCGAATTG GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGC ACATCAATGG GGAAGCGAAC AGAGGGCCA AGAGGACCAAAAGAGCAAAAACAAAAAAAA  | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAA AACACCAAAAA TGGGAACCAG AACACCAAAAA TGGGAACCAG ATGATTACCT GAGAGGTGAA CTGGCTCGCC AGGCAGCCAG TTACTGACAG TTACTGACAG GCAGCCTCAA   | GCTTCTTGCT TTATGACCTG TTGGCTCTCTTATGACCTG ACATGATGGC CGCTTGTAT CAGGATTACAG GATGACATTA AGAATGGCCT AGTACTACAG GAAGCACTAT AGAGCACTAT AGAGCACTAT AGGCACTAT AGGCACTAT AGCGACCGG TGTATCTGAG TGGCTCTGGCC AGGTTCCACC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGCA GAGTTTTTA AAACCAAGTT ACAGCAAATC ACTTGACAG AGTTGTACAG AGTTGCAGAC ATTCCAGAC ATTCCAGAC ATTCCAGAC ACTGCAGCAAC ACTGCAGCAAC ACTGCAGCAAC ATCCCTGCTTG   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT AAGCTCGACC TCTCTGCTGT AACCAAAACC AAATCCAAAGCT ATAGCACATC CAAATCCAAAC CCAGGTTAAG TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TTTCACCAGTTAAG TTTCACGGGT TTCACCAGT  | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT AAAGCACAAT GAAGGTCATT TGCAGTAGCA ACTACCAGAA ACTACACCAGAA ACTACACCAGAA ACTACACCAGAC ACAGGTCGAC CATTAGTCCA CCCCAGTTCT TTCAGGAGTG   | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>22100<br>22160<br>2220<br>2280<br>2340   |
| 65<br>70       | GGAGTTTGCT CTGTGCCTTTT CATGTTCGAC ATTCGAATTCG ATTCGACTTATGA GGAGCAAAA CCAATCAGTGC TCTAAAGTTA TCCAAATCCA ATTACTAGGC ACATCAATGC ACATCAATGC ACATCAATGC ACATCAGGGGAAGGGCC AAGAGTGAT TCAGAACCCAA AGAAAAGAGA   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AGGTCATACA GAGTCATACA GAGTCTTAG AGCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAC AAAGTCGAA TGGGAACCAC ATGATTACCT GAGAGGGTGAA CTGCCTCGCC AGGCAGCCAC ATTACTGACAC CGCAGCCTCAA AGGGAGGTGAA AGGGAGGTGAA  | GCTTCTTGCT TTATGACCTG TTGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGATGGGCT AGTACTACAG GAAGCACTAT CACAGGAGCT AGGACACTAT AGCGGACGGA TGTATCTGAT CACAGGAGCT AGGACTGCT AGGCTGCCT AGGCTTGCAC AGGTTCCACAG AGGTTCCACAG   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGCAAA ATTGTTGGCA ATTGTTGGCA AACCAAGTT AAACCAAGTT ACAGCAAATCA ACTTTGACAG ACTTGCAGAC AACTTCCAGAC AACTCCCAGAC AACTCCCAGAC AACTCCCAGAC AACTCCCAGAC AACTCCCAGAC AACTCCCAGAC AACTCCCAGAC AACTCCCAGAC AACTCCAGAC AACTCCTGCTTGAAC AGAACCAACAT AGAACCAACAT AGAACCAACAT AGAACCAACAT AGAACCAACAA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTGGACC TCTCTGCTGT AACGAAATCG AGTTTTTCT CACACAAGCT AATCCAAAC CCAGGTTAAG TCTCTGGGA GTGAAGGAAG ATTTGCAGGT TTCACCAGT TTCACCAGT AGACATTTC   | CAACATTAGT ACTCTTGCCA TTCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGGT CAAGAGACAT AAAGCACAAT GAAGTCATT TGCAGTAGCA ACTACCAGAA ACAACAGGAC ACAGGTCACC GATTAGTCCA CCCCAGTTCT TTCAGGAGTCAC TTCAGGAGTCAC TTCAGGAGTCAC TTCAGGAGTCAC TTCAGGAGTCAC TTCAGGAGTCAC TTCAGGAGTCAC TCCCGGTTCT TCCAGGAGTCAC TCCCGTTACT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>2040<br>2100<br>2220<br>2280<br>2340<br>2400   |
| 65             | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG TACGTCTATG CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGCC ACATCAATGA TGGTGAAAC GGGAAGGGCC AAGAGGACCAAA CCAGAACCAAC CAGAAAGACCAAC CAGAAAGACCAAC   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AAGTCAAGTGAA ATATCCCATG TAAAATACCT AGACATGCAA AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG AAGACAAGAA TGGGAACCAG CAGGAAGTGAA TTGCTGCTCGCC AGCAGGCAG TTACTGACAC AGCAGGCAG TTACTGACAC AGCAGGCAG TTACTGACAC TTGTGTTAC                                   | GCTTCTTGCT TTATGACCTTTATTAGCT TTATGACCTT ACATGATGGC CGGCTTGTTACAG TCCTTATCAG GATGACATTACAG GATGACATTACAG GATGACATTACAG GAAGCACATTACAGAG AGAGCACACAGAGCATCCC AGGACAGGAC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA GATCATGTG AAACCAAGTT ACAGCAATC ACTTTGACAG ACTTTGACAG ACTTTGACAG ACTTTGACAG ACTTTGACAG ACTTTGACAG ACTTCCAGAC CATCTCTGACAG ACTGCTGACAC ATCTCTGACAG ACTGCTGACAG ACTGCTGACAG ACTGCTGACAG ACTGCTGACAG ACTGCTGACAG ACTGCTGACAG ACTGCTGACAG ACTGCTGCTTG GGATACTTGAAAG ACTTATGACAG   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG ACGTAATCG AAGTTACCAAGCT CACACAAGCT AATCCAAAC CCAGGTTAAG TCTCTCGGGA ATTCCAGGA ATTTCCAGGT TTCACCCAGT TTACCCAGGT TTACCCAGGT TTACCCAGGT TTACCCCAGGT TTACCCAGGT TTACCCCAGGT TTACCCAGGT TTACCAGGT TTACCCAGGT TTACCAGGT TTACCAGGT TTACCAGGT TTACCAGGT TTACCAGGT TTACCAGGT TTACCAGGT TTACCAGGT TTAC | CAACATTAGT ACTCTTGCCA TCCTTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT CAAGAGAGAT CAAGGACAAT GAAGGTCATT TGCAGTAGT CTCACCAGAA AGAACAGGAC ACAGGTCGAC ACAGGTCGAC CCCCAGTTCT TTCAGGAGTC TCTCAGGAGTC TCTCAGGAGTC TCTCAGGAGTC TCTCAGGAGTC TCTCAGGAGTC TCTCAGGAGTC GAATCACTGT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1860<br>1980<br>2040<br>2100<br>2100<br>2220<br>2280<br>2340<br>2400<br>2460   |
| 65<br>70       | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG ATTCGACTATT TACGTCTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGC ACATCAATGA TGTGGTGAAC GGGAAGGGCC AAGAAGTGAT TCAGAACCAA AGAAGTGATT TCAGAACCAA AGAACCAA AGAACCAA AGAACCAA AGAACCAA TACGTTCTTC  | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCATGCAA ATATCCCATG TAAAATACCT AGACATGCAA AACACAAAAA TGGGAACCAG AACACCAAAAA TGGGAACCAG ATGATTACCT GGGAGGTGAA CTGCCTCGCC AGGCAGGCAG TTACTGACA TTACTGACA TTACTGACAC TTGTGTTAC TTTTGCACT   | GCTTCTTGCT TTATGACTGT TTATGACTGT ACATGATGGC CGGCTTGTAT CAGGATTACAC GATGACATTA AGAATGGCT AGTACTACAC GAAGCACTAT AGGACACTAT AGGACACTAT AGGACACTAT AGGACACTAT AGCAGGACCT TGTATCTGAA TGGCTGGCC AGGTTCCACC TTGTCATCTCACC AGGTTCCACC ACTGGACATC AGGTTCCACC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACACC ACTGGACATC AAAGTTGCAACC AAAGTTGCAACC ACTGGACACC AAAGTTGCAACC AAAGTTGCAACC ACTGGACACC AAAGTTGCAACC ACTGGACACC AAAGTTGCAACC AAAGTTGCAACC ACTGGACACC ACTGGACACC AAAGTTGCAACC ACTGGACACC ACTGCACC ACTCCACC ACTGCACC A | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GGAATATTTTAG GGATTTTTTAG GAATCAAGTT ACAGCAAATC ACTTGACAG AGTTGTCAGA AGTGCCCGA AGTGCCCGAA CTGAGCACC TCTCTGCTTG AGATACTTGAAG ACAGAGCAACA TCTCTGCTTG AGATACTTGAAG AGATACTTCAAGA TCTCTGCTTG AGATACTTCAAGACA TCTCTGCTTG AGATACTTCAAGACA TCTCTGCTTG AGATACTTCAA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT ACCGAAATCG AGATTTTCTT CACACAAGCT AAATCCAAAC CCAGGTTAAG TCTCTGGGGA TCTCTGGGGA TTTCTGGGGA TTTGCAGGT TTCACCGGT ATTTGCAGT TTCACCCAGT AGACATTTTC TTTTTTTAA   | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT GAAGGTCATT TGCAGTAGCA ACACCAGAA ACAACAGGAC ACAGGTCGAC GATTAGTCCA TCCAGGTTCT TTCAGGAGTG TTCAGGAGTG TCTCGTTACT GAAATCACTGT AAAATAGACT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>2040<br>2100<br>2220<br>2280<br>2340<br>2400   |
| 65<br>70       | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG ATTCGACTATT TACGTCTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGC ACATCAATGA TGTGGTGAAC GGGAAGGGCC AAGAAGTGAT TCAGAACCAA AGAAGTGATT TCAGAACCAA AGAACCAA AGAACCAA AGAACCAA AGAACCAA TACGTTCTTC  | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCATGCAA ATATCCCATG TAAAATACCT AGACATGCAA AACACAAAAA TGGGAACCAG AACACCAAAAA TGGGAACCAG ATGATTACCT GGGAGGTGAA CTGCCTCGCC AGGCAGGCAG TTACTGACA TTACTGACA TTACTGACAC TTGTGTTAC TTTTGCACT   | GCTTCTTGCT TTATGACTGT TTATGACTGT ACATGATGGC CGGCTTGTAT CAGGATTACAC GATGACATTA AGAATGGCT AGTACTACAC GAAGCACTAT AGGACACTAT AGGACACTAT AGGACACTAT AGGACACTAT AGCAGGACCT TGTATCTGAA TGGCTGGCC AGGTTCCACC TTGTCATCTCACC AGGTTCCACC ACTGGACATC AGGTTCCACC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACATC ACTGGACACC ACTGGACATC AAAGTTGCAACC AAAGTTGCAACC ACTGGACACC AAAGTTGCAACC AAAGTTGCAACC ACTGGACACC AAAGTTGCAACC ACTGGACACC AAAGTTGCAACC AAAGTTGCAACC ACTGGACACC ACTGGACACC AAAGTTGCAACC ACTGGACACC ACTGCACC ACTCCACC ACTGCACC A | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GGAATATTTTAG GGATTTTTTAG GAATCAAGTT ACAGCAAATC ACTTGACAG AGTTGTCAGA AGTGCCCGA AGTGCCCGAA CTGAGCACC TCTCTGCTTG AGATACTTGAAG ACAGAGCAACA TCTCTGCTTG AGATACTTGAAG AGATACTTCAAGA TCTCTGCTTG AGATACTTCAAGACA TCTCTGCTTG AGATACTTCAAGACA TCTCTGCTTG AGATACTTCAA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT ACCGAAATCG AGATTTTCTT CACACAAGCT AAATCCAAAC CCAGGTTAAG TCTCTGGGGA TCTCTGGGGA TTTCTGGGGA TTTGCAGGT TTCACCGGT ATTTGCAGT TTCACCCAGT AGACATTTTC TTTTTTTAA   | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT GAAGGTCATT TGCAGTAGCA ACACCAGAA ACAACAGGAC ACAGGTCGAC GATTAGTCCA TCCAGGTTCT TTCAGGAGTG TTCAGGAGTG TCTCGTTACT GAAATCACTGT AAAATAGACT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1860<br>1980<br>2040<br>2100<br>2100<br>2220<br>2280<br>2340<br>2400<br>2460   |
| 65<br>70       | GGAGTTTGCT CTGTGCCTTTT CATGTTCGAC ATTCGAATTCG ATTCGACTTATGA CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCCAAATCCA ATTACTAGGC ACATCAATGA TGTGGTGAAC GGGAAGGGCC AAGACCAAT TCAGAACCAA AGAAAAGAGCAAT ACAGAAGCAAT ACAGAAGCAAT ACAGAACCAAT ACAGAACTAAT ACAGAATTAT CCAAGAATTAT TCAAGAATTAT   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA TAAAATACCT AGACATGCAA AAAGTCCAAG AACACAAAAA TGGGAACCAAG ATGATTACCT CGGGGGCAG CTGCCTCGCC AGGCAGGCAG TTACTGACA CGCAGCTCAA CGCAGCCTCAA CGCAGCCTCAA CTTGTGTTAC TTTTGTGTTAC TTATGACTCAT TATGACTCAT                                 | GCTTCTTGCT TTATGACCTG TTGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGATGGGCT AGTACTACAG AGAGCACTAT AGGGCACAG TGGCTTGTACAG AGCACAGGAGC TGGTATCTGAC TGGCTGGCT AGGCTTCCCC TTGTCTCACCC TTGTCTCACCC TTGTCACCC TTGTCACCC TTGTCACCC TTGTCACCC TTGTCACCC TTGTCACCCACAC TTCCACCCACAC TTCCACCCACAC TTCCACCCAC  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA AATCATGTG AAACCAAGTT ACAGCAAATCA ACTTTGAGAC AGTGTGCGGAA AGTGCGGGAA ACAGACACA ATCTCCAGAC ATCTCCAGAC AGTGCGCGGAA ACAGACAACA ACAGACAACA ACAGACAACA ATCTCTGCTTGAA AGATACTTGAAACA ATCTCTGCTTGAACACACACACACACACACACACACACAC  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTGGGTCTC CTGGGTCTC AAGCTCGACC AGCTCGACC AGTTTTTCTT CACACAAGCT CACACAAGCT CACACAAGCT CACACAAGCT TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TTTTCTGGGA TTTTCCTGGGA ATTTGCAGGT TTCACCCAGT GAACATTTC TGTTTTTTAAA TAACTGGAA AACAATATAC  | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT AAAGCACAAT AGAGGTCATT TGCAGTAGCA ACACGGAC ACAGGTCGAC GATTAGTCCA ACAGGTCGAC GATTAGTCCA TCCAGGAGC TCCAGTTCT TTCAGGAGTG TCTCGTTACT GAATCACTGT AAAATAGAGT CTGAAAACAG   | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1980<br>2040<br>2160<br>2220<br>2280<br>2340<br>2400<br>2400<br>2520<br>2580   |
| 65<br>70       | GGAGTTTGCT CTGTGCCTTGT CATGTCTCTA ATTCGAATTG TACGTCTATA CGTCAGTAC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGCC ACATCATGG GGGAAGGCCA AGGATGATT CCAGAACCAT AGGAAAGCCA AGAAAAGACCA AGAAAAGACCA AGAAAAGACCA AGAAAAGACCA AAAAGTCTCTTC TACAGAATAA AAATGTGCAA  | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG ATATCCCATG TAAAATACCT AGACATGCAC AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG AAGGTCGAAG ATATCCCT GAGAGGTGAA TTGGCTCGCC CTGCCTCGCC CAGCAGGCAG TTACTGACAC TTTGTGTTAC TTTTTGCACTT TATGACTTAG TATGACTCAAT GTTAATAATAT                        | GCTTCTTGCT TTATGACCTTTATTAGCT TAGGGCTTCTTA ACATGATGGC CGGCTTCTTATCAG GATGACATTACAG GATGACATTACAG GATGACATTACAG GAAGCACATTACAG GAAGCACATTACAG GAAGCACATTACAG AGAGCACCATTACAGAGAC TGGACAGGAC TGGACAGGAC TGGACTCCACC TGTATCTGAA TTGCACAGAA TTTTTTTAACACAA   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAACAAG ATTGTTGGCAA ATTGTTGGCA GGATCATGTG AAACAAGTT ACAGCAATAA ACTTTGACAG ACTTTGACAG ACTTTGACAG ACTTTGACAG ACTTCCAGAC ATCTCTGAGAC ATCTCTGAGAC ATCTCTGGTTG AGATACTTGATGGCAGA AGTGGCGGAA AGTGGCGGAA ACTTGATGGCGGAA AGTGGCTGATGGCTGCTTG   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTGTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGTTTTCTT CACACAAGCT ATTGCACTTC AAATCCAAAC CCAGGTTAAG TCTCTGGGAG ATTTGCAGGA ATTTGCAGGT TTACCCAGGT TGACACTTC TGTTTTGTAG TATACTGGAA TATACTGGAA AACAATATAC GACAAGATTA  | CAACATTAGT ACTCTTGCCA TCCTTTAAAT GAAATTTATG TCATCGATGT TGATCATTGT AGAATTGCT CTTCTGGGTT CAAGAGAGAT AAAGCACAAT GAAGGTCATT TGCAGTAGCA ACTCACCAGAA AGAACAGGAC ACAGGTCCAC CCCCAGTTCT TTCAGGAGTCA TCTAGGAGTCA TCTCAGGAGTCA TCTCAGGAGTCA TCTCAGGAGTCA CCCCAGTTCT TCTAGGAGTCA TCTCAGGAGTCA TCTCAGGAGTCA CCCCAGTTCT TCTAGGAGTCA CCCCAGTTCT TCTAGGAGTCA CCCCAGTTCT TCTAGGAGTCA CCCCAGTTCT TCTAGGAGTCA CCCAGTTCT TCTAGGAGTCA CAAAACAGGAGAAACCAG GAGGAAATCTT | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1980<br>2040<br>2100<br>2220<br>2280<br>2340<br>2400<br>2460<br>2520<br>2580<br>2640   |
| 65<br>70<br>75 | GGAGTTTGCT CTGTGCCTTT CATGTTCTATC ATTCGAATTG ATTCGAATTG TACGTCTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGC ACATCAATGA GGGAAGGCAA TCAGAGCCA AGAGTGAAT TCAGAACCA AGAAAAGAGG CAGAAGCAAA TACGTTCTTC TCAGAATTCT TCAGAATTA AAATGTGCAC CCTTTTCTAT  | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCATGCAA ATATCCCATG TAAAATACCT AGACATGCAA AAGCCAGAAA TGGGAACCTGAA CAGGAGCTGAA ATATCCCTAGGAACCAA AGGGAGCTGAA ATGACTGCAA AGGAGGTGAA TTGCACCTCACC AGGGAGCTGAA TTGTGTTTAC TTTTGCACTT ATATGACACA TTTATGAAGAT TTATGAAGAT                      | GCTTCTTGCT TTATGACCTT TATGACTGT ACATGATGGC CGGCTTGTAT CAGGATTACAG TCCTTATCAG GATGACATTACAG GAAGACACTAT AGAACACTAT AGACACAGAGCT AGGACACAGAA AGCGGACGGC TGTATCTGAC TGGCCTGGCC  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GGATATAGCAA ATTGTTGGCA GATCATGTG AAACCAAGTT ACAGCAATTTA ACGCAATCA ACTTGACAGA ACTTGACAGA ACTTGACAGA ACTTGACAGA ACTTGCTGGACA ACTTCTGCTGG AGATACTTGCTGC ATCTCTGCTGC ATCTCTGCTGC ATCTCTGCTGC AGATACTTGACAGACACACACACACACACACACACACACA  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CAGGTCGACC TCTCTGCTGT AACGAAGCT AGCTAGACC CACACAAGCT AAGCCAAAGCT CACACAAGCT CAAGCTAAG CCAGGTTAAG TTCTCTGGGAA ATTTGCAGGA ATTTGCAGGT TTCACCCAGT TTAACATATACT CACACAAGCT TTTAACATTTC TTTAACATTTC TTTAACATTTC TTTAACATTTC TTTAACATTTC TTTAACATTTC  | CAACATTAGT ACTCTTGCCA TCCTTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGAGAT AAAGCACAAT GAAGGACAT TCCACAGAA AGAACAGGAC ACAGGTCGAC CATTAGTCCA TCCACCAGTTCT TTCAGGAGTG TCTCGTTACT TCAAGAGTG AAAATAGAGT CTGAAAACAG GAGGAATCTT ACTATGCTAT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>1920<br>1920<br>2140<br>2220<br>2220<br>2240<br>240<br>2520<br>2520<br>2580<br>2580<br>2700  |
| 65<br>70       | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTCG ATTCGACTTATGA CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCCAAATCCA ATTACTAGGC ACATCAATGA TGTGGTGAAC GGGAAGGCCA AGAACCAAT AGAACCAA AGAAAAGAC CAGAAGCAAT TCAAGATCAT TCAAGAATCAT AGAACCAA AGAAAAGAC CCTTTCTTT TTTACCTTTT   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA TAAAATACCT AGACATGCAA AAAGTCGAAG AACACAAAAA TGGGAACCAG ATGATTACCT AGACAGTGAAG ATGATTACCT AGAGGGGGCAG CTGCCTCGCC AGGCAGGCAG TTACTGACAC TTGTGTTAC TTTGTGTTAC TTATGACTCAT TTATGACAC TTATGACTCAT                                  | GCTTCTTGCT TTATGACCTG TTGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGATGGGCT AGTACTACAG AGAGCACTAT AGGGCACAG TGGCTGTAT CACAGGAGCA AGGCACAGC TGGCTGGCT AGGCACAGC TTGTCTCACC TTGTCACCACAA ATTTTTTACACAAA ATTTTTTACACAAA ATTTTTTACACCAAA ATTTTTTACACCACAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTACACCACAAA ATTTTTACACCACAAAA ATTTTTTACACCACAAAAAATTTTACACCACAAAAATTTTACACCAC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA AATCATGTG AAACCAAGTT ACAGCAAATCA ACTTTGAGAC AGTGCGCGAA ACTGGCGCGAA ACGAGCAACA ACGAGCAACA ACGAGCAACA CGAGCAACA CGAGCCACC TGCCTCTGCTTGAA GATACTTGAACA ATCTTGCTGAACA ATCTTGCTTGAACACACACACACACACACACACACACACA   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC CTGGGTCTC AAGCTCGACC TCTCTGCTGT AACCAAATCG AGTTTTTCTT CACACAAGCT CACAGAGCT CACAGGTTAAG TCTCTGGGGA GTGAAGGAG TTTCCTGGGGA ATTTGCAGGT TTCACCCAGT GAACATTTC TGTTTTTTAAA AACAATATAC GACAGAGTTA ACAATATAC GTTAAGGAGTTAA  | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT AAAGCACAAT AGAGGTCATT TGCACCAGAA ACAGGTCGAC ACAGGTCGAC CCCCAGTTCT TTCAGGAGTG TCTCGTTACT GAATCACTGT AAAATAGAGT AAAAACAG GAGGAATCTT ACTAAGACTGT ACTAAGACTGT ACTAAGACTGT ACTAAGACTGT ACTAAGACTGT ACTAAGACTGT ACTAAGACTGT ACTAAAACAG GAGGAATCTT ACTATAGCTTT ACTATAGCTTT TCTTATCCTT   | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1980<br>2040<br>2100<br>2220<br>2280<br>2340<br>2400<br>2460<br>2520<br>2580<br>2640   |
| 65<br>70<br>75 | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTCG ATTCGACTTATGA CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCCAAATCCA ATTACTAGGC ACATCAATGA TGTGGTGAAC GGGAAGGCCA AGAACCAAT AGAACCAA AGAAAAGAC CAGAAGCAAT TCAAGATCAT TCAAGAATCAT AGAACCAA AGAAAAGAC CCTTTCTTT TTTACCTTTT   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCAAGTGAA TAAAATACCT AGACATGCAA AAAGTCGAAG AACACAAAAA TGGGAACCAG ATGATTACCT AGACAGTGAAG ATGATTACCT AGAGGGGGCAG CTGCCTCGCC AGGCAGGCAG TTACTGACAC TTGTGTTAC TTTGTGTTAC TTATGACTCAT TTATGACAC TTATGACTCAT                                  | GCTTCTTGCT TTATGACCTG TTGGGCTCTCT ACATGATGGC CGGCTTGTAT CAGGATTACAG GATGACATTA AGATGGGCT AGTACTACAG AGAGCACTAT AGGGCACAG TGGCTGTAT CACAGGAGCA AGGCACAGC TGGCTGGCT AGGCACAGC TTGTCTCACC TTGTCACCACAA ATTTTTTACACAAA ATTTTTTACACAAA ATTTTTTACACCAAA ATTTTTTACACCACAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTTACACCACAAA ATTTTTACACCACAAA ATTTTTACACCACAAAA ATTTTTTACACCACAAAAAATTTTACACCACAAAAATTTTACACCAC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA AATCATGTG AAACCAAGTT ACAGCAAATCA ACTTTGAGAC AGTGCGCGAA ACTGGCGCGAA ACGAGCAACA ACGAGCAACA ACGAGCAACA CGAGCAACA CGAGCCACC TGCCTCTGCTTGAA GATACTTGAACA ATCTTGCTGAACA ATCTTGCTTGAACACACACACACACACACACACACACACA   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAAACTAAA TAGTGACACT CTTGGGTCTC CTGGGTCTC AAGCTCGACC TCTCTGCTGT AACCAAATCG AGTTTTTCTT CACACAAGCT CACAGAGCT CACAGGTTAAG TCTCTGGGGA GTGAAGGAG TTTCCTGGGGA ATTTGCAGGT TTCACCCAGT GAACATTTC TGTTTTTTAAA AACAATATAC GACAGAGTTA ACAATATAC GTTAAGGAGTTAA  | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT AAAGCACAAT AGAGGTCATT TGCACCAGAA ACAGGTCGAC ACAGGTCGAC CCCCAGTTCT TTCAGGAGTG TCTCGTTACT GAATCACTGT AAAATAGAGT AAAAACAG GAGGAATCTT ACTGAAACAG GAGGAATCTT ACTGAAACAG GAGGAATCTT ACTGATAGCTT ACTGATAGCTT ACTGATAGCTT TCTGATAGCTT TCTGATAGCTT TCTGATAGCTT TCTGATAGCTT TCTGATAGCTT TCTGATAGCTT TCTGATAGCTT TCTTATCCTT                               | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>1920<br>1920<br>2140<br>2220<br>2220<br>2240<br>240<br>2520<br>2520<br>2580<br>2580<br>2700  |
| 65<br>70<br>75 | GGAGTTTGCT CTGTGCCTTTT CATGTTCGAC ATTCGAATTCG ATTCGACTTATCC TTATTTATGA GGAAGCAAAA CCAATCAGTGC ATTACTAGCC ACATCAATCCA ATTACTAGCC ACATCAATCCA ACATCAATCCA ACATCAATCCA ACATCAATCCA ACATCAATCCA ACATCAATCCA ACATCAATCCA ACATCAATCCA CGGAAGCCAAA AGAAGCCAA AGAAAAGAC CAGAAGCAAA TACGTTCTTT TCAAGAATTA AAATGTGCAC CCTTTTCTAAT GTATCTTTTT GTATCTTTTTTTTTT   | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG GAGTCTTCAG ATATACCATG TAAAATACCT AGACATGCAA AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG AAAGTCGAAG ATATACCT CAGAGGTGAAG ATGGAACCAG ATGATTACCT AGGAGGTGAA TTACTGACAC TTTTTGCACTT TTTTTGCACTT TTTTTGCACTT TTTTTTTTTT | GCTTCTTGCT TTATGACCTT TATTAGCTT TAGGGCTTCTT ACATGATGGC CGGCTTGTACAG TCCTTATCAG GATGACATTACAG GATGACATTACAG GAAGCACTTAT AGAACACAGAAGAA AGCGGACGGG TGTATCTGAA TGGCTTGGAAGT AAGATTCCACT ACTGGAAGT AAGATTCCACT TTCACACAAA TTTTTTTAACT TCTAACACTT TCTAACACT TCTACCT TC | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAACAAG GCAAAAGCAA ATTGTTGGCA GATCATGTG AAACAAGTT ACAGCAAATC ACTTGACAGCAAATC ACTTGACACGC ATCTCCAGCA ACTCTCGCTGC ACGCAACACAGTT TGCTACGCACCC TGCCTACGCACCC TGCCTACGCACCC TGCCTACGCACCC TGCCTACGCACCC TGCCTACTGCTTC TGCTACGCACCC TGCCTACTGCACCC TGCCTACTGCTTC TGCTACTGCACCC TGCCTACTGCACCC TGCCTACTGCACCC TGCCTACTGCACCC TGCCTACTGCACCC TGCCTACTGCACCC TGCCTACTGCACCC TGCCTACTGCACCC TGCCTACTGCACCC TTATATGCACCC TTATATGTAT | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTGTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGTTTTCTT CACACAAGCT ATTGCACTTC AAATCCAAAC CCAGGTTAAG TTCACCCAGT TTCACCCAGT TTCACCCAGT TTAACTGAA CAGACATTTC CACAGAGTTA CAGACATTTC CACAGAGTTA CAGACATTTT CACAGAGTTA CAGACATTTT CACAGAGTTA CAGACATTT CACAGAGTTA CAGACATTT CACAGAGTTA CAGACATTT CACAGAGTTA CAGACATTT CACAGAGTTA CAGACATTT CAGACATT CAGACAT CAGACA | CAACATTAGT ACTCTTGCA TTCCTTAAAT GAAATTTATG TCATCGGATTGT TGATCATTGT TGATCATTGT CAAGAGACAAT GAAGGTCAAT TGCAGTAGCA ACTCACCAGAA AGAACAGGAC ACAGGTCGAC CCCCAGTTCT TTCAGGATTG TCTCAGGATG GAATCACTGT GAATCACTGT AAAATAGACT CTGAAAACAG GAGGAATCTT ACTTATCTTT ACTTATCTTT ACTTATCCTT TCTTATCCTT TCTTATCCTT TTTTAACCTTT TCTTATCCTT TTTTAACCCTT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1800<br>1860<br>1920<br>2040<br>2160<br>2220<br>2280<br>2340<br>2400<br>2460<br>2520<br>2580<br>2640<br>2700<br>2760<br>2820   |
| 65<br>70<br>75 | GGAGTTTGCT CTGTGCCTTT CATGTTCTATC ATTCGAATTG ATTCGAATTG TACGTCTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGGC ACATCAATGA TGTGGTGAAC ACATCAATGA TGTAGACCAA AGAAACAGAC CAGAAGCAAA TACGTTCTTC TCAAGAATAAT TCAAGAATAA TACGTTCTTC TCAAGAATAA TACGTTCTTC TCAAGAATAA TTTCAAGTAT TTTACCTTTTT GTATCTTTTTTACTTTTTTACTTTTTTTACTTTTTTTACTTTTTT  | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCATGCAA ATATCCCATG AAAGTCGAAA ACACAAAAAA TGGGAACCTGAA GAGCATGCAA CTGCTCGCC CAGGCAGCAA TTACTGACAC TTACTGACTCACAC TTATGACTCACACACACACACACACACACACACACACACA   | GCTTCTTGCT TTATGACCTTT TTATGACCTT ACATGATGGC CGGCTTGTAT CAGGATTACAC TCCTTATCAG GATGACATTACAC GATGACATACAC GAAGACACTAC AGAACAACAC AGAGCACCTA AGGAGCATCCAC TGTATCTGAC TGTATCTGAC ATTGCATTCACACAA TTTTTTACACAAAT TTTTATTTAAC TCAAGATAAC TGAAGATAAC CTATTGGAAGAC CTATTGCATGAC TTAACACAACAC   | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GCAAAAGCAA ATTGTTGGCA GGGTTTTTA GGATCATGTG AAACCAAGTT ACAGCAATCA ACTTGACAG ACTTGACAGA ACTGCGCGAA ACTGCGCGAA ACTGCTGCAA ACTGCTGCTACAG ACTGCTGCTACAG ACTGCTGCAGA ACTGCTGCAGA ACTGCTGCAGA ACTGCTCAGACA ACTGCTGCTTGAAA GCTAACTGAA ACTTTGCTTGA GGTAACTGAA CGTAACTGAA CTTTTGCTAG GTTAATGAAC TTCTTTGCTAG CTTATATGTAI TTTTTAGCAC   | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT CTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG ACGAAATCG ACGACACTTC CACACAAGCT ATGGCACTTC ATGGCACTTC ATTGCAGGA CTCTCTGGGGA ATTTGCAGGA ATTTGCAGGT TTAACCCAGT CGACACATTTC TGTTTTTTTAA TATACTGGAA TTTAACAGTTT TTTAACATTTT TTTAACATTTT TTTAGCACTTT  | CAACATTAGT ACTCTTGCCA TCCTTTAAAT GAAATTATG TCATCAGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGAGAT AAAGCACAAT GAAGGTCAAT TCCAGATGT ACTCACCAGAA AGAACAGGAC ACAGGTCGAC CCCCAGTTCT TTCAGGAGTG TCTCGTTACT GAATCACTGT AAAATAGAGT ACTGACACTACT ACTATCCTT ACTATCCTT TCTAAAACAG GAGGAATCTT TCTAAAACAG TCTTATCCTT TTTAAAATCCT TTTAAAATCCTT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1980<br>2040<br>2100<br>2100<br>2220<br>2280<br>2340<br>2400<br>2520<br>2520<br>2520<br>2560<br>2640<br>2700<br>2760<br>2820<br>2880                 |
| 65<br>70<br>75 | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG ATTCGAATTG CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGCC ACATCAATGA GGGAAGGGCC AGGAGCAAA AGAAGAGGATAT TCAGAACCAA AGAAAGAGC CAGAAGCAA AGAAGATTA TACGTTCTTC TCAAGAATTA AAATGTGCAC CCTTTTTCTAATTACTTTT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTC | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCATGCAA ATATCCCATG TAAAATACCT AGACATGCAA ACACAAAAA TGGGAACCAG AACACCAAAAA TGGGAACCAG AGGCAGCTCAA GGAGGTGAA TTACTGACA TTACTGACA TTTTTGCACTT ATAGACTCAT TTTTACATAAT TTTTACATAATA TTATACATAATA TTATACATAC                                 | GCTTCTTGCT TTATGACTGT TTATGACTGT ACATGATGGC GGCTTGTAT CAGGATTACAC GATGACATTACAC GATGACATTACAC GAATGACACTAT AGAATGACACTAT AGGACACTAT AGGACACTAT AGGACACTAT AGCAGGACCT TGTATCTGAA AGCGGACGGC AGGTTCCAC AGGTTCCAC AGGTTCCAC AGGTTCCAC TTGTCATTCT AAAGTTGCAT TTTTTTTTACACACAAA TTTTTTTTTACACTACACAAA TTCTACTCTTC ACAGGACTAT TCAACACAAA TTTTTTTTTACACTACAC  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GGATATATG GAATATATG AAACCAAGTT ACAGCAAATC ACTTTGACAG A GGTACCACAA A TCTCCAGAC A AGTGCCCGAG A CATGCCCGAC A TCTCTGCTTG A GATACTTGAA A CAGAACAACA TCTCTGCTTG A GATACTTGAA A GATACTTGAA A TCTTTGCTGG TGCTTATATGTAT TTTATACCAG TTTTATACCAG TTTTATACCAG  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT TCTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGATTTTCTT CACACAGGCT AAGCTCGGGAC CCACGGTAAG TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TTTCACCAGT ATTTGCAGGT TTCACCCAGT GAACATTTTC TGACCTTGTAAG TTTTAGAACTTTT AGACATTTAAAG TTTAAAGATTT AGTATTTAAAG TTTGAACTTTT TTTGAACTTTT TTTTGAACCTTT TTTTGAACCTTT TTTTGAACCTTT TTTTGAACCTTT TTTTGAACCTTT TTTTTTTTT  | CAACATTAGT ACTCTTGCCA TCCTTAAAT GAAATTTATG TCTCGGATGT TGAGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGACAT GAAGGTCATT TGCAGTAGCA ACAACAGGAC ACAGGTCGAC GATTAGTCCA TTCAGGAGTG TCCGGTTCT TTCAGGAGTG AAAATAGACT CAGAAACAG GAGGAATCTT ACTTAGCCTT TTTTAAAATCCT TTTTAAAATCAT TTTTACACTGA ATACCCGAAAAAAAAAA  | 1260<br>1320<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>2940<br>2100<br>2210<br>2280<br>2340<br>2400<br>2520<br>2580<br>2640<br>2700<br>2760<br>2820<br>2820<br>2700<br>2760<br>2820<br>2880<br>2940 |
| 65<br>70<br>75 | GGAGTTTGCT CTGTGCCTTT CATGTTCGAC ATTCGAATTG ATTCGAATTG CGTCAGTACC TTATTTATGA GGAAGCAAAA CCAATCAGTG TCTAAAGTTA TCCAAATCCA ATTACTAGCC ACATCAATGA GGGAAGGGCC AGGAGCAAA AGAAGAGGATAT TCAGAACCAA AGAAAGAGC CAGAAGCAA AGAAGATTA TACGTTCTTC TCAAGAATTA AAATGTGCAC CCTTTTTCTAATTACTTTT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTCAAGTAT ATTCTAAGTAT ATTC | TGACTGTTAT TTGTTGGCCT GTGTGTTTGT AAGTCATACA GAGTCTTCAG AGCATGCAA ATATCCCATG TAAAATACCT AGACATGCAA ACACAAAAA TGGGAACCAG AACACCAAAAA TGGGAACCAG AGGCAGCTCAA GGAGGTGAA TTACTGACA TTACTGACA TTTTTGCACTT ATAGACTCAT TTTTACATAAT TTTTACATAATA TTATACATAATA TTATACATAC                                 | GCTTCTTGCT TTATGACTGT TTATGACTGT ACATGATGGC GGCTTGTAT CAGGATTACAC GATGACATTACAC GATGACATTACAC GAATGACACTAT AGAATGACACTAT AGGACACTAT AGGACACTAT AGGACACTAT AGCAGGACCT TGTATCTGAA AGCGGACGGC AGGTTCCAC AGGTTCCAC AGGTTCCAC AGGTTCCAC TTGTCATTCT AAAGTTGCAT TTTTTTTTACACACAAA TTTTTTTTTACACTACACAAA TTCTACTCTTC ACAGGACTAT TCAACACAAA TTTTTTTTTACACTACAC  | CTGAACAAAG GATGCTTCTC CTTCTTTTAG CGGAACCAAG CTTGTGCCAT TGGGAGATAA GGATATATG GAATATATG AAACCAAGTT ACAGCAAATC ACTTTGACAG A GGTACCACAA A TCTCCAGAC A AGTGCCCGAG A CATGCCCGAC A TCTCTGCTTG A GATACTTGAA A CAGAACAACA TCTCTGCTTG A GATACTTGAA A GATACTTGAA A TCTTTGCTGG TGCTTATATGTAT TTTATACCAG TTTTATACCAG TTTTATACCAG  | TTGAAGGAGA GCTACTTTGT CTGGCATTAT AAAACTAAA TAGTGACACT TCTTGGGTCTC AAGCTCGACC TCTCTGCTGT AACGAAATCG AGATTTTCTT CACACAGGCT AAGCTCGGGAC CCACGGTAAG TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TCTCTGGGGA TTTCACCAGT ATTTGCAGGT TTCACCCAGT GAACATTTTC TGACCTTGTAAG TTTTAGAACTTTT AGACATTTAAAG TTTAAAGATTT AGTATTTAAAG TTTGAACTTTT TTTGAACTTTT TTTTGAACCTTT TTTTGAACCTTT TTTTGAACCTTT TTTTGAACCTTT TTTTGAACCTTT TTTTTTTTT  | CAACATTAGT ACTCTTGCCA TCCTTTAAAT GAAATTATG TCATCAGATGT TGATCATTGT AGAATTGGCT CTTCTGGGTT CAAGAGAGAT AAAGCACAAT GAAGGTCAAT TCCAGATGT ACTCACCAGAA AGAACAGGAC ACAGGTCGAC CCCCAGTTCT TTCAGGAGTG TCTCGTTACT GAATCACTGT AAAATAGAGT ACTGACACTACT ACTATCCTT ACTATCCTT TCTAAAACAG GAGGAATCTT TCTAAAACAG TCTTATCCTT TTTAAAATCCT TTTAAAATCCTT  | 1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1860<br>1920<br>1920<br>2100<br>2160<br>2220<br>2340<br>2400<br>2450<br>2520<br>2580<br>2640<br>2700<br>2760<br>2820<br>2880<br>2940                 |

| 5  | GGTGCTTACT<br>ATATTTAAAA<br>GGCCAAGTGC<br>AACCACTTAC<br>TACATTTTGT | CAAAGAGTGT<br>TAAAATGTCC<br>AATTGACTTC<br>AGTTGCTTAT<br>ATTATACAGT | CCACTATIGA<br>TAAAGGGTTA<br>CCTTTTTTAA<br>ATTTTTTGTT<br>ACCTTTCTCA | TCACAGATCT TTGTATTATG GTAGACAAAA TGTTTCATGA TTAACTTTTG GACATTTTGT | CTGCTCACTG<br>TGTTAGTCTT<br>CCACCCATTG<br>TTTCTTAACA | ATCCTTCTGC<br>TTGTATATTA<br>ATTGTATTAT | 3060<br>3120<br>3180<br>3240<br>3300<br>3342 |
|----|--|--|--|---|--|--|--|
| 10 |  |  | 1#: NM_0005  | 82  |  |  |  |
|    | 1  | 11   | 21   | 31  | 41   | 51                                     |  |
|    | <br>  GCAGAGCACA   | GCATCGTCGG   | GACCAGACTC   | GTCTCAGGCC  | AGTTGCAGCC   | TTCTCAGCCA                             | 60   |
| 15 | AACGCCGACC   | AAGGAAAACT   | CACTACCATG   | AGAATTGCAG  | TGATTTGCTT   | TTGCCTCCTA                             | 120  |
|    |  |  |  | GCTGATTCTG<br>ACATGGCTAA  |  |  | 180<br>240                                   |
|    | CAGAATCTCC   | TAGCCCCACA   | GACCCTTCCA   | AGTAAGTCCA  | ACGAAAGCCA   | TGACCACATG                             | 300  |
| 20 |  |  |  | CATGTGGACA<br>GATTCTCACC  |  |  | 360<br>420                                   |
| -0 | TCTGATGAAT   | CTGATGAACT   | GGTCACTGAT   | TTTCCCACGG  | ACCTGCCAGC   | AACCGAAGTT                             | 480  |
|    |  |  |  | TATGATGGCC<br>AGACCTGACA  |  |  | 540<br>600                                   |
|    |  |  |  | GAGGAGTTGA  |  |  | 660  |
| 25 | CCCGTTGCCC   | AGGACCTGAA   | CGCGCCTTCT   | GATTGGGACA  | GCCGTGGGAA   | GGACAGTTAT                             | 720  |
|    |  |  |  | GAAACCCACA<br>GAGCATTCCG  |  |  | 780<br>840                                   |
|    | CTTTCCAAAG   | TCAGCCGTGA   | ATTCCACAGC   | CATGAATTTC  | ACAGCCATGA   | AGATATGCTG                             | 900  |
| 30 |  |  |  | AAACACCTGA<br>AAGGAGAAAA  |  |  | 960<br>1020                                  |
| 20 |  |  |  | AAAATGAAAG  |  |  | 1080   |
|    |  |  |  | TGAGTCTGGA<br>CCCTGTAAAC  |  |  | 1140<br>1200                                 |
|    |  |  |  | TATCACTGTA  |  |  | 1260   |
| 35 |  |  |  | AAAATACTTT  |  |  | 1320   |
|    |  |  |  | TTTTTAAGTT<br>TCTTGAATGT  |  |  | 1380<br>1440                                 |
|    | AATTGCTTAT   | TIGITITICCC  | ACCGTTGTCC   | AGCAATTAAT  |  |  | 1500   |
| 40 | GCCTAAAAA  | AAAAAAAA   | AAAA   |   |  |  | 1524   |
|    | Seq ID NO:   | C171 DNA S   | equence  |   |  |  |  |
|    |  | id Accessio  | _  | 2821  |  |  |  |
|    | 1  | quence: 150.<br>11   | 21   | 31  | 41   | 51                                     |  |
| 45 | 1  | 1  | 1  |   | 1  | Transportation I                       | 60   |
|    |  |  |  | GCTCCGGCTG<br>CCGCGGAGCA  |  |  | 120  |
|    | CCTCAGCTCC   | TITTCCTGAG   | CCCGCCGCG  | TGGGAGCTGC  | GCGGGGATCC   | CCGGCCAGAC                             | 180  |
| 50 |  |  |  | : TGCTGCCGCT<br>: AGGATGCACT                                      |  | ACCCAGACAG                             | 240<br>300                                   |
|    | TTCGCTGTG  | GGTTGAGGCT   | CCCCCCCCCC   | TACATGTGTA  | CTGGCTGCTC   | GATGGGGCCC                             | 360  |
|    |  |  |  |   |  | GCAGCTGTGG<br>ACTGGAGAAG               | 420<br>480                                   |
|    | AAGCCCGCAG   | G TGCCAACGC  | TCCTTCAAC  | A TCAAATGGAT  | TGAGGCAGGT   | CCTGTGGTCC                             | 540  |
| 55 |  |  |  |   |  | CTTCGTTGCC                             | 600<br>660                                   |
|    |  |  |  |   |  | CGGCCAGCTG                             | 720  |
| *  |  |  |  |   |  | CAGGCTTGCA                             | 780<br>840                                   |
| 60 |  |  |  |   |  | GTGCTGGCAC<br>TTCTCAGCCC               | 900  |
|    |  |  |  |   |  | AACCGCAGTC                             | 960  |
|    | TCCGGCCAC  | A CCTCCGCAG  | A GCCACAGTG  | r Trgccaacgo<br>r gcattggcca                                      | GCCCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC               | GCCCACCCA                              | 1020<br>1080                                 |
| CE | TCATCCTGG  | A AGCCACACT  | r CACCTAGCA  | 3 AGATTGAAGA  | CATGCCGCT  | TTTGAGCCAC                             | 1140   |
| 65 |  |  |  |   |  | GGTCTGCCAG<br>AGGGTCTACC               | 1200<br>1260                                 |
|    | AGAAGGGCC  | A CGAGCTGGT  | G TTGGCCAAT  | A TIGCIGAAAC  | TGATGCTGG  | GTCTACACCT                             | 1320   |
|    |  |  |  |   |  | GTGGCCACTG A CCCGGCTACT                |  |
| 70 |  |  |  |   |  | AACCAGATGC                             |  |
|    |  |  |  |   |  | ATCAACAGCG                             | 1560   |
|    |  |  |  |   |  | C GGCAGCATCG<br>A CCCCAGCCAC           | 1620<br>1680                                 |
| 75 | AGCAGTGCA  | T GGAGTTTGA  | C AAGGAGGCC  | A CGGTGCCCT   | TTCAGCCAC  | A GGCCGAGAGA                           | 1740   |
| 75 |  |  |  |   |  | G GTGACAGACA<br>C TACACTTGCA           | 1800<br>1860                                 |
|    | TTGCCTCCA  | A CGGGCCGCA  | G GGCCAGATI  | C GIGCCCATG   | T CCAGCTCAC  | I GTGGCAGTTT                           | 1920   |
|    | TTATCACCI  | T CAAAGTGGA  | A CCAGAGCGT  | A CGACTGTGT   | A CCAGGGCCA  | C ACAGCCCTAC                           |  |
| 80 |  |  |  |   |  | C AAGGACCGCA<br>C TCCCTGGTGA           | 2040<br>2100                                 |
|    |  |  |  |   |  | C AACAGCTGCA                           | 2160   |
|    |  |  |  |   |  |  |  |
|    | ACATCAAGO  | A CACGGAGGC  | C CCCCTCTAT  | G TCGTGGACA   | A GCCTGTGCC  | G GAGGAGTCGG                           | 2220   |
|    | ACATCAAGO<br>AGGGCCCTO   | CA CACGGAGGO<br>GG CAGCCCTCO                                       | C CCCTCTAT   | 'G TCGTGGACA<br>IA TGATCCAGA                                      | A GCCTGTGCC<br>C CATTGGGTT                           |  | 2220   |

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|     | GCAGTGTGCA  | GGCAGGTCCT                | GAGGCCTGGG   | GTTGGGGTGG | AGGGTGCGGC | CCGGAGTTGT | 2820         |
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|     |             |                           | CAAGACGAGG   |            |            |            | 2880         |
|     | CCCTTGTCCA  | GGATGCAGGG                | ACTGCCTTCT   | CCTTCCTGCT | TCATCCGGCT | TAGCTTGGGG | 2940         |
| _   | CTGGCTGCAT  | TCCCCCAGGA                | TGGGCTTCGA   | GAAAGACAAA | CTTGTCTGGA | AACCAGAGTT | 3000         |
| 5   | GCTGATTCCA  | CCCGGGGGGC                | CCGGCTGACT   | CGCCCATCAC | CTCATCTCCC | TGTGGACTTG | 3060         |
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|     | GGACTTGGCC  | CCATGGGACC                | CATCCTCAGT   | GCTCCCTCCA | GATCCCGTCC | GGCAGCTTGG | 3180         |
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| 10  | CCGGGAGCTG  | GGTTTCTCTT                | CCCTTTTTAT   | CTGCTGGTGT | GGACCACACC | TGGGCCTGGC | 3300         |
| 10  | CGGAGGAAGA  | GAGAGTTTAC                | CAAGAGAGAT   | GTCTCCGGGC | CCTTATTTAT | TATTTAAACA | 3360         |
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| 15  |             |                           | CGCCCACGTG   |            |            |            | 3660         |
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|     |             |                           | GATGTTTCAT   |            |            |            | 3780         |
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| 20  | GAGAAATGAA  | TAAAGAATCT                | ACTCTTCG     |            |            |            | 3868         |
| 20  | 0 TD 110    | G1 63 644 6               |              |            |            |            |              |
|     |             | C173 DNA Se               |              |            |            |            |              |
|     |             | lo Accession<br>Jence: 44 | 1 #: XM_0975 | 808        |            |            |              |
|     | courng sequ | nence: 44                 | . 700        |            |            |            |              |
| 25  | 1           | 11                        | 21           | 31         | 41         | 51         |              |
|     | ī           | ī                         | ī            | ī          | Ĩ          | Ī          |              |
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|     | GACACTTGTT  | TGTCACGTGT                | CAATAATCAT   | CTCTGCCCGG | GACCTCAGCA | TGAACAACCT | 120          |
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|     |             |                           | TAGATGCCAA   |            |            |            | 360          |
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| 40  |             |                           | CTAAACTCCA   |            |            |            | 840          |
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|     |             |                           | AGGAGCTGCC   |            |            |            | 1020         |
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| -13 |             |                           | TCAAGCTGGAA  |            |            |            | 1140<br>1200 |
|     |             |                           | TGATGCATCT   |            |            |            | 1260         |
|     |             |                           |              |            |            | ATGCCTACCA | 1320         |
|     |             |                           |              |            |            | GGGAGGCTGA | 1380         |
| 50  |             |                           |              |            |            | TTGCCAGACA | 1440         |
|     |             |                           |              |            |            | AGGACTCAAA | 1500         |
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|     | CTTTGAAAGC  | TGGGGCATCC                | GCCTGGCCGT   | GTGGGCCATC | GTGTTGCTCT | CCGTGCTCTG | 1620         |
| ~ ~ | CAATGGACTG  | GTGCTGCTGA                | CCGTGTTCGC   | TGGCGGGCCT | GTCCCCCTGC | CCCCGGTCAA | 1680         |
| 55  |             |                           |              |            |            | GTGGCCTTCT | 1740         |
|     |             |                           |              |            |            | GCTGGGAGAC | 1800         |
|     |             |                           |              |            |            | CATCGGTGCT | 1860         |
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| UU  |             |                           |              |            |            | CACTCTGCCT | 2040         |
|     |             |                           |              |            |            | CCCTGGTGAT | 2100         |
|     |             |                           |              |            |            | ACTGTGACCT | 2160<br>2220 |
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|     |             |                           |              |            |            | ATGTGGATCT | 2520         |
|     |             |                           |              |            |            | GCTTCCCCTC | 2580         |
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|     |             |                           |              |            |            | AACTGCTGCT | 2700         |
|     |             |                           |              |            |            | GCTTTCAGCC | 2760         |
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|     |             |                           |              |            |            | CTTCCTCAGC |              |
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| 00  |             |                           |              |            |            | TCCCGTGTGA |              |
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Seq ID NO: C174 DNA Sequence Nucleic Acid Accession #: NM\_130849

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|      |            | TCCGGCGAGG |            |            |            |            | 960  |
|      |            | AAGGCCCTGC |            |            |            |            | 1020 |
|      |            | CAGGACCTGC |            |            |            |            | 1080 |
|      |            | AACCCCATGG |            |            |            |            | 1140 |
| 15   |            | ATGATGCAGT |            |            |            |            | 1200 |
|      |            | TTTCGTACTG |            |            |            |            | 1260 |
|      |            | AAACGTGCGT |            |            |            |            | 1320 |
|      |            | ATGGACCTTG |            |            |            |            | 1380 |
|      |            | ATCTACTTCC |            |            |            |            | 1440 |
| 20   |            | TTGCTGATTC |            |            |            |            | 1500 |
|      |            | ATGAAATTGA |            |            |            |            | 1560 |
|      |            | CTGAAGCTGT |            |            |            |            | 1620 |
|      |            | GAGCTCCAGC |            |            |            |            | 1680 |
|      |            | TGCAGCCCCT |            |            |            |            | 1740 |
| 25   |            | AATGTGCTGG |            |            |            |            | 1800 |
|      |            | CCCCTCAACA |            |            |            |            | 1860 |
|      |            | CGGATCCAGC |            |            |            |            | 1920 |
|      |            | ATCTCCCCAG |            |            |            |            | 1980 |
|      |            | CCCCCCACTC |            |            |            |            | 2040 |
| 30   |            | GGGCCTGTGG |            |            |            |            | 2100 |
| 20   |            | CTAGAAGGCA |            |            |            |            | 2160 |
|      |            | CAGAACTGCA |            |            |            |            | 2220 |
|      |            | CAGCAGACTC |            |            |            |            | 2280 |
|      |            | CAGACAGAGA |            |            |            |            | 2340 |
| 35   |            | CTGGCTCGAG |            |            |            |            | 2400 |
| 20   |            | GTGGACTCTC |            |            |            |            | 2460 |
| •    |            | GCAGGCAAGA |            |            |            |            |      |
|      |            |            |            |            |            |            | 2520 |
|      |            | ATCATTGTGC |            |            |            |            | 2580 |
| 40   |            | CGCAACGGCT |            |            |            |            | 2640 |
| 70   |            | CTGGAGGACA |            |            |            |            | 2700 |
|      |            |            |            |            |            | CAGTCACCTA | 2760 |
|      |            | AAGCAGTTTA |            |            |            |            | 2820 |
|      |            | GTACCCCGGA |            |            |            |            | 2880 |
| 45   |            | GGGGCACTGA |            |            |            |            | 2940 |
| 73   |            | GATTATGCCA |            |            |            |            | 3000 |
|      |            |            |            |            |            | CCTGGACAAA | 3060 |
|      |            |            |            |            |            | TCTATGCTGC | 3120 |
|      |            |            |            |            |            | CAGCGGGTGG | 3180 |
| - 50 |            |            |            |            |            | GCTCGCCACA | 3240 |
| . 50 |            |            |            |            |            | AGGACATCTA | 3300 |
|      |            | GAGGTTCTGG |            |            |            |            | 3360 |
|      |            |            |            |            |            | TCATCCTGCC | 3420 |
|      |            |            |            |            |            | GGCAACTGAA | 3480 |
| 55   |            |            |            |            |            | CAGTGACTGG | 3540 |
| 33   |            |            |            |            |            | GTGATACTAA | 3600 |
|      | GGTGGATGCC | AACCAGAGAA | GCTGCTACCC | CTACATCATC | TCCAACCGGT | GGCTGAGCAT | 3660 |
|      |            |            |            |            |            | CCGTCATCGG | 3720 |
|      |            |            |            |            |            | TGCAGGTGAC | 3780 |
| 60   |            |            |            |            |            | TCGTGGCTGT | 3840 |
| OU   |            |            |            |            |            | TGGAAGGCAG | 3900 |
|      | CCGCCCTCCC | GAAGGTTGGC | CCCCACGTGG | GGAGGTGGAG | TTCCGGAATT | ATTCTGTGCG | 3960 |
|      |            |            |            |            |            | ACGGTGGCGA | 4020 |
|      |            |            |            |            |            | TTTGCCTGTT | 4080 |
| 65   |            |            |            |            |            | TGGCAGACAT | 4140 |
| 03   |            |            |            |            |            | TCCTGTTCTC | 4200 |
|      |            |            |            |            |            | ACATTTGGTG | 4260 |
|      |            |            |            |            |            | GCCTGGACTT | 4320 |
|      |            |            |            |            |            | TGTGCCTGGC | 4380 |
| 70   | CCGAGCCCTG | CTCCGCAAGA | GCCGCATCCT | GGTTTTAGAC | GAGGCCACAG | CTGCCATCGA | 4440 |
| 70   |            |            |            |            |            | CCTGCACTGT | 4500 |
|      | CCTGACCATC | GCACACCGGC | TTAACACTAT | CATGGACTAC | ACCAGGGTCC | TGGTCCTGGA | 4560 |
|      | CAAAGGAGTA | GTAGCTGAAT | TTGATTCTCC | AGCCAACCTC | ATTGCAGCTA | GAGGCATCTT | 4620 |
|      | CTACGGGATC | GCCAGAGATG | CTGGACTTGC | CTAAAATATA | TTCCTGAGAT | TTCCTCCTGG | 4680 |
| 7.   |            |            |            |            |            | ATGGACTTGA | 4740 |
| 75   |            |            |            |            |            | AGGGTAACTG | 4800 |
|      |            |            |            |            |            | CTAAGGTCAC | 4860 |
|      |            |            |            |            |            |            | 4920 |
|      |            |            |            |            |            |            | 4980 |
| 00   |            |            |            |            |            | TCCTCCTGGA | 5040 |
| 80   |            |            |            |            |            | TCTGGGGTGC | 5100 |
|      |            |            |            |            |            | CAACAGTAAA | 5160 |
|      | AAAAAAAA   |            |            |            |            |            | 5176 |
|      |            |            |            |            |            |            |      |

Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM\_004626 Coding sequence: 124..1188

| 5          | 1          | 11         | 21                       | 31         | 41         | 51                           |              |
|------------|------------|------------|--------------------------|------------|------------|------------------------------|--------------|
| 5          | TAACCCGCCG | CCTCCGCTCT | CCCCGGCTGC               | AGGCGGCGTG | CAGGACCAGC | GGCGGCCGTG                   | 60           |
|            |            |            | GGCTCCTCCT               |            |            |                              | 120          |
|            |            |            | GGTCTGCGAG               |            |            |                              | 180          |
| 10         |            |            | GTGGCTGGCG               |            |            |                              | 240          |
| 10         |            |            | GCAGCTGGAG<br>GCACACGGTG |            |            |                              | 300<br>360   |
|            |            |            | CATGOSCTGS               |            |            |                              | 420          |
|            |            |            | AGGGACCCGG               |            |            |                              | 480          |
|            |            |            | CGCCCGGGCC               |            |            |                              | 540          |
| 15         |            |            | GCCACCCGGG               |            |            |                              | 600          |
|            |            |            | CATGGGGGCC               |            |            |                              | 660          |
|            |            |            | TAAACTGATG<br>AATGAAGTGT |            |            |                              | 720<br>780   |
|            |            |            | GCTGCAGGAG               |            |            |                              | 840          |
| 20         |            |            | GGTAGTGCAC               |            |            |                              | 900          |
|            |            |            | GCCTGTGAAG               |            |            |                              | 960          |
|            |            |            | TGAGAAGGTG               |            |            |                              | 1020         |
|            |            |            | CGACAGCTGC               |            |            |                              | 1080         |
| 25         |            |            | CGAGCGGTGC               |            |            |                              | 1140<br>1200 |
|            |            |            | ACTCTGCTCA               |            |            |                              | 1260         |
|            |            |            | TGCTTGTGAA               |            |            |                              | 1320         |
|            |            |            | GCCACCAGGA               |            |            |                              | 1380         |
| 30         |            |            | ACAAGATTAA               |            |            |                              | 1440         |
| 30         |            |            | AGCGGGGCTT               |            |            | CAGAATGTTC                   | 1500<br>1560 |
|            |            |            | CCTGGGGTCT               |            |            |                              | 1620         |
|            |            |            |                          |            |            | GGATGTGGAA                   | 1680         |
| 25         |            |            | ACATAGCTTT               |            |            |                              | 1740         |
| 35         |            |            | AATATATATG               |            |            |                              | 1800         |
|            |            |            |                          |            |            | ·CCCTGCAGTT                  | 1860         |
|            | CCAGGCA    | TCAAGTGAAC | TCGGCAGACC               | CIGGGGCIGG | CAGAGGGAGC | TCTCCAGTTT                   | 1920<br>1927 |
|            | COMOGN     |            |                          |            |            |                              | 1,2,         |
| 40         | Seq ID NO: | C181 DNA S | equence                  |            |            |                              | •            |
|            |            |            | n #: NM_031              | B66        |            |                              |              |
|            | Coding seq | uence: 62  | 090                      |            |            |                              |              |
|            | 1          | 11         | 21                       | 31         | 41         | 51                           |              |
| 45         | ī          | ī          | ī                        | ĭ          | Ĩ          | ī                            |              |
|            |            |            |                          |            |            | TTGGCGCTGC                   | 60           |
|            |            |            |                          |            |            | CAAGAGATCA                   | 120          |
|            |            |            |                          |            |            | CAGTTCAACC                   | 180          |
| 50         |            |            |                          |            |            | GTGGAGATCC<br>TGCCTAGAGG     | 240<br>300   |
|            |            |            |                          |            |            | GCCGGCTGCG                   | 360          |
|            | CGCCGCTCAT | GCGCCAGTAC | GGCTTCGCCT               | GGCCCGACCG | CATGCGCTGC | GACCGGCTGC                   | 420          |
|            |            |            |                          |            |            | CTAACCACCG                   | 480          |
| 55         |            |            |                          |            |            | CCGCCTTCGG                   | 540          |
| JJ         |            |            |                          |            |            | GGCAGGGGCG<br>GGGAAGGCGC     | 600<br>660   |
|            |            |            |                          |            |            | GCGCCTATGG                   | 720          |
|            |            |            |                          |            |            | CAGATCGCTA                   | 780          |
| <b>6</b> 0 |            |            |                          |            |            | TTCACCGTCT                   | 840          |
| 60         |            |            |                          |            |            | GTCTCCACCT                   | 900          |
|            |            |            |                          |            |            | CTCTCGGCCT<br>GAGAAGGTGG     | 960<br>1020  |
|            |            |            |                          |            |            | GOGGOGGCGG                   | 1080         |
| ~=         |            |            |                          |            |            | TACGAGGAGC                   | 1140         |
| 65         |            |            |                          |            |            | TGCACCGTGG                   | 1200         |
|            |            |            |                          |            |            | ATCTTGTCGC                   | 1260         |
|            |            |            |                          |            |            | GGCTACTCGC<br>GTGCTGGCGC     | 1320<br>1380 |
|            |            |            |                          |            |            | CAGAGCCTGG                   | 1440         |
| 70         |            |            |                          |            |            | GGCACCATGT                   | 1500         |
|            | TCCTGCTGGC | CGGCTTCGTC | TCCCTGTTCC               | GCATCCGCTC | GGTCATCAAC | CAACAGGACG                   | 1560         |
|            |            |            |                          |            |            | TTCACCGTGC                   | 1620         |
|            |            |            |                          |            |            | CACAACCGCC                   | 1680         |
| 75         |            |            |                          |            |            | GACCAGGCAC<br>GGGGGCATCA     | 1740<br>1800 |
| , ,        |            |            |                          |            |            | CTGTGCACCC                   | 1860         |
|            |            |            |                          |            |            | CACGGCCGCGG                  | 1920         |
|            | GGGGTGGCGC | ccccccccc  | GGGGGGGGG                | GCGGGGGACC | CGGCGGCGG  | C GGGGGGCCGG                 | 1980         |
| 80         |            |            |                          |            |            | CGGTCGGGCA                   | 2040         |
| οU         |            |            |                          |            |            | A GCGGAGGGGA                 | 2100<br>2160 |
|            |            |            |                          |            |            | C GAAGGGACAC<br>C GATAATGAAC | 2220         |
|            |            |            |                          |            |            | TACCTGGCAT                   | 2280         |
|            |            |            |                          |            |            | r ccrcccgcca                 | 2340         |
|            |            |            |                          |            |            |                              |              |

| 5<br>10<br>15 | TGGAGCCTC GAGAACCTCT GAGGAGGGT AAATGCCTTA TTCTTACATT TACATTT AAAATATGTA TACCCTGTA GATTTAACCA AGGACGCATG TGGAGAAAAT TGAACTGAAA CTCTTTTCTG AGGCAGTAAT AACCCTGAAA | CCTGGCTGCA<br>TTTTCTCCT<br>GACCGCCACC<br>AGTAAACAAA<br>AGAGGATGTA<br>TATATCCAAA<br>AGAACAGATA<br>TTGCCCTCTC<br>GGGAAAATGG<br>TACTTGTTAA<br>ATCCATGGAT<br>TCCCCTTAGG | GAGGAGGTG CTTGGCTGGG CGACTCTTCC TGATGGGATT CAAGAAATGT TTTATATAAT GATATAGTGT TAAGTATTCT CCCCGCCTCT ACATTTTCTG ACTTTTCTG GTTTTTGCAC AACAACTCTC CCTTGTTATT | TTTGCAGTCA TACGTAAACT GCACGGTTTG CTTAATTATA TATTTGTTAA GTACATTTTT ATTTTGTCAA TCTGAGCTGT GCTTGTCATT TTAAGTTGTT CTTCCCCAAA ACTTTAGTGG | GATACACAGA<br>CCCACCCTG<br>GGTATTCTTA<br>CACCCCACGT<br>ATTGTAAAAA<br>TTGTAAAAAG<br>TAAAATGACT<br>CACCTTTAAA<br>CTGTACACTG<br>AGCCAAGTAA<br>GACGGTGTTT<br>ATGTAAATGG | TTTCACCTGG ACTTACCCTG ACTTACCCTG AAAAACGGCT AAAAAAGTGT TTTAGAGGCT TTTGATAAAT GTGCTTGCTA ACCTTAGGCA ATATCATTGT TTCATGGGGA AAATCATTGT ACCTTAGGAGA AACTTCTGCA | 2400<br>2460<br>2520<br>2580<br>2640<br>2700<br>2760<br>2820<br>2820<br>2940<br>3000<br>3060<br>3120<br>3180<br>3195 |
|---------------|--|---|---|---|---|--|--|
| 20            | Nucleic Aci  |   | #: XM_0506  | 525   |   |  |  |
| 25            | CCGGTGTCCC<br>GCACCCAGCG<br>CGGCTCCGCT<br>CGCTGCTGCT<br>TCTTTGGCCA   | GCTTCTCCGC<br>AAGAGAGCGG<br>CCCTCTGCCC<br>GCTCTTCCTC<br>GCCCGACTTC  | 21<br> <br>GCTGCGCGCG<br>GCCCAGCCG<br>GCCCGGGACA<br>CCTCGGGGTC<br>GCCTCGCACT<br>TCCTACAAGC  | CCGGCTGCCA<br>AGCTCGAACT<br>GCGCGCCCAC<br>GCTGCCTGGG<br>GCAGCAATTG  | GCTTTTCGGG<br>CCGGCCGCT<br>GATGCTGCAG<br>CTCGGCGCGC<br>CAAGCCCATC   | GCCCGAGTC<br>CGCCCTTCCC<br>GGCCCTGGCT<br>GGGCTCTTCC<br>CCTGCCAACC  | 60<br>120<br>180<br>240<br>300<br>360  |
| 30            | AGACCATGAA<br>GCCACCCGGA<br>TAGACGAGAC<br>CGGTCATGTC   | GGAGGTGCTG<br>CACCAAGAAG<br>CATCCAGCCA<br>CGCCTTCGGC  | GAATACCAGA<br>GAGCAGGCCG<br>TTCCTGTGCT<br>TGCCACTCGC<br>TTCCCCTGGC<br>CCCCTCGCTA  | GCGCTTGGAT<br>CGCTCTTCGC<br>TCTGCGTGCA<br>CCGACATGCT  | CCCGCTGGTC<br>CCCCGTCTGC<br>GGTGAAGGAC<br>TGAGTGCGAC  | ATGAAGCAGT<br>CTCGATGACC<br>CGCTGCGCCC<br>CGTTTCCCCC   | 420<br>480<br>540<br>600<br>660  |
| 35            | AAGCTCCAAA<br>AAACGCTTTG<br>ACCGAGATAC<br>TGTCCGAAAG   | GGTATGTGAA<br>TAAAAATGAT<br>CAAAATCATC<br>GGACCTGAAG  | GCCTGCAAAA<br>TTTGCACTGA<br>CTGGAGACCA<br>AAATCGGTGC<br>AACGCGCCCT  | ATAAAAATGA<br>AAATAAAAGT<br>AGAGCAAGAC<br>TGTGGCTCAA  | TGATGACAAC<br>GAAGGAGATA<br>CATTTACAAG<br>AGACAGCTTG  | GACATAATGG<br>ACCTACATCA<br>CTGAACGGTG<br>CAGTGCACCT   | 720<br>780<br>840<br>900<br>960<br>1020  |
| 40            | AGCTGGTGAT<br>CCCGCAGCAT<br>CTCCAGAGCA<br>TCCTAGCTGC   | CACCTCGGTG<br>CCGCAAGCTG<br>CGGCTGACCA<br>TCCAGTCTCA  | AAGCGGTGGC<br>CAGTGCTAGT<br>TTTCTGCTCC<br>GCCTGGGCAG<br>AGGCCACAGG  | AGAAGGGGCA<br>CCCGGCATCC<br>GGGATCTCAG<br>CTTCCCCCTG  | GAGAGAGTTC<br>TGATGGCTCC<br>CTCCCGTTCC<br>CCTTTTGCAC  | AAGCGCATCT<br>GACAGGCCTG<br>CCAAGCACAC<br>GTTTGCATCC   | 1080<br>1140<br>1200<br>1260<br>1320   |
| 45            | GCCCACCCGA<br>TT   | ATCTTGTAGA  | AATATTCAAA  |   |   |  | 1380<br>1382   |
| 50            | Nucleic Act  | C183 DNA Se<br>id Accession<br>mence: 199.  | #: NM_0013  | 306.1   |   |  |  |
|               | 1  | 11  | 21  | 31  | 41  | 51   |  |
| 55            | GCGCGCGCCG<br>CGCCAGGCCC<br>GGCCTTGCCG<br>CTGGGCTGGC   | TCGGTGAGTC<br>AGCGGCCCCG<br>CGGCAGCCAT<br>TGGGCACCAT  | GCAGGCGCAC<br>AGTCCGTCCG<br>GCCCCTCGTC<br>GTCCATGGGC<br>CGTGTGCTGC  | TCCGTCCGTC<br>TCCCCGCACC<br>CTGGAGATCA<br>GCGTTGCCCA  | CGTCGGGGCG<br>CGGAGCCACC<br>CGGGCACCGC<br>TGTGGCGCGT  | CCGCAGCTCC<br>CGGTGGAGCG<br>GCTGGCCGTG<br>GTCGGCCTTC   | 60<br>120<br>180<br>240<br>300   |
| 60            | GTGCAGAGCA<br>GACCTTCAGG<br>CTAGTGGCGC<br>AAGATCACCA   | CCGGCCAGAT<br>CGGCCCGCGC<br>TGGTGGCAGG  | GTCGCAGAAC<br>GCAGTGCAAG<br>CCTCATCGTG<br>CCAGTGCACC<br>CGTGCTGTTC  | GTGTACGACT<br>GTGGCCATCC<br>AACTGCGTGC<br>CTTCTCGCCG  | CGCTGCTGGC<br>TGCTGGCCGC<br>AGGACGACAC<br>CCCTGCTCAC  | ACTGCCACAG<br>CTTCGGGCTG<br>GGCCAAGGCC<br>CCTCGTGCCG   | 360<br>420<br>480<br>540<br>600  |
| 65            | CAGAAGCGCG<br>CTGGGGGGCG<br>AAGGTCGTCT<br>GACCGCAAGG   | AGATGGGCGC<br>CGCTGCTCTG<br>ACTCCGCGCC<br>ACTACGTCTA  | GGGCTGTAC<br>CTGCTCGTGT<br>GCGCTCCACC<br>AGGGACAGAC   | GTGGGCTGGG<br>CCCCCACGCG<br>GGCCCGGGAG<br>GCAGGGAGAC  | CGGCCGCGC<br>AGAAGAAGTA<br>CCAGCCTGGG<br>CCCACCACCA   | GCCCGAGGCG<br>GCTGCAGCTG<br>CACGGCCACC<br>CACAGGCTAC<br>CCACCACCAC<br>GTGCAGCCTT   | 660<br>720<br>780<br>840<br>900  |
| 70            | GCCTCGGAGG<br>TCCCCAGCAG<br>GCATGGACTG<br>ACCACCCCGT   | CCAGCCCACC<br>CCACGGCTTT<br>TGAAACCTCA<br>CGAGCCCCAT  | CCCAGAAGCC<br>GCGGGCCGGG<br>CCCTTCTGGA<br>CGGGCCGCTG  | AGGAAGCCCC<br>CAGTCGACTT<br>GCACGGGGCC<br>CCCCCATGTC  | CGCGCTGGAC<br>CGGGGCCCAG<br>TGGGTGACCG<br>GCGCTGGGCA  | TGGGGCAGCT<br>GGACCAACCT<br>CCAATACTTG<br>GGGACCGGCA   | 960<br>1020,<br>1080<br>1140<br>1200   |
| 75            | Seq ID NO:   | C184 DNA S  | TATTTTTCAA<br>equence<br>n #: NM_012  |   | ICGITTIAGC  |  | 1250   |
|               |  | uence: 66   |   | ****.T  |   |  |  |
| 80            | 1<br>  | 11<br>  | 21<br>i   | 31<br>  | 41  | 51<br>1  |  |
|               | AATTAATGGA   | AAGCAGAAAA  | AAGGCGAAGA<br>GACATCACAA<br>GATTATTTGC  | ACCAAGAAGA  | ACTTTGGAAA  | TATTTTATAG<br>ATGAAGCCTA<br>AGCATGCTAA   | 60<br>120<br>180   |

```
AAAGACCTGT GCTTTTGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT
       CAGAACTTCA GCACACAG GAACTCTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG
                                                                                    300
       CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG
                                                                                    360
       CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCATCAAC AAAGTCTTGC
                                                                                    420
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       CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG
                                                                                    480
       TCCAACTTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT
       TAACAAGAAA GCAGTTTGGG CTTCTCAGTT TCTTTTTTGC TGTACTGCAT GCAATTTATA
                                                                                    600
       GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC AGGTCCAACA AAATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT
                                                                                    660
                                                                                    720
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       ATGTGTCTCT GGGAATTGTG GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC
                                                                                    780
       CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA
                                                                                    840
       TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCTGGAAT AAGTGGATAG ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCCTTCCAA
                                                                                    900
                                                                                    960
        TTGTTGTCCT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA
                                                                                    1020
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       AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCCCAGT
                                                                                    1080
       TGTAGAATTA CTGTTTACAC ACATTTTTGT TCAATATTGA TATATTTTAT CACCAACATT
                                                                                    1140
        1195
        Seq ID NO: C185 DNA Sequence
20
       Nucleic Acid Accession #: NM_001775.1
Coding sequence: 70..972
                                                         41
                                                                     51
25
        CTAAAGCTCT CTTGCTGCCT AGCCTCCTGC CGGCCTCATC TTCGCCCAGC CAACCCCGCC
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        CTCTCTAGGA GAGCCCAACT CTGTCTTGGC GTCAGTATCC TGGTCCTGAT CCTCGTCGTG
                                                                                    180
        GTGCTCGCGG TGGTCGTCCC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG
                                                                                    240
        CGCTTTCCCG AGACCGTCCT GGCGCGATGC GTCAAGTACA CTGAAATTCA TCCTGAGATG
30
        AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAAGG GTGCATTTAT TTCAAAACAT
                                                                                    360
        CCTTGCAACA TTACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA
                                                                                    420
        CCTTGCAACA AGATTCTTCT TTGGAGCAGA ATAAAAGATC TGGCCCATCA GTTCACACAG
                                                                                    480
        GTCCAGCGGG ACATGTTCAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC
                                                                                    540
       ACATGGTGTG GTGAATTCAA CACTTCCAAA ATAAACTATC AATCTTGCCC AGACTGGAGA
AAGGACTGCA GCAACAACCC TGTTTCAGTA TTCTGGAAAA CGGTTTCCCG CAGGTTTGCA
                                                                                    600
35
                                                                                    660
        GAAGCTGCCT GTGATGTGGT CCATGTGATG CTCAATGGAT CCCGCAGTAA AATCTTTGAC
                                                                                    720
        AAAAACAGCA CTTTTGGGAG TGTGGAAGTC CATAATTTGC AACCAGAGAA GGTTCAGACA
        CTAGAGGCCT GGGTGATACA TGGTGGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC
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        ACCATAAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT
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        ATCTACAGAC CTGACAAGTT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGCACA
                                                                                    960
        TCTGAGATCT GAGCCAGTCG CTGTGGTTGT TTTAGCTCCT TGACTCCTTG TGGTTTATGT
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        CATCATACAT GACTCAGCAT ACCTGCTGGT GCAGAGCTGA AGATTTTGGA GGGTCCTCCA
                                                                                    1080
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                                                                                                                                1920
 50
             GAGGACCAGC GCCGTGACTC CTGCGGTCCG GTTGAATAGC ACCGGGGCCC CCGCGAGCTT
                                                                                                                               1980
             GGGCGCAGGC GGAGGGGCGT CGTCGGTGCC CTTGTCTGTG TTAATTCTCA GCCTCCTGCT
                                                                                                                                2040
             GGTTTTCATC ATGTCCGTCT TCGTGGCCGC CGGGCTCTTC GTGCTGGTCA TGAAGCGCAG
                                                                                                                                2100
             GAAGAAGAAC CAGAGCGACC ACACCAGCAC CAACAACTCC GACGTGAGCT CCTTTAACAT
                                                                                                                                2160
             GCAGTACAGC GTGTACGGCG GCGGCGGCGG CACGGGCGGC CACCCACACG CGCACGTGCA
                                                                                                                                2220
             TCACCGCGGG CCCGCGCTGC CCAAGGTGAA GACGCCCGCG GGCCACGTGT ATGAATACAT
 55
                                                                                                                                2280
             CCCCCACCCA CTGGGCCACA TGTGCAAAAA CCCCATCTAC CGCTCCCGAG AGGGCAACTC
                                                                                                                                2340
              CGTAGAGGAT TACAAAGACC TGCACGAGCT CAAGGTCACC TACAGCAGCA ACCACCACCT
                                                                                                                                2400
             GCAGCAGCAG CAGCAGCCGC CGCCGCCACC GCAGCAGCCA CAGCAGCAGC CCCCCGCCGCA
GCTGCAGCTG CAGCCCGGGG AGGAGGAGAG GCGGGAAAGC CACCACTTGC GGAGCCCCGC
                                                                                                                                2460
                                                                                                                                2520
 60
              CTACAGCGTC AGCACCATCG AGCCCCGGGA GGACCTGCTG TCGCCGGTGC AGGACGCCGA
                                                                                                                                2580
              CCGCTTTTAC AGGGGCATT TAGAACCAGA CAAACACTGC TCCACCACCC CCGCCGGCAA
TAGCCTCCCG GAATATCCCA AATTCCCGTG CAGCCCCGCT GCTTACACTT TCTCCCCCAA
                                                                                                                                2640
                                                                                                                                2700
              CTATGACCTG AGACGCCCCC ATCAGTATTT GCACCCGGGG GCAGGGGACA GCAGGCTACG
                                                                                                                                2760
              GGAACCGGTG CTCTACAGCC CCCCGAGTGC TGTCTTTGTA GAACCCAACC GGAACGAATA
                                                                                                                                2820
              GACCACGTT ACCAGTATA AAAACGTAGA GACCACGTT AGCAAAACA TAAAACGAAAAA AAACTCTCTT GGAGCTTTT CATTTAAAAC
 65
                                                                                                                                2880
              AAACAAGCAA GCAGACACAC ACAGTGAACA CATTTGATTA ATTGTGTTGT TTCAACGTTT
                                                                                                                                3000
              AGGGTGAAGT GCCTTGGCAC GGGATTTCTC AGCTTCGGTG GAAGATACGA AAAGGGTGTG
CAATTTCCTT TAAAATTTAC ACGTGGGAAA CATTTGTGTA AACTGGGCAC ATCACTTTCT
                                                                                                                                3060
                                                                                                                                3120
  70
              CTTCTTGCGT GTGGGGCAGG TGTGGAGAAG GGCTTTAAGG AGGCCAATTT GCTGCGCGGG
                                                                                                                                 3180
              TGACCTGTGA AAGGTCACAG TCATTTTTGT AGTGGTTGGA AGTGCTAAGA ATGGTGGATG
                                                                                                                                 3240
              ATGGCAGAGC ATAGATTCTA CTCTTCCTCT TTTGCTTCCT CCCCCTCCCC CGCCCCTGCC
                                                                                                                                 3300
               CCACCTCTCT TTCTCCCCTT TTAAGCCATG GGTGGGTCTA ACTGGCTTTT GTGGAGAAAT
                                                                                                                                 3360
               TAGCACACCC CAACTITAAT AGGAAATTTG TTCTCTTTTT CCGCCCCTCT CCTTCTCTCC
                                                                                                                                 3420
  75
               TCCCCTCCCC TCCCTTCTCA TTCCTTTTCT TTGTTTTTAA AGGATGTGTT TGTATGCATT
                                                                                                                                 3480
               CTGGACATTT GAATTAAAAA AAAAGTATTG TGATCCTGTA AAGGATCACC ATAGATGTGG
                                                                                                                                 3540
              ACABATCATT ABABITACAG AGCTATATGA TCCATAATTG ATTAGTCABA ATBACTTATT
                                                                                                                                 3600
               GATGAAATAT ACAAATATTT TATTGTAGCA CCTATTTTTA TATGCACATT TAGCATTCCT
                                                                                                                                 3660
               CTTTCCTTCA CTATTTAGCC TATGATTTTG CAGAGGTGTC ACACTGTATT AGGATCTGCA
TTTCTAAAAC TGACGTGGTA TCAGGAAGGC ATTTTCAATC ATTCAAAATG TGGAGAATTT
                                                                                                                                 3720
  80
                                                                                                                                 3780
               AATGGCTAAA TCTTTAAAAG CCAATGCAAC CCACCCAATT GAATCTGCAT TTTCTTTTAA
               GAAAACAGAG CTGATTGTAT CCCAATGTAT TTTAAAAAAT AGGGCAATTG ATTGGGCCAT
                                                                                                                                 3900
               TCCGAGAGAA TTGTTTGCAA GTTTTGGGTT TTATTAGAAA ATATTTGAAA GTATTTTAT
TAATGAACCA AAATGACATG TTCATTTGAC TACTATTGTA GCCGATTTTC GATTGTTTAA
                                                                                                                                 3960
                                                                                                                                 4020
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|    | CCAAACCCAG<br>GGACTGTACA<br>TGACAAACAG<br>CACATGTAAT | AGTCTCTATA<br>GATATCTGTA | CAATGTCTTT<br>AGATGGGGCT   | ATCCCTGTGG<br>ACTGTTGTTA     | GCAGCAAGCA<br>CAGTCTCATA   | ATGATGATAA                     | 4080<br>4140<br>4200<br>4250 |
|----|--|--------------------------|----------------------------|------------------------------|----------------------------|--------------------------------|------------------------------|
| 5  | Seq ID NO:<br>Nucleic Aci<br>Coding sequ             | d Accession              | #: NW_000.                 | 793.2                        |                            |                                |                              |
| 10 |  | 11                       | 21                         | 31                           | 41                         | 51                             |                              |
|    | <br>GCCTGCAGAG                                       | i<br>AGAGGCACTT          | TGCACCACAG                 | ACAGATAGCA                   | AGAAGGGAAA                 | GACAGAGAGT                     | 60                           |
|    | GAGAAAAAAG<br>AAGCACAGAA                             | AGGAGTCAGT               | CGCTCCTGGG                 | GAAGGGAGAG                   | AGTGAGACTG                 | GGAGAAAGAG                     | 120<br>180                   |
| 15 | GCACATTTAA   | <b>АДДДДДДДД</b>         | CTCTGGCAAT                 | TCAAGAAAGA                   | AACAGGCTAC                 | GTTTAAAGAG                     | 240                          |
|    |  |                          |                            | TTAAAATCTC                   |                            | TCATAGGTGC<br>GTGAAGGGGA       | 300<br>360                   |
|    |  |                          |                            |                              |                            | TCAGCGTAGA                     | 420                          |
| 20 | CTTGCTGATC   | ACACTGCAAA               | TTCTGCCAGT                 | TTTTTTCTCC                   | AACTGCCTCT                 | TCCTGGCTCT                     | 480                          |
| 20 | CTATGACTCG   | GTCATTCTGC               | TCAAGCACGT                 | AGAGGGACTG                   | CGCTGCGTCT                 | CCAAGTCCAC<br>GGAAGAGCTT       | 540<br>600                   |
|    | CCTCCTCGAT   | GCCTACAAAC               | AGGTGAAATT                 | GGGTGAGGAT                   | GCCCCCAATT                 | CCAGTGTGGT                     | 660                          |
|    |  |                          |                            |                              |                            | AGAAGATAGC<br>TAGTGGTCAA       | 720<br>780                   |
| 25 | CTTTGGCTCA   | GCCACTTGAC               | CTCCTTTCAC                 | GAGCCAGCTG                   | CCAGCCTTCC                 | GCAAACTGGT                     | 840                          |
|    | GGAAGAGTTC   | TCCTCAGTGG               | CTGACTTCCT                 | GCTGGTCTAC                   | ATTGATGAGG                 | CTCATCCATC                     | 900<br>960                   |
|    |  |                          |                            |                              |                            | AGCACCAGAA<br>TGCCGCCCCA       | 1020                         |
| 20 | GTGCCGAGTT   | GTGGCTGACC               | GCATGGACAA                 | TAACGCCAAC                   | ATAGCTTACG                 | GGGTAGCCTT                     | 1080                         |
| 30 | TGAACGTGTG   | TGCATTGTGC               | AGAGACAGAA                 | AATTGCTTAT                   | CTGGGAGGAA                 | AGGGCCCCTT<br>AGAGATGAAA       | 1140<br>1200                 |
| •  | GAAAACTAGA   | TTAGCTGGTT               | AAAGGTATGA                 | TTATAAGAGA                   | GCTTATTGTT                 | TTAAAAAGTT                     | 1260                         |
|    | ATATAAAGGC   | AAGGAAATTA               | AGAACTGAAT                 | CCATATTTCA                   | ACAGAGCCCT                 | ATTGGCTTAC                     | 1320<br>1380                 |
| 35 |  |                          |                            |                              |                            | TTAGTAAAAA                     | 1440                         |
| 55 | GCCCTATGTG   | AAAAGATCCC               | AAGATGGAGA                 | GGAAGAAACG                   | CTAATTCAGC                 | ATGTGTTCAT                     | 1500                         |
|    | TCTGCATTGA   | GAAGGAACTG               | ATACATCTG                  | TGCATGCTTT                   | GAGACCAGAA                 | GAAAAGACTT                     | 1560<br>1620                 |
|    | TGGCTCTATT   | TGGCATGGAT               | GGAGCCCAG                  | TGGAAAATTC                   | CCARATATTA                 | GGTATTGCCT                     | 1680                         |
| 40 | TTGAACCCAG   | GCCATGTGGT               | TAGACGTTGC                 | TGTTAAGGTT                   | AGACCTTATO                 | TTAGAGTCAT                     | 1740                         |
|    | TTCTGATGTT   | CCAGCTTCTA               | GCCATGTAGT                 | GCTCTCAGTC                   | TTCATACCCC                 | GATCATCTGT                     | 1800<br>1860                 |
|    | AATCTGAGGG   | TTAATTTCTA               | GGCAGGTGG                  | GAGAGTGGTA                   | AAAAAGAAA?                 | GAAATTGACA                     | 1920                         |
| 45 | AGCTAGGAAA   | GAGGAGGCAG               | AAAGATTTG                  | BAAATTCACA                   | GAGTTTCACC                 | CTTAAGCTGT                     | 1980                         |
| 43 |  |                          |                            |                              |                            | GCCAGAAAAA<br>A ATATATTTGT     | 2040<br>2100                 |
|    | CATATGCTCC   | TAGAGAGGAG               | AAAGGGGTG                  | TTGAAAGAA                    | AAAAAATAC                  | DTTTATAAAT 1                   | 2160                         |
|    | TAATTGTGAG   | GGGTTTCTTT               | TGGAAATAA                  | TACTTTTGA                    | CONTGTATG                  | r GGTATGTATA<br>r GGGTCTGGTG   | 2220<br>2280                 |
| 50 | GTGCTGGTCT   | TTTCCTCCCC               | ATTCCTACA                  | A TTTCTATGT                  | GCCCAAGTC                  | TTCCTAATCT                     | 2340                         |
|    | TGGTCTCTAT   | AGCAGTGTT                | CTCTGAAT                   | G CTGAGCTGA                  | GAAATTATA                  | C GTACATACAC                   | 2400                         |
|    | ACATACATAC   | TTCAGCACAC               | ATATATGTA                  | r atataticio<br>c ctcccaaagi | C AGCTGCTGCT               | G GGAGGTAGGT<br>A TAGTGAAGAA   | 2460<br>2520                 |
| 66 | TAGGTGCAAA   | CAAACAAGC                | TACTTCCAT                  | r gcaaaatag/                 | A AGAAGAGGA                | A GTTAGAGATA                   | 2580                         |
| 55 | ATTCTGATCA   | ATCATTTTG                | AGGCTTTGT                  | T ATAAGGCAA                  | CCCCGGTAT                  | A TCATGGAATT<br>I GAGGTTTAGT   | 2640<br>2700                 |
|    | AATCTAAAGT   | CCCTATAGT                | A TATGATTAT                | A ATGCTATTT                  | TATAAAAA 1                 | TATATAAAAT                     | 2760                         |
|    |  |                          |                            |                              |                            | T TAAAGATTAT                   | 2820<br>2880                 |
| 60 |  |                          |                            |                              |                            | G TAAATATGAG<br>G ATCTTTTGTC   | 2940                         |
|    | CATTCCATTA   | ATAACTGAA'               | AAAAAAAA                   | A TAAAATGGA                  | T AGAAAAAA                 | C TAAAGTTGAA                   | 3000                         |
|    | AATACATTCI   | TAAACTAGT                | r gtctgaaat                | G AGAAAAGAG<br>G GGAGCAACA   | T GAGAACTAG<br>T ATCAGTOGT | G TGTGCAAGAA<br>G TCACCAGCTG   | 3060<br>3120                 |
|    | GTATATTGTC   | TAAATATTA                | A AGCTCCATT                | G GGACTGATT                  | T TTCATGGCA                | A CATCAGCTTT                   | 3180                         |
| 65 |  |                          |                            |                              |                            | T TCATTATCTA                   | 3240<br>3300                 |
|    | TACATTCAA  | GGAAAATCA<br>GGCTTATCT   | r atigagaat<br>c tgcccccat | A ATTATTICA<br>T GATTTTTAA   | C CTCAAAATG                | T TGTTAACTTC<br>G TGTGAGATTT   | 3360                         |
|    | ACTGTGGAAG   | CCTAAAGCA                | <b>G ТААААТААА</b>         | A AACCTGGTT                  | G CAGCACATT                | C ACACTGTTGT                   | 3420                         |
| 70 |  |                          |                            |                              |                            | A GATAAGCCGG<br>G ATGATGGAAA   | 3480<br>3540                 |
| ,, | AATCACCCAC   | TTGTGCTAT                | A TTTTTAAAG                | A AGGAGGTCG                  | T TTATGTGTG                | C AGACAATTCT                   | 3600                         |
|    |  |                          |                            |                              |                            | A AGACATGGGC                   | 3660                         |
|    |  |                          |                            |                              |                            | A GGCTGTGGAA<br>G TAGAATGTTC   | 3720<br>3780                 |
| 75 | TTGGTGTTA'   | r cagggttaa              | G CCCTGTAAT                | T ATGTAACCT                  | A TITATOGCA                | A CATGAATTT                    | 3840                         |
|    |  |                          |                            |                              |                            | T TTTGAGGTAG A TACTCATGTG      | 3900<br>3960                 |
|    |  |                          |                            |                              |                            | A GTCCCACAGG                   | 4020                         |
| 80 | GAAATGTGT  | A TCTATTTAT              | A TATCATAG                 | A TAAATCTAT                  | ATTTATATA D                | T ATCATATATA                   | 4080                         |
| οU |  |                          |                            |                              |                            | T GTGTTTACAT A ATAGTTTCCA      | 4140<br>4200                 |
|    | AGAAATTTT  | A GATATTATO              | A TAACATCTO                | G GTCTACTCA                  | A ACACTTATI                | NG TTTGAAAGAC                  | 4260                         |
|    |  |                          |                            |                              |                            | NA TACTAGTGGG<br>TA ATGTAGAAAT | 4320<br>4380                 |
|    | ALCONOMI   |                          | ALGORAL                    |                              |                            |                                |                              |

|  | Ommoo ma ca  | COM 2 mm 2 2 2 2   |  |  |  |  |   |
|--|--|--|--|--|--|--|---|
|  |  |  | TGTAACTGAC   |  |  |  | 4440  |
|  |  |  | AGTCACTTAA   |  |  |  | 4500  |
|  | CTCTGGTCCT   | GTGTCTTCAC   | CTCATTTATA   | GCACGTCTCC   | TTGATTTTTG   | GTAGTATCAA   | 4560  |
| ~  | CTTCCCAGTG   | ATCTGTTCAG   | TTAAGTTCTT   | CTCCCGTTAA   | CCAGGAAGTG   | CTTATTCTCT   | <b>4620</b>   |
| 5  |  |  | CCTATTGTCT   |  |  |  | 4680  |
|  |  |  | TGAAATATGG   |  |  |  | 4740  |
|  |  |  | GTTAGGAGAC   |  |  |  | 4800  |
|  |  |  |  |  |  |  |   |
|  |  |  | TTCCTCAGGC   |  |  |  | 4860  |
| 10   |  |  | GACTTCTCTT   |  |  |  | 4920  |
| 10   | GGACATTTGT   | TCCACCCGAC   | CTCTGACTGA   | TGGTTTGGAA   | AATAACTTTA   | ATTAGGATCA   | 4980  |
|  | TATGACCATT   | GAAAAAGGAA   | AAATGTAGAC   | TCTGACTTCC   | GTCCCACTGA   | AGGATTAATG   | 5040  |
|  |  |  | GAGCTTTTCA   |  |  |  | 5100  |
|  |  |  | TTTAATTTTA   |  |  |  | 5160  |
|  |  |  | CAGAGTTAAA   |  |  |  |   |
| 15   |  |  |  |  |  |  | 5220  |
| 13   |  |  |  |  |  | GGGGCTTAAG   |   |
|  |  |  | TGGGCACAAT   |  |  |  | 5340  |
|  | AGAGAGGATC   | TAGGATGGGA   | GAGCTAGAAA   | GTTGCTAACT   | GGGAAGAACA   | AGGCCCTGAG   | 5400  |
|  | GGGTTGGTCT   | ACCAATCTGG   | GAAGATTTGA   | AAACAAACTT   | CTCGCAACTG   | AAGGAAGGCT   | 5460  |
|  |  |  | GAGTGACTTT   |  |  |  | 5520  |
| 20   |  |  | CAGAAGCAAG   |  |  |  | 5580  |
|  |  |  | AGAAAGCAAA   |  |  |  |   |
|  |  |  |  |  |  |  | 5640  |
|  |  |  | CCGTCTTAGG   |  |  |  | 5700  |
|  |  |  | AAGACCCAGC   |  |  |  | 5760  |
| 0.5  | AAACCCTCCA   | CTTCTCCCCC   | TCCCCTCAAA   | AAGCCAACAG   | GTAAACACAT   | AAATGAAAGA   | 5820  |
| 25   |  |  | AAATAAAGAA   |  |  |  | 5880  |
|  |  |  | ATGTGTATTA   |  |  |  | 5940  |
|  |  |  | ATTAAATGAT   |  |  |  | 6000  |
|  |  |  |  |  |  |  |   |
|  |  |  | TCACCCAGAC   |  |  |  | 6060  |
| 30   |  |  | GCCAGAGTTG   |  |  |  | 6120  |
| 30   |  |  | AGTGGTTGGA   |  |  |  | 6180  |
|  | TTTGTCTCCC   | TGGCAAGGAG   | AATATGCGGG   | ACATGATGCT   | AAGAGCCCTG   | GGTAAATGTG   | 6240  |
|  | GTGAGAATGC   | ACGCGTGCAT   | ATGCTACACA   | TATGTGCTTC   | TCAGTTGCAG   | AAAATGAACT   | 6300  |
|  |  |  | GAAAGAGTGT   |  |  |  | 6360  |
|  |  |  | TTTTAATAAA   |  |  |  | 6420  |
| 35   |  | IGIICIIGIA   | IIIIAAIAAA   | CITIGAATAA   | MAGMAIAMAM   | AAAAAAAAA  |   |
| 33   | ААААААА  |  |  |  |  |  | 6429  |
|  |  |  |  |  |  |  |   |
|  |  | C192 DNA S   |  |  |  |  |   |
|  | Nucleic Act  | ld Accession   | n #: NM 006  | 549.2  |  |  |   |
|  | Coding sem   | ience: 824.  | .2590  |  |  |  |   |
| 40   |  |  |  |  |  |  |   |
| . •  | 1  | 11   | 21   | 31   | 41   | 51   |   |
|  | ÷  |  | 21   | 31   | 41   | 21   |   |
|  |  | 1  |  | b  | 1  | 1  |   |
|  | 1  | 1  | 1  | 1  | 1  | 1  |   |
|  |  |  | TGCAGCGAGC   | CGTGATCGTG   |  |  | 60  |
| 45   |  |  |  | CGTGATCGTG   |  |  | 60<br>120   |
| 45   | CAACACAGAG   | AGACCCTGTC   | TGCAGCGAGC   | CGTGATCGTG<br>CAAACAAACA   | AACAAACAAA   | CAAAACAAAG   |   |
| 45   | CAACACAGAG<br>AAAAAAAAAT   | AGACCCTGTC<br>GGGAGTGGGC   | TGCAGCGAGC<br>TCAAAACAAA<br>CGGGCGCGGT   | CGTGATCGTG<br>CAAACAAACA<br>GACTCACACC   | AACAAACAAA<br>TGTAATCCCA   | CAAAACAAAG<br>GCACTTTCGG   | 120<br>180  |
| 45   | CAACACAGAG<br>AAAAAAAAAT<br>AGGCCAAGGC   | AGACCCTGTC<br>GGGAGTGGGC<br>GGGTGGATCA   | TGCAGCGAGC<br>TCAAAACAAA<br>CGGGCGCGGT<br>CGAGGTCAGG   | CGTGATCGTG<br>CAAACAAACA<br>GACTCACACC<br>AATTCAAGAT   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC   | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA   | 120<br>180<br>240   |
| 45   | CAACACAGAG<br>AAAAAAAAAT<br>AGGCCAAGGC<br>AACCCCATCT   | AGACCCTGTC<br>GGGAGTGGGC<br>GGGTGGATCA<br>CTACGAAAAA   | TGCAGCGAGC<br>TCAAAACAAA<br>CGGGCGCGGT<br>CGAGGTCAGG<br>TACAAAAATT   | CGTGATCGTG<br>CAAACAAACA<br>GACTCACACC<br>AATTCAAGAT<br>AGCCAAGTAT   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC   | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC   | 120<br>180<br>240<br>300  |
| 45   | CAACACAGAG<br>AAAAAAAAAT<br>AGGCCAAGGC<br>AACCCCATCT<br>CCAGCTACTC   | AGACCCTGTC<br>GGGAGTGGGC<br>GGGTGGATCA<br>CTACGAAAAA<br>GGGAGACTGA   | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAA  | CGTGATCGTG<br>CAAACAAACA<br>GACTCACACC<br>AATTCAAGAT<br>AGCCAAGTAT<br>TGCTTGAACC   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC<br>TGGGAGGCAG   | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC<br>AGGTTGCAGT   | 120<br>180<br>240<br>300<br>360   |
|  | CAACACAGAG AAAAAAAAAT AGGCCAAGGC AACCCCATCT CCAGCTACTC GATCCGAGAT  | AGACCCTGTC<br>GGGAGTGGGC<br>GGGTGGATCA<br>CTACGAAAAA<br>GGGAGACTGA<br>CGCGTCACTG   | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAAC CACTCCAGCG  | CGTGATCGTG<br>CAAACAAACA<br>GACTCACACC<br>AATTCAAGAT<br>AGCCAAGTAT<br>TGCTTGAACC<br>TGGGCGACAG   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC<br>TGGGAGGCAG<br>AGCGAGACTC   | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC<br>AGGTTGCAGT<br>CGTTTCAGAA   | 120<br>180<br>240<br>300<br>360<br>420  |
| <b>45</b><br><b>50</b>   | CAACACAGAG AAAAAAAAAA AGGCCAAGGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAA   | AGACCCTGTC<br>GGGAGTGGGC<br>GGGTGGATCA<br>CTACGAAAAA<br>GGGAGACTGA<br>CGCGTCACTG<br>AAAAAAAAA  | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG  | CGTGATCGTG<br>CAAACAAACA<br>GACTCACACC<br>AATTCAAGAT<br>AGCCAAGTAT<br>TGCTTGAACC<br>TGGGCGACAG<br>TCGGGGTGGA   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC<br>TGGGAGGCAG<br>AGCGAGACTC<br>GCTCTCATTG   | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC<br>AGGTTGCAGT<br>CGTTTCAGAA<br>GCTCGTTGCA   | 120<br>180<br>240<br>300<br>360<br>420<br>480   |
|  | CAACACAGAG AAAAAAAAT AGGCCAAGGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC   | AGACCCTGTC<br>GGGAGTGGGC<br>GGGTGGATCA<br>CTACGAAAAA<br>GGGAGACTGA<br>CGCGTCACTG<br>AAAAAAAAA<br>CCTACGGCCT  | TGCAGCGAGC TCAAAACAAA CGGGGCGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCAGCG AAAAAGGGAG AGAAATACCA  | CGTGATCGTG CAAACAACA GACTCACACC AATTCAAGAT AGCCAAGTAT TGCTTGAACC TGGGCGACAG TCGGGGTGGA GAGAAGCACA  | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC<br>TGGGAGGCAG<br>AGCGAGACTC<br>GCTCTCATTG<br>TCGGAACGGG   | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC<br>AGGTTGCAGT<br>CGTTTCAGAA<br>GCTCGTTGCA<br>CTGGAAATCC   | 120<br>180<br>240<br>300<br>360<br>420  |
|  | CAACACAGAG AAAAAAAAAT AGGCCAAGGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTC ACCCAGTTAA  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGAACCTTT  | CGTGATCGTG CAAACAACA GACTCACACC AATTCAAGAT AGCCAAGTAT TGCTTGAACC TGGGGGACAG TCGGGGTGGA GAGAAGCACA TATTAACTTG   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC<br>TGGGAGGACTC<br>GCTCTCATTG<br>TCGGAACGGG<br>GAGCTTGACT  | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC<br>AGGTTGCAGA<br>GCTCGTTGCA<br>GCTCGTTGCA<br>CTGGAAATCC<br>CTCCTGTCAA   | 120<br>180<br>240<br>300<br>360<br>420<br>480   |
|  | CAACACAGAG AAAAAAAAAT AGGCCAAGGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTC ACCCAGTTAA  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGGCGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCAGCG AAAAAGGGAG AGAAATACCA  | CGTGATCGTG CAAACAACA GACTCACACC AATTCAAGAT AGCCAAGTAT TGCTTGAACC TGGGGGACAG TCGGGGTGGA GAGAAGCACA TATTAACTTG   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC<br>TGGGAGGACTC<br>GCTCTCATTG<br>TCGGAACGGG<br>GAGCTTGACT  | CAAAACAAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC<br>AGGTTGCAGA<br>GCTCGTTGCA<br>GCTCGTTGCA<br>CTGGAAATCC<br>CTCCTGTCAA   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
| 50   | CAACACAGAG AAAAAAAAAAAAAAAAAAAAAAAAAAAA  | AGACCCTGTC GGGAGTGGGCA CTACGAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA  | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGAACCTTT TTGGCAGGGT   | CGTGATCGTG CAAACAACA GACTCACACC AATTCAAGAT TGCTTGAACC TGGGCGACAG TCGGGGTGGA GAGAAGCAC ATTTAACTTG CAGTGAGACA CAGTGAGACA   | AACAAACAAA<br>TGTAATCCCA<br>TAGCCTGGAC<br>GGTGGCCGGC<br>TGGGAGGCAG<br>AGCGAGACTC<br>GCTCTCATTG<br>TCGGAACGG<br>GAGGTTGACT<br>TCCCCTGGGT  | CAAAACAAAG GCACTTTCGG AACATGGTGA GCCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAATCC CTCCTGTCAA CGCTCGACCC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600   |
|  | CAACACAGAG AAAAAAAAAT AGGCCAAGGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC ACCCAGTTAA CTCCAGTTACCC CGTAGGACGG   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGAACCTTT TTGGCCAGGT CCTCCAGGT CCTCCAGGTC  | CGTGATCGTG CAAACAACA GACTCACACC AATTCAAGAT AGCCAAGTAT TGCTTGAACC TCGGCGACAG TCGGGGTGGA GAGAAGCACA TATTAACTTG CAGTGAGACA TTGTGAGACA TTGTTGACAC TTGTTGACACA TTGTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTC   | AACAAACAAA TGTAATCCCA TAGCCTGGAC GGTGGCCGGC TGGGAGGCAG AGCGAGACTC GCTCTCATTG TCGGAACGGG GAGGTTGACT TCCCCTGGGT CTCTCCCCG  | CARAACAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCCTGTAATC<br>AGGTTGCAGT<br>GCTTTCAGAA<br>GCTCGTTGCA<br>CTGGAAATCC<br>CTCGGACCC<br>CACAGTGCTG   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660  |
| 50   | CAACACAGAG AAAAAAAAAAAAAAAAAAAAAAAAAAAA  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGGAACTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT  | CGTGATCGTG CAAACAAACA GACTCACACC AATTCAAGAT AGCCAAGTAT TGGTTGAACC TGGGGGTGGA GAGAAGCACA TATTAACTTG CAGTGAGACA TTGGTTCTCTC AAGGCTCCAG   | AACAACAAA TOTAATCOCA TAGCCTGGAC GGTGGCGGC TGGGAGGCAG AGCAGACTC TCGGAACGGG GAGGTTGACT TCCCCTGGGT TCCCCTGGGC CAAAGTGGCC  | CARAACAAG<br>GCACTTTCGG<br>AACATGGTGA<br>GCTGTTAATC<br>AGGTTGCAGT<br>GCTCGTTGCA<br>CTGGAAATCC<br>CTCCTGTCAA<br>CGCTCGACCC<br>CTCCACGCCG<br>CCCCGGCCGG  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780   |
| 50   | CARCACAGAG ANANANAN AGGCCAAGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAANANA TGTGAGTGTC ACCCAGTTAA CTCGATTCCC GTAGGACAG TTATCCAGCT ATGCAGTTA   | AGACCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CCTACGACACA AAAAAAAAA CCTACGGCCT CTTAGGGCGT TTCTAGGGGATCCA GGGGATCCA CCCAGTGTGC CCCAGTGTGC   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGGACTTT TTGGCAGGT ACGCACACTT TGGCACACTT TGGAAGAGC  | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTAT TGCTTGAACC TGGGGGACAG TCGGGGTGGA GAGAAGCACA TATTAACATG CAGTGAGAC TATTACATG CAGTGAGAC TCGGTTCAC TTCGTTTCTC AAGGCTCCAG TCGCGCATGC   | AACAACAAA TGTAATCCCA TGGCCGGC TGGCAGGCAG GGTGGCCGGC TGGGAAGGCAG GCGAACGGG GAGGTTGACT TCCCCTGGGT TCCCCTGGGT CCAAAGTGGCT ACCATGTCAA  | CARAACAAAG GCACTTTCGG AACATGGGG ACCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCGTCAA CGCTGCACC CACAGTGCTG CACAGTGCTG CATGTGCTGCTGCAGCCC CACAGTGCTG CATGTGTCTC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>'720<br>780<br>840  |
| 50   | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTA ACCCAGTTAA CTCGATTCCC CGTAGGACGG TTATCCAGCT ATGGCAGTGC TAGCCAGCCC  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG CTACGGCCT CTACGGCCT CTACGGCCT TTTTTGGCTGT TTCAGGCAGC GGGGGATCCA CCCAGTGCGA AGCAGCAACC  | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG ATGAACTTT TTGGCAGGGT CCTCCAGGT ACGCACACTT TGGATGAACC GGGCCGCCCC  | CGTGATCGTG CAAACAAACA GACTACACCC GACTCACACC GACTTGAACA AGCCAAGTAT TGGGGGACAG TCGGGGGACAG TCGGGGTGAA GAGAAGCACA TATTAACTTG TCGTTTCTC AAGGCTCCAG TGGCGCATGC CCAGGATGAAC CCAGGATGAAC CCAGGATGAAC CCAGGATGAG CCAGGATGAG CCAGGATGAG   | AACAAACAAA TGTAATCCCA TGGGCGGC GGTGGCCGGC TGGGAGCCG GCTCTCATTG TCGGAACGG GAGTTGACT TCCCCTGGGT TCCCCTGGGT CTCTTCCCCG CAAGTGGCT ACATTGTCAT TCGGGGGCA   | CARAACAAG GCACTTTCGG AACATGGTGA GCCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGCTGCACCC CACAGTGCTG CGCTGCCGG GGGCAGCAG  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900  |
| 50   | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC GATCCCAGGAT AAGAAAAAAA TGTGAGTGTC ACCCAGTTAAA CTCGATTCCC CGTAGGACGG TTATCCAGCT ATGGGATGCC CTAGCCAGCCC CAGCAGCCCA  | AGACCCTGTC GGGATGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA  | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAAATACCA TTGAACCTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT TGGATGAAGCT TGGATGAAGGC CGGGCCCCC CCTGTGAGGGC   | CGTGATCGTG CAAACAAACA GACTCACACC GACTCACACC GACTGAGATAT TGCTTGAACC TGGGCGACAG TCGGGGTGGA GAGAAGCACA TATTAACTTG CAGTGAGAC TTCGTTCTCC AAGGCTCCAG TCGCGCATGG CCAGCGATGAG CCAGCGATGAG CCTGCGGGGCC  | AACAAACAAA TGTAATCCCA TGGCAGGCAG GGTGGCCGGC TGGGAGGCTG TCGGAACGGG GAGTTGACT TCCCCTGGGT TCCCCTGGGT ACCATGTCATC CTGTGCCACC CAAAGTGCCT ACCATGTCAT CCTGGGGCGC CTGCGCGCC CTGCGCGCCC CTGCGCGCCC CTGCGCGCCC CTGCGCGCCC CTGCGCGCCC CTGCGCCCCC CTCTCCATCCCT   | CARAACAAG GCACTTTCGG AACATGGTGA ACATGGTGA GCTGTTAATC AGGTTGCAGT GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGCTCGACCC CACAGTGCTG CACAGTGCTG CACGTGCTGCAG CATGTGTCTCA CGGGCAGCAG TGAGCATCCA   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960   |
| 50<br>55   | CAACACAGAG AAAAAAAAAAAAAAAAAAAAAAAAAAAA  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGCTGA CCTACGGCT CTAGGGCT CTAGGGCT TTTTGGCTGT TTCAGGGGGC CCCAGTGTGC CCCAGTGTGC CCCAGTGTGC AGCCAGCAACC AGCCAGCAACC AGCCAGCAACC GGGGAACC AGCCAGAACC GAGTCCTTCA  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGAACTTT TTGGCAGGT CCTCCAGGTC CCTCCAGGTC TGGATGAAG CGGGCCCCCC CCTGTGAGGC TTGTGTCAC  | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTAT TGCTTGAACC TGGGGGACAG TCGGGGTGAA CAGGAGCACA TATTAACTTG CAGTGAGACA TATTACTTG CAGTGAGACA TCGGGTGACAC TGGGCGACAG CCGGACAG CCGGACAG CCGGACAG CCAGCATGAC CCAGCATTAC CCAGCATTAC CCAGCATTAC CCAGCATTAC CCACCATTAC CCACCAT | AACAACAAA TGTAATCCCA TGGAGCCGG GGTGGCCGGC TGGGAGGCAG AGCGAGACTC GCTCTCATTG TCGGAACGGG GAGGTTGACT TCCCCTGGGT TCCTCCCCG CAAAGTGCCT ACCATGTCAT CTCGGGGCCA ACCATGTCAT CTCCTCCTCCT CCGGGCTGTG CCCGGGTTGTC CCGGGCTGTG  | CARAACAAG GCACTTTCGG AACATGGTGA GCTCGTTAATC AGGTTGCAGT GCTCGTTGCA CTGGGAAATCC CTCCTGTCAA CGCTCGACCC CACAGTGCTG CCACTGCCGG CATGTGCCCGG CATGTGCCCC CTGGCAGCCC CTGGCAGCCC CTGGCAGCCC CTGGCAGCCC CTGTGGCACCC CTGTGGCACCC CTGTGGCACCC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>'720<br>780<br>840<br>900<br>960<br>1020  |
| 50   | CAACACAGAG AAAAAAAAAA AGGCCAAGCC AACCCCATCT CCAGCTACTC GATCOGAGAT AAGAAAAAAA TGTGAGTGTA ACCCAGTTAA CTCGATTCOC CGTAGGACGG TTATCCAGCT TAGCCAGCCC CAGCAGCGAA CCTGGGCATG CCGGCTTGGCC   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGCGGGT CGAGGTCAGG TACAAAAATT GGCAAGAGAAA CCACTCCAGCG AAAAAGGGAG ATGAACTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT TGGATGAAGC GGGCCCCCC CTGTGAGGC TTGTGTCAC   | CGTGATCGTG CAAACAAACA GACTACACCC AATTCAAGAT AGCCAAGTAT TGGGGGACAG TCGGGGGACAG TCAGGAGCACAG TATTAACTTG TAGGTTTCTC AAGGCTCAG TCGCGCATGC CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CGAGTGTAGA CGAGTGAG  | AACAAACAAA TGTAATCCCA TGGCCGGC GGTGGCCGGC TGGGAGGCAG AGCAGGAGCTC CTCTCATTG TCCCCTGGGT TCCCCTGGGT CTCTTCCCCG CAAGTGGCT TCTTCCCCG CAAGTGGCT TCTGCGGGCCAC CTCTCATCCT CCGGGGCCAC CTCTCATCCT CGGGGCCAC CCGGGCTGTG GAGGTCCCCC  | CARAACAAG GCACTTTCGG AACATGGGGG ACCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGCTGGACCC CACAGTGCTG CAGCTGCCGG CATGTGCTC GGGGCAGCAG TAGGCATCCA CTGGACACC TTGACCCT TTGACTCCT TTGACTCCTC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960   |
| 50<br>55   | CAACACAGAG AAAAAAAAAA AGGCCAAGCC AACCCCATCT CCAGCTACTC GATCOGAGAT AAGAAAAAAA TGTGAGTGTA ACCCAGTTAA CTCGATTCOC CGTAGGACGG TTATCCAGCT TAGCCAGCCC CAGCAGCGAA CCTGGGCATG CCGGCTTGGCC   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGAACTTT TTGGCAGGT CCTCCAGGTC CCTCCAGGTC TGGATGAAG CGGGCCCCCC CCTGTGAGGC TTGTGTCAC  | CGTGATCGTG CAAACAAACA GACTACACCC AATTCAAGAT AGCCAAGTAT TGGGGGACAG TCGGGGGACAG TCAGGAGCACAG TATTAACTTG TAGGTTTCTC AAGGCTCAG TCGCGCATGC CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CGAGTGTAGA CGAGTGAG  | AACAAACAAA TGTAATCCCA TGGCCGGC GGTGGCCGGC TGGGAGGCAG AGCAGGAGCTC CTCTCATTG TCCCCTGGGT TCCCCTGGGT CTCTTCCCCG CAAGTGGCT TCTTCCCCG CAAGTGGCT TCTGCGGGCCAC CTCTCATCCT CCGGGGCCAC CTCTCATCCT CGGGGCCAC CCGGGCTGTG GAGGTCCCCC  | CARAACAAG GCACTTTCGG AACATGGGGG ACCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGCTGGACCC CACAGTGCTG CAGCTGCCGG CATGTGCTC GGGGCAGCAG TAGGCATCCA CTGGACACC TTGACCCT TTGACTCCT TTGACTCCTC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>'720<br>780<br>840<br>900<br>960<br>1020  |
| 50<br>55   | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTC ACCCAGTTAAA CTCGAATTCCC CGTAGGACGG TTATCCAGCT ATGGGAGTGC TAGCCAGCCC CAGCAGCGAA CCTGGGCATGC CGGCTTGGCAC CGGGTCCCAG   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG CTACGGCCT CTACGGCGCT TTTTGGCGTG TTTCAGGGAGC GGGGATCCA CAGGGGATCCA CAGGAGCAACC AGCAGAAGC GAGTCCTTCA GGCAGCAACC GGGACCGG GCGGCCCCGGGCCC  | TGCAGCGAGC TCAAAACAAA CGGGCGGGT CGAGGTCAGG TACAAAAATT GGCAAGAGAAA CCACTCCAGCG AAAAAGGGAG ATGAACTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT TGGATGAAGC GGGCCCCCC CTGTGAGGC TTGTGTCAC   | CGTGATCGTG CAAACAAACA GACTCACACC GACTCACACC GACTCAGACA AGCCAAGTAT TGCTTGAACA TGGGGGACAC TGGGGGACAC TATTAACTTG TGGTTTCTC AAGGCTCCAG TGGCGCATGC CCAGGATGAG CCTGCGGGCC CGAGTGTGAA CTGCGCATGC CGATGCGCATGC CGAGGATGAG CCTGCGGGC CGATGTGAA TGGCAGCAC TGCCAGGCTCAACAC TGGCAGCAC TGCGCAGGC TGGCAGGC TGGCAACAC TGGCAGGCT TGGCAGGCT TGGCAACGCT  | AACAAACAAA TGTAATCCCA TGGGACCGGC GGTGGCCGGC TGGGAGGCTG GCTCTCATTG TCGGAACGGG GAGTTGACT TCCCTGGCT TCCCTGGCT TCCCTGGCT TCCCTGCCC CAAAGTGGCT ACCATGTCAT CCTGGGGGCA CTCTCATCCT CCGGGCTTGC CAGGCTCTCC CCGGCTTGC CAGGCTCTCC TCTCTCCCC TCTCTCCCC CTCTCATCCT CCGGCTTTGC CCGGCTTTGC CAGGCTCCCC TCTCTCCACCC TCTCTCCACCC TCTCTCCACCC TCTCTCCACCC TCTCTCCACCC TCTCTCCACCC  | CARAACAAAG GCACTTTCGG AACATGGTGA ACCTGTAATC AGGTTGCAGT CGTTTCAGAA CTGGAAATCC CTCCTGTCAA CGCTCGACCC CACAGTGCTG CACAGTGCTG CACGTGCAG CATGGCAG TGAGCATCCA CTGTGGACT TTGACTCCTC AGCGGTCCCA AGCGGTCCCA  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080   |
| 50<br>55   | CAACACAGAG AAAAAAAAAAAAAAAAAAAAAAAAAAAA  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGGACGGT TTGGCAGGGT CCTCCAGGT TGGATGAAGC CCTGTAGGC TTGTGTCAC CCCTGTAGGC ACCTCTCAGGT ACCCACACTT TGGATGAGGC CCTGTAGGC ACCTCTCAGGGT ACCTCTCAGGGT ACCTCTCAGGGGAGCC ACCTCTCAGGGC ACCTCTCAGG  | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTAT TGCTTGAACC TGGGCGACAG TCGGGGTGGA CAGGAGCACA TATTTAACTTG CAGTGAGCAC TGGGCGACAG TCGGGGTGAC TGGGCGACAG CCGGGTGGACAG CCGGGGGCC CCGGGGGCC CCGGGGGCC CCGGGGGCC CGAGTGTAG CGATGGCCAA CGATGACCAA CGATGACCAA CGATGACAACTG CATGAACGGA   | AACAAACAAA TGTAATCCCA TGGAGCCGG GGTGGCCGGC TGGGAGGCAG AGCGAACGGG GAGTTGACT TCCGCAACGGG CAAAGTGGCT ACCATGTCATCC CCGGGTTCATCC CCGGGTTGAC CTCTCATCCT CCGGGCTGTG GAGGTCCCCA CGGGCTGTG GAGGTCCCCA CCTCTCATCCAC CACCATCCAC CCGGGCTGTG CACCATCCAC CCGGGCTGTG CACCATCCAC CCGGGCTGTG CACCATCCAC CCGGGCTATCAC CCGGCTCATCT CCGGGCTATCT CCGGGCTATCT CCGGGCTATCT CCGGGCTATCT  | CAAAACAAAG GCACTTTCGG AACATGGTGA AGCTGTAATC AGGTTGCAGT GCTCGTTGCA CTCGGTAATC CTCGTTGCA CTCGGTCAA CGCTCGACCG CACAGTGCTG CACAGTGCTG CACAGTGCTG CAGCGCAG TGAGCATCCA CTGTGACCCT TTGACTCCTC AGCGGTCCCCT   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>6720<br>780<br>840<br>900<br>900<br>1020<br>1080<br>1140<br>1200  |
| 50<br>55<br>60   | CAACACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CCAGCTACTC GATCOGAGAT AAGAAAAAAA TGTGAGTGTC ACCCAGTTAA CTCGATTCCC CGTAGGACG TATCCAGCT TAGCCAGCT TAGCCAGCT CAGCAGCACC CAGCAGCACC CAGCAGCACC CGGCTCCCAG CGGGTCCCAG GGGTGCCCTAG GCCTTACTCA   | AGACCTGTC GGGATGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CCTACGGCAC AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAAATACCA TTGGACTT TTGGCAGGT CCTCCAGGTC ACGCACACTT TGGATGAAGC GGGCCGCCC CCTGTGAGGC CTTGTGGTCAC CCCTGGAGGC CCTGGAGGC ACCTCTCCAGGTC CCCTGGAGGC CCCTGGAGGC ACCTCTCCAG   | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTAT TGCTTGAACCC TGGGGGACAG TCGGGGTGGA CAGGAGCACA TTOGTTTCTC CAGTGAGACA TCGGTCAGC TCGGCTCAG TCGCGCGCC CCAGGATGAG CCAGGATGAG CCTGCGGGGC CAGGATGAGACA TCGCAGCAC CGAGTGTGAG CGAGTGTGAG CGAGTGTAGA CGACCAACCC CAGAACGAC TCGCAGCCC CAGAACGAC TCGCAGCCC CTCAGCAGCCC CTCAGCAGCCC CTCACCTCCGC  | AACAAACAAA TGTAATCCCA TGGCCGGC GGTGGCCGGC TGGGAGCCGC GCTCTCATTG TCGGAACGGG GAGGTTGACT TCCCCTGGGT CTCTTCCCCG CAAGTGCCT CTCTCATCCT CTGGGGGCA CTCTTCATCCT CTGGGGCCA CTCTTCATCCT CTGGGGCCA CTCTTCATCCT CTGGGGCCA TCTTGATCCT CTGGGGCATCT CTGCCCCGC CTCTCTGCAAG GCCCCCGCCCCG   | CARAACAAAG GCACTTTCGG AACATGGGTGA GCCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGGTCGACCC CACAGTGCTG CAGCTGCCG CAGTGCTG CAGTGCTG CAGTGCTCC GGGGCAGCAG TGAGCATCCA CTTGACTCCC AGGGGTCCCA AGGGGTCCCA AGCGGTCCCT GGCCGACAGT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>900<br>900<br>1020<br>1140<br>1200<br>1260  |
| 50<br>55<br>60   | CAACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC ACCCAGTTACA CCGATTCAC CGTAGGACGG TTATCCAGCT ATGGGATGC CTAGCCAGCCA CCTGGCCAG CGGTTGGCG CGGGTTCCCAG GGGTGCCCAG GCGTCCCAG GGGTCCCAG GGGTCCCAG GGGTCCCAC   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTCA CGCGTCACTG CTACGGCCT CTACGAGCCT TTTTGGCTGT TTCAGGGAGC CCCAGTGTGC CCCAGTGTGC AGCACAAAA AGCACAAAC AGCACAAAC AGCACAACCGC GCGGCCCCGCCCC CCAGCTCACCT CACGCCGTCACCT CACGCCCGTCACCT CACGTCACCC CACGTCACCC CACGTCACCT CACGCCCCCCC CACGCCCCCC CACCCCCCCC CACCCCCCCC  | TGCAGCGAGC TCAAAACAAA CGGGCGCGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGAACCTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT GGGTCAAGC CCTGTGAGGC CCTGTGAGGC TTGTGGTCAC ACCTCTCCGGGCCACCC CCTGTGAGGC TCCTGGAGGC ACCTCTCCGG   | CGTGATCGTG CAAACAAACA AGACTAACAC AATTCAAGAT AGCCAAGTAT TGGTTGAACC TGGGGGACAG TCGGGGGACAG TCGGGTGGA CAGTAACTTG TCGTTTCTC AAGGCTCCAG TCGCGGATCAG CCTGCGGGGGC CCAGGATCAG CGTGGGGGC CGAGTGTGAG TGGCGCAT TGGCGCATCAG TCGCAAGCTG CATGAACGAA TCGCAAGCTG CATGAACGAA TCGCCTCGG GCAGGACTGT   | AACAAACAAA TGTAATCCCA TGGGACGGGC GGTGGCCGGC TGGGAGGCTG GCTCTCATTG TCGGAACGGG GAGATTGACT TCCCCTGGGT TCCCCTGGGT TCTCCCCG CAAAGTGGCT TCTCATCCT CCGGGTCTTCC CCGGGTCTTCC CCGGGTCTTCC CCGGCTCTTCC TCTCCATCCT TCTCGCAGCTCTCATCCT CCGGGTCTTCC TCTCTGCAAG GCTGCATCCT TCTCTGCAAG GCTGCATCCT TCTCTCCCCGG TGCAGCTCCCCGGC TCTCTGCAAG  | CARAACAAAG GCACTTTCGG AACATGGTGA GCTGTTAATC AGGTTGCAGT CGTTTCAGAA CCTGGAAATCC CTCCTGTCAA CGTCGGACCC CACAGTGCTG CACAGTGCTG CAGTGCTCT CAGGCAGCC CATGGGACT TGAGCATCCA CTGGGACT AGCGGTCCCA GCCGGTCCCA GCCGGCCACAGT ATCAGTATAC  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1260<br>1320  |
| 50<br>55   | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC GATCCCAGGTACTC ACCCAGTTAAA CTCGATTCCC CGTAGGACGG TTATCCAGCT ATGGAGATGC CTAGCCAGCCC CAGCAGCCCA CCTGGGCATGC CGGTTGGCC CGGTCCCAG GGGTCCCAG GGGTGCCCAG GCGTTCACC CCTAACGACC CCTCAACGAC CCTGAAGGAC CCTGAAGGAT  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG CTACGGCCT CTACGAGGCCT TTTTGGCTGT TTTCAGGGAGC GGGGATCCA AGCCAGAAGC AGCCAGAAGC AGCCAGAACC GCGGACCCG GCAGCCGGTCCCC GCAGCCGGTCCC GCAGCCGGTCCCC GCAGCCCGGTCAGCT CCCGTCAGCT CCCGTCAGCT CCCGAAATTGGAA   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGGAG AGAAATACCA TTGGACGGT TTGGCAGGGT CCTCCAGGT TGGATGAGC CCTGTAGGC TTGTGTCAC CCCTGTAGGC CCCTGTAGGC TCCCGGTAC CCCCCCCAGTC CCCCCCAGTC CCCCCCAGTC CCCCCAGTAC CCCCCAGTAC CCCCCAGTAC CCCCCAGTAC CCCCCAGTAC CCCCCAGTAC CCCCCAGTAC ACGCGTAT AGGGCTCCTA  | CGTGATCGTG CAAACAACAA AGCCAAGTAT AGCCAAGTAT TGCTTGAACC TGGGCGACAG TCGGGGTGGA CAGGAGCACA TATTAACTG CAGTGTGTTATACTG CAGTGTGACAC TGGCCCAGG CGGAGTGGA CGAGTGTGAG CGAGTGGAG CGAGTGGAG CGAGTGGAG CGAGTGGAG CGAGTGGAG CGAGTGGAG CGAGTGGAG CGAGTGGAG CGAGTGGAG CGAGTGAG CGAGCGAG CTGCCCCGG CCAGGACTGC TGGCCTCGG CGAGCTGT TGGTTCCTC   | AACAAACAAA TGTAATCCCA TGGCAGGCAG GGTGGCCGGC TGGGAGGCCG TGGGAGGCTC TCGGAACGGG GAGTTGACT TCCCCTGGGT TCCCTGGCT CAAGTGCAT ACCATGTCAT CCTCTCCCC CAAGTGCAT CCTCTCATCCT CCGGGCTGTG GAGGTCCCCC CTCTCATCCT CCGGGCTGTG GAGGTCCCCC CTCTCATCCT CCGGCTGTGAACACAAACAACAAAAAAAAAA   | CARAACAAAG GCACTTTCGG AACATGGTGA ACCATGATGATC AGGTTGCAGT CGTTTCAGAA CGTCGTTGCA CTCGGAAATCC CTCCTGTCAA CGCTCGACCC CACAGTGCTG CACAGTGCTG CAGGCAGCAG TGAGCATCCA CTGTGGACCT TTGACTCCTC AGCGGTCCCA GCCCGTCCCT GGCCGACAGT ATCAGTATAC ACAATGAAAA  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1260<br>1320<br>1380  |
| 50<br>55<br>60   | CARCACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC CAGCTACTC GATCCGAGAT AAGAAAAAA TGTGAGTGTC ACCCAGTTAA CTCGATTCCC CGTAGGACGG TTATCCAGCT ATGCAGCT CAGCAGCAA CCTGGGATGC CGGCTTGGCG CGGGTCCCAG GGGTGCGCT GCCTACTCA CCTGAAGGAT CCTGAAGGAT CCTGAAGGAT TGACAATACC   | AGACCTTOTC GGGATGGGC GGGTGGATCA CTACGAAAAA GGGAGACTCA AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CGGGGGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAAATACCT TTGGCAGGT CCTCCAGGTC CCTCCAGGTC TGGATGAAG CCTCTCAGGTC CCTGTGAGGC TTGTAGGC CCTGGAGGC CCTGGAGGC TTGTCAGGTC CCTGGAGGC TTGTCAGGT TCACGGTAT TCACGGTAT TCACGGTAT TGAGGCTCTA  | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTTA TGCTTGAACC TGGGGGACAG TCGGGGTGGA GAGAAGCACA TATTTAACTTG CAGTGAGCA TGGTTGATCC CAGGATTAGTTCCC AAGGCTCCAG TGGCGCATGC CCAGGATTAG CCAGGATTAG CCAGGATTAG CCAGGATTAG CCAGGATTAG CGAGTTTAGA CGAGTTTAGA CGAGTTTAGA CGAGTTTAGA CGAGTTTAGA CGAGTTTAGA CGAGTTTAGA CGAGCTAGC CTGCAGCTGG CTGCAAGCTG CTGCATCCAG CTGCCTCGG CCAGGATTAG CTGCCTCGG CGAGTTTAGA CTGCCTCGG CTGCAGCTG CTCCAAAAAAG CTCCCTCGG CTCCAAAAAAAG CTCCCTCGG CTCCAAAAAAAG CTCCCTCGG CTCCAAAAAAAG CTCCCTCGG CTCCAAAAAAAAG   | AACAAACAAA TGTAATCCCA TGGCCGGC TGGCAGGCCG GCTCCCATTG TCGCAACGGG GAGGTTGACTT TCGCAACGGG CTCTCATCT TCCCCTGGGT CTCTCCCGG CAAGTGCCT CTCGCGGCC CAAGTGCCT CTCGCGCT CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGCGGCCA TCTCTGCAAG GGCTCTTG GAGGTCCCC TCTCTGCAAG GGCTGCAGCTGA AGCTGCATCT AAGCTGACTCA AAGCTGACTCA AAGCTGACTCA AAGCTGACTCA AAGCTGACTCA AAGCTGACTCA  | CARAACAAAG GCACTTTCGG AACATGGTGA GCCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CATGTGTCT GGGGCAGCAG TGAGCATCCA CTGCAGCCC AGGGCCCG AGGGGCCCCT AGCAGTCCCA AGCAGTCCCA AGCAGTCCCA AGCAGTCCCA AGCAGTCCAT ACACAGTATACA ACAATGAAAA AGGCAGGCCGG  | 120<br>180<br>340<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>900<br>91080<br>1140<br>1200<br>1260<br>1380<br>1440   |
| 50<br>55<br>60   | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTA ACCCAGTTAA ACCCAGTTAC CGTAGGACGG TTATCCAGCT TAGCCAGCAC CAGCAGCAGCA CCTGGGCATG CGGGTTCCCAG GGGTGGGCTG GGCTCCCAG GGCTGGCAGC GGCAGCAGAA CCTGAAGAAT CCTGAAAGAAT TGAACAATACC CCTTTCCACGT   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG CTAGGGCCT CTAGGGCCT TTTTGGCTGT TTCAGGGAGC AGCCAGTAGGCCA AGCCAGTAGGCC AGCCAGAACC AGCCAGAACC CGGACCGCC GCAGCCGCCC GCAGCCGCCC GCAGCCGCCC GCAGCCGCCC CCGTCTCCA AGCCAGTAGC CCCGTCAGCT CACGTCTCCA AGCTCTCCA AGCTCTCCA AGCTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACCTCCCAC CCCCTCCACC CCCCTCCCAC CCCCTCCACC CCCCTCCCAC CCCCCTCCAC CCCCCCCC   | TGCAGCGAGC TCAAAACAAA CGGGCGGGT CGAGGTCAGG TACAAAAAT GGCAGAGAAA CCACTCCAGGG AAAAAGGGAG AGAAATACCAA TTGAACCTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT GGGTGAGGC CCTGTGAGGC CCTGTGAGGC TTGTGGTCAC CCCTGCAGGTC ACGCCCCC CTGTAGGC TCCCGCAGTC ACGCCTCCCGCAGTC CCCGCAGTC CCCGCAGTC TCACGGGTAT AGGGCTCCTA   | CGTGATCGTG CAAACAACA GACTACACCC AATTCAAGAT AGCCAAGTAT TGGTGGACAG TCGGGGGACAG TCGGGGTGAA TATTAACTTG TGGGCGACAG TCGGTTCTCC CAGGAGCACAG TCGGTTCCC CAGGATGAG CCTGCGGGGGC CGAGCTGTAACCG CGAGCTGAG CCAGCATGC CAGGATGAG CCTGCGCGGGGC CATGAACGGA TCGCCTCGG CAGGACTGT TGGCCTCAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAAACAG CCGCCAACACAG CCGCCAACACAG CCGCCAGCT CGCCAACAACAG CCGCCAGCT   | AACAAACAAA TGTAATCCCA TGGCAGCCGGC TGGGAGCCGG GGTGGCCGGC GCTCTCATTG TCGGAACGGG GAGTTGACT TCCCCTGGGT TCTTCCCCG CAAGTGGCT TCTTCCCCG CAAGTGCCT TCTGGGGGCA CTCTCATCCT CCGGGTGTCATC TCGGGGCTGCATCCT TCTGCAGGCTGATCCT TCTGCCAGC TCTCTCCACCC TCTCTCCACC TCTCCACC TCTCTCCACC TCTCTCCACC TCTCCACC TCTCCACC TCTCACC TC | CARAACAAAG GCACTTTCGG AACATGGTGA GCCTGTTAATC AGGTTGCAGT CGTTTCAGAA CCTCGGTGCAC CCTCCTGTCAA CCTCGGAATCC CACAGTGCTG CACAGTGCTG CACAGTGCTG CAGCTGCCGG CATGTGTCTC GGGGCAGCAG TGAGCATCCA CTTGGACTC AGCGGTCCCA GCCCGTCCCT AGCGGTCCCA GCCCGTCCCT ACAGTATAC ACAATGAAAA AGCAGGCCGG GCATCCAGCCGG GCATCCAGCCGG GCATCCAGCCGG GCATCCAGCCGGCCGG GCATCCAGCCGG GCATCCAGCCGG  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1080<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500  |
| 50<br>55<br>60   | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTA ACCCAGTTAA ACCCAGTTAC CGTAGGACGG TTATCCAGCT TAGCCAGCAC CAGCAGCAGCA CCTGGGCATG CGGGTTCCCAG GGGTGGGCTG GGCTCCCAG GGCTGGCAGC GGCAGCAGAA CCTGAAGAAT CCTGAAAGAAT TGAACAATACC CCTTTCCACGT   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CGCGTCACTG CTAGGGCCT CTAGGGCCT TTTTGGCTGT TTCAGGGAGC AGCCAGTAGGCCA AGCCAGTAGGCC AGCCAGAACC AGCCAGAACC CGGACCGCC GCAGCCGCCC GCAGCCGCCC GCAGCCGCCC GCAGCCGCCC CCGTCTCCA AGCCAGTAGC CCCGTCAGCT CACGTCTCCA AGCTCTCCA AGCTCTCCA AGCTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACGTCTCCA CACCTCCCAC CCCCTCCACC CCCCTCCCAC CCCCTCCACC CCCCTCCCAC CCCCCTCCAC CCCCCCCC   | TGCAGCGAGC TCAAAACAAA CGGGCGGGT CGAGGTCAGG TACAAAAAT GGCAGAGAAA CCACTCCAGGG AAAAAGGGAG AGAAATACCAA TTGAACCTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT GGGTGAGGC CCTGTGAGGC CCTGTGAGGC TTGTGGTCAC CCCTGCAGGTC ACGCCCCC CTGTAGGC TCCCGCAGTC ACGCCTCCCGCAGTC CCCGCAGTC CCCGCAGTC TCACGGGTAT AGGGCTCCTA   | CGTGATCGTG CAAACAACA GACTACACCC AATTCAAGAT AGCCAAGTAT TGGTGGACAG TCGGGGGACAG TCGGGGTGAA TATTAACTTG TGGGCGACAG TCGGTTCTCC CAGGAGCACAG TCGGTTCCC CAGGATGAG CCTGCGGGGGC CGAGCTGTAACCG CGAGCTGAG CCAGCATGC CAGGATGAG CCTGCGCGGGGC CATGAACGGA TCGCCTCGG CAGGACTGT TGGCCTCAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAACAG TCGCAAACAG CCGCCAACACAG CCGCCAACACAG CCGCCAGCT CGCCAACAACAG CCGCCAGCT   | AACAAACAAA TGTAATCCCA TGGCAGCCGGC TGGGAGCCGG GGTGGCCGGC GCTCTCATTG TCGGAACGGG GAGTTGACT TCCCCTGGGT TCTTCCCCG CAAGTGGCT TCTTCCCCG CAAGTGCCT TCTGGGGGCA CTCTCATCCT CCGGGTGTCATC TCGGGGCTGCATCCT TCTGCAGGCTGATCCT TCTGCCAGC TCTCTCCACCC TCTCTCCACC TCTCCACC TCTCTCCACC TCTCTCCACC TCTCCACC TCTCCACC TCTCACC TC | CARAACAAAG GCACTTTCGG AACATGGTGA GCCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CATGTGTCT GGGGCAGCAG TGAGCATCCA CTGCAGCCC AGGGCCCG AGGGGCCCCT AGCAGTCCCA AGCAGTCCCA AGCAGTCCCA AGCAGTCCCA AGCAGTCCAT ACACAGTATACA ACAATGAAAA AGGCAGGCCGG  | 120<br>180<br>340<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>900<br>91080<br>1140<br>1200<br>1260<br>1380<br>1440   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>            | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTC ACCCAGTTACA CCTGAGACGG TTATCCAGCT ATGGGAGTGC CAGCAGCCAC CAGCAGCCAA CCTGGGCATG CGGCTTGGCG CGGCTTGGCG GGCTCCCAG GGGTGCCCAC GGAGTCCCAC CCTGAAGGAT TGACAATACC CCTGAAGGAT CCTTCCACGC CAGGGGCCCC CAGCAGGAC CCTCCCACGC CCTCCCACGC CCTCCCACGC CAGCAGCCCC CCTCCCACGC CAGCAGCCCC CCTCCCACGC CAGCAGCCCC CAGCAGCCCC CAGCAGCCCCC   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGCTCACTG GCGTCACTG CTACGGCCT CTACGAGCGCT TTTCAGCGAGC TTTTCAGCGAGC AGCAGCAGC AGCAGCAGC AGCAGCAGC AGCAGCAGC CCCGGCCCC CACGCCGGCCC CACGCCGGCCC CACGCCGGCCC CACGCCGGCCC CACGCCGGCCC CACGCCCGCC   | TGCAGCGAGC TCAAAACAAA CGGGCGGT CGAGGTCAGG TACAAAAATT TGGCAGGGAGAC CACTCCAGCG AAAAAGGAGA AGAAATACCA TTGAACCTT TTGGCAGGT CCTCCAGGT ACGCACACT TGGATGAAG GGACCCCCC CCTGTAGGG TCTTGTGTCAC CCCCGCAGGT TCACGGTAC ACCTCTCAGG CCCCCCAGTC TCACGGTAC ACGCAGTC TCACGGTAC TCACGGTAC AGGCTCCT TGAAGTTCT TGAAGTTCT TGAAGTTCT TGAAGTTCT CCCGAGGTAC TCTACCAGGAC TGTACCAGGA  | CGTGATCGTG CAAACAACAA AGCCAACTAA AGCCAACTAA AGCCAACTGAAC TGGGCGACAG TATTAAACT TGGGCGACAG AGAAGACACA TATTAACTTG CAGTGAGACA TTCGTTTCTC CAGTGAGACA TGCGCATGC CCAGGGTGAA TGGCAATGAC CCAGGGTGAA TGCCAAA TGCCCAGG CATGAACGAC CTCGCCTCGG CATGAACGAC TGGCCTCGG CATGAACGAC TGGCTCTCGC TGGCCTCGG CCAGGACTTT TGGTTCTCT TGGTCCTCCAAAAAG CCGGCCAGCT AATTGCCAACAAA   | AACAAACAAA TGTAATCCCA GGTGGCCGGC TGGGAGGCGG AGGGAGACTC CCTCTCCCGG CAAAGTGGCT ACCATGTCATC CCGGGTTCACCC CAAAGTGGCT ACCATGCAT CCGGGTCTCATCCC CGGGTTCACCC CTGGGGGCAC CTCTCATCCT CCGGGTTGAC CTGCGGGTCACC TCTCATCCT CCGGGTTGAAC CGTGCATCC TCTCGCAAG CGTGCATCC TCTCGCAAG CGTGCATCC CTGCAAGTCCC CTCTGCAAG CCTGCAAGTCC CTCAGCAGC CTGCAAGTGCC CTCAGAGAGC CTCCAAGAACC CTCCAAGAAGC CTCCAAGAAGC CTCCAAGAAGC CTCCAAGAAGC CTCCAAGAAGC CTCCAAGAAGC   | CARAACAAAG GCACTTTCGG AACATGGTGA GCCTGTTAATC AGGTTGCAGT CGTTTCAGAA CCTCGGTGCAC CCTCCTGTCAA CCTCGGAATCC CACAGTGCTG CACAGTGCTG CACAGTGCTG CAGCTGCCGG CATGTGTCTC GGGGCAGCAG TGAGCATCCA CTTGGACTC AGCGGTCCCA GCCCGTCCCT AGCGGTCCCA GCCCGTCCCT ACAGTATAC ACAATGAAAA AGCAGGCCGG GCATCCAGCCGG GCATCCAGCCGG GCATCCAGCCGG GCATCCAGCCGGCCGG GCATCCAGCCGG GCATCCAGCCGG  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560  |
| 50<br>55<br>60   | CARCACAGAG ANANANAN AGGCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC CATCCGAGAT AAGAANANA TGTGAGTGTC ACCCAGTTAC CTGATTCCC CGTAGGAGG TTATCCAGCT ATGGGATGC CAGCAGCAA CCTGGGATGC CGGCTTCCAG GGGTCCCAG GGGTCCCAG GGGTCCCAG CCTGAAGGAT TGACAATACC CTTTCCACGT CAGGGCCCC CTGTCCACG CCTGAAGGAT TGACAATACC CTTTCCACGT CAGGGCCCC CAGTGGCCC CAGGGCCCC CAGGGCCCC CAGGGCCCCC CAGGGCCCCC CAGGGCCCCC CAGGGCCCCC CAATGTGGTG   | AGACCTITIC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CCTACGGACAC AAAAAAAAAA  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGAAG AGAAATACCA TTGGACAGGT TTGGCAGGT TTGGCAGGT CCTCCAGGTC CCTGTGAGGC TTGTAGGC ACCTCTCAGGT TTGGCAGGT TTGGCAGGT TCTGGAGGC TTGTGGTCAC CCCTGGAGGC CCCCGCAGTC TCACGGGTAT TGAAGGTGCT TGAAGGTGCT TGAAGGTGCT TGAAGGTGCT TGTACAGGAAAAAAAAAA   | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTAT TGCTTGAACCC TGGGGGACAG TCGGGGTGAA CAGGGTGGA CAGGGTGGA TATTAACTG CAGTGAGACA TGCTTATTACTTG CAGTGAGACA TGCGCATGAC TGCGCATGAC CCAGGATTAG CCAGGATTAG CCAGGATTAG CCAGGATTAG CCAGGATTAG CATGAACGA CTCGCCTCGG CCAGGATTAG CCACAGTTGG CCAAAAAAG CCGCCAGCT GTCCAAAAAAG CCGCCAGCT TGGTCCAAAAAAG CCGCCAGCT TGACCCAAT TGACCCAAC   | AACAAACAAA TGTAATCCCA TGGCCGGC TGGGAGCCAG GGTGGCCGGC TGGGAACGGG GAGGTTGACT TCGCAACGGG CCAAAGTGGCT TCCCCTGGGT CCATTGCCCG CAAAGTGCCT TCTCATCCT CCGGGCCACTCATCCT CCGGGCCACTCATCCT CCGGGCCACTCCTCATCCT CCGGGCCACTCCTCCACCCT CCTCTGCAAG AGCTCATCCT CTGCCAGGG TGCCACCTA AAGTTGGCCT AAGTGGACT AAGTGGACT AAGTGAACACC CCTGGAGGCC CCTGAAGAAGC GAGGACCATC   | CARAACAAAG GCACTTTCGG ACCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CACAGTGCTG CCGCTGCAC CACAGTGCTG CCGCTGCAG CTGTGCAG CTGTGCAG CTGTGCAG CTGTGCAG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTC CACAGTGCTC CACAGTGCTC CACAGTGCTC CACAGTGCTC CGGCCAGCAG TGAGCATCCA ACCAGTCCCT GGCCGACAGT ATCAGTATAC ACAATGAAAA GCCAGCCGG GCATCCAGCC TGGACCACC TGGACCACC TGGACCACC TGTACATGGT TTGACTCGT TTGACTCGT TTGACTCGT TGGACCAC TGGACCACC TGTACATGGT   | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1260<br>1380<br>1440<br>1560<br>1620  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>            | CAACACAGAG AAAAAAAAA AGGCCAAGC AACCCCATCT CCAGCTACTC GATCOGAGAT AAGAAAAAAA TGTGAGTGTC CCTGAGTACAC CGTAGGACGA TATCCAGCT TATCCAGCT TAGCCAGCC CAGCAGCAGCA CCTGGGCATG GGGTTCCC GGGTTCCC GGGTTCCC GGGTTCCCA GGGTTCCC CCTGAAGGAC CCTGAAGGAC CCTGAAGGAC CCTGAAGGAC CCTTACCCG CATTCCACGT CAGGGCCCC CAGGGGCCCC CAATGTGGGT GTTCCAACTG  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTCA CGCGTCACTG CGCGTCACTG CTACGGCCT CTACGGCCT TTTTGGCTGT TTCAGGGAGC TTCAGGGAGC GGGGATCCA AGCCAGAAGC AGCCAGAAGC GCGGCCCGGCC  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAAATACCA TTGGACTT TTGGCAGGT CCTCCAGGTC ACGCACACTT TGGATGAGC CCTGTGAGGC CTTGTGGTCAC CCCTGGAGGC CCTGGAGGC CCCTGGAGGC TGTACAGGT TCACGGTAT AGGGCTCCTA AGGGCTCCTA AGGGCTCCT CCCGAGGCAC TGTACCAGGA TGTACCAGGA AGGTCCTGAA  | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTTA TGCTTGAACCC TGGGGGACAG TCGGGGTGAA CAGTACACA CAGTGAGACA TCGGTTGAACCC CAGGAGCACA TCGGTTGAACCC CAGGAGCACA TCGGTTCACC CAGGATGAG CCTGCGCGGCC CAGGATGAG CCAGCATGC CAGGATGAG CCTCCAGG CAGCTTCAACCGA CTCGCCTCGG GCAGCTTCACCAACTGC CTCGCCTCGG GCAGCTTCACCCAACTGC CCGCCCCCAGCT TGGTCCCTCC TGCTCCAACACAACA   | AACAAACAAA TGTAATCCCA TGGCCGGC GGTGGCCGGC TGGGAGACTC GCTCTCATTG TCGCAACGG GAGATGACT TCCCCTGGGT TCTCCCCG CAAGTGGCT TCTTCCCCG CAAGTGCCT TCTGCATCCT CCGGGTCTCATCCT CCGGGTCTTC CCGGGCTCTC CCGGGCTCTC CCGGCCTGCACCCC TCTCACCCC TCTCACCCC TCTCGCAGC TCTCCCCGCC TCTCCCCCGCC TCTCCCCCGCC TCTCCCCCGCC TCTCCCCCGCC TCTCCCCGCC TCTCCCCCGCC TCTCCCCCGCC TCTCCCCCGCC TCTCCCCGCC TCTCCCCCGCC TCTCCCCCGCC TCTCCCCCGCC TCTCCCCCCCC   | CARAACAAAG GCACTTTCGG AACATGGGGGGGGGGGGGGGG  | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>900<br>1080<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>            | CAACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC CCTAGGATCCC CGTAGGACGA ATGGAGTGCC CAGCAGCCC CAGCAGCCC CAGCAGCCC CAGCAGCACC CGGGGCCCC CGGGGCCCC CGGAGCCCC CAACGTACCCC CAACGCCC CAACGCCC CAACGCCC CAACGCCC CAACGCCC CAACGCCC CAACGCCC CAACGCCC CAACGCCC AGCCCCCCAACGCCC AGCCCCCCAACGCCC AGCCCCCCAACGCCC CAACGCCCC  | AGACCTGTC GGGATGAGC GGGTGGATCA CTACGAAAAA GGGAGCTCACTG CTACGACCT CTACGACCT CTACGACCT CTACGACCT TTCAGGCGCT TTCAGGCGCT TTCAGGCAGC GCGCAGTAGCC CCAGTGCGC GCAGCCAGCAGC GCCCGCCCG CCAGCCGCCC GCAGCCGCC GCAGCCCGCC GCAGCCCC ATCAGCC ATCAGCCAGAC ATCAGCAGA AGCCTGCTCCA ATCAGCAGA CGCCTTCCAC CGCCTCCCAC ATTGAGCAGC GCCTTCCAC CGCCTTCCAC CGCCTCCAC CGCCCTCCAC CGCCCCTCCAC CGCCCTCCAC CGCCCTCCAC CGCCCTCCAC CGCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCAC CGCCCCTCCCCCCCCCC   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT TGGCAGGGAAC CACTCCAGGG AAAAAGGAG AGAAATACCA TTGAACCTT TTGGCAGGGT CCTCCAGGT CCTCCAGGT ACGCACACT TGGATGAGC CCTTTGAGG CCCTTTGAGG CCCTTTCAGG GCAGCCCCC TCACGGGTAC ACGCACACT TGAGGTCCAGGT TGAGGCCCCCC TCACGGGTAC CCCCGCAGTC TCACGGGTAC TGAAGGTCCTA AGGGCTCCTA AGGGCTCCTAC TGAAGGTCCT TCCAGGGAC TGTACCAGGA AGGTCCTGGA AGGTCCTGGA   | CGTGATCGTG CAAACAAACA GACTACACCC GATTCAACAC AATTCAAGAT AGCCAAGTAT TGGTGGACAG TGGGGGACAG TCGGGGGACAG TATTAACTTG CAGTAGACAC TTCGTTTCTC CAGGAGCTCAG TGGCGCATGC CCAGGATGAG CCTGCGGGGGC CGAGCTGAG CGATGAACGAA TCGCTCAG CCAGCATGC CATGAACGAC TTGCCTCAG CCAGCATGC CATGAACGAC TTGCCAAAAAG CCGGCCAGCT AATTGCCATC TGACCCAAC TGGCCAGCT CAGCACACG CCGGCCAGCT CGGACCAGCT CGGACCAGCT CGGACCAGC CATCAAAAAGGC GATCAAAAGGC GATCAAAAGGC GATCAAAAGGC  | AACAAACAAA TGTAATCCCA TGGCAGCCAG GGTGGCCGGC TGGGAGCAG GCTCTCATTG TCGGAACGG GAGATTGACT TCCCCTGGGT TCCCCTGGGT TCTCCCCG CAAAGTGGCT ACATTCCT CCGGGGTCATCCT CCGGGTCATCCT CCGGGTCATCCT TCTGCAGGCTTACCT TCTGCAGGCTTACCT TCTGCAAGCTGCATCCT TCTCTGCAAG CCTGCATCCT TCTCTGCAAG CCTGCAGCTTAACT AAGTTGGCCT AAGTTGGCT AAGTTGGCCT AAGTTGGCCT AAGTTGGCCT AAGTTGGCCT AAGTTGGCCT AAGTTGGCCT AAGTTAGCCT CCTGAGAGGCT CTCAAGAAGC GGGACCATC CTCAAGAAGC ATCCAATAC ATCCAGTATAC   | CARAACAAAG GCACTTTCGG AACATGGTGA GCTGTTAATC AGGTTGCAGT CGTTTCAGAA CCTGGAAATCC CTCCTGTCAA CGTCGACCC CACAGTGCTG CCGCTGCCG GCGCACAGTCCTC AGCGGTCCCA GCCCGTCCCT AGCGGTCCCA GCCCGTCCCT GGCCGACAGT ATCAGTATTAC ACAATGAAAA GGCAGCCCC TGGACCACCC TGGACCACCC TGGACCACCC TGGACCACCC TGTACATGGA TACACTCTCTGA  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1260<br>1380<br>1440<br>1560<br>1560<br>1680<br>1740  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>            | CARCACAGAG ANANANAN AGGCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC CATCCGAGAT AAGAANANA TGTGAGTGTC ACCCAGTTACA CTGGATTCCC CGTAGGAGGG TTATCCAGCT TAGCCAGCC CAGCAGCAA CCTGGAATGC CGGTTCCAG GGGTGCCCAG GGGTGCCCAG CCTGAAGGAT TGACAATACC CTTTCCACGT CAGGGCCCC CAATGTGGT CAGGGCCCC CAATGTGGTA CTTCCAAGT CAGGGCCCC CAATGTGGTA CGGTTCGAACTG GTTCGAACTG GTTCGAACTG GAGACCACC CAAGACCACC CAAGACCACC CAAGACATCACC CGAAGATCATC CGAACGCC CAAGACATCATC CGAACACCC CGAAGATCATC   | AGACCTIGNE GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CCTACGGCACT CTAGGGCGT CTTAGGGGGT CTTTTTGGCTGT TTCTAGGGGATC CCCAGTGTGC CCCAGTGTGC AGCAGAAGC AGCCAGAAGC AGCCAGAGC CCCGTCCCC CCGGCCCC CAGTTCTCACAGC CAGTCTCCACAGAGC CAGTCTCCACAGAGC CAACTAGCAACAGAGC CACCTCCCACC CACCTCCCACC CCCCTCCCCC CCCCCCCC   | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGAAG AGAAATACCA TTGAACTTT TTGGCAGGGT CCTCCAGGTC ACGCACACTT TGGATGAGC CTTGTGTCAC CCCTGTAGGC TTGTGTCAC CCCTGTAGGC TCCCGCGTAT AGGGCTCCTA TGAAGGTCCTA AGGTCCTGGA AGGTCCTGGA AGGTCCTGGA AGGTCCTGAT TCAAGATCT TCCAGGATCT TCCAGGATCT TCCAGGATCT TCCAGGATCT TCAAACCTTC   | CGTGATCGTG CAAACAACAA AGCAACAA AGCAACAACA AGTTCAAGAT AGCCAACTGAACC TGGGGGACAG TCGGGGTGGA CAGGAGCACA TATTTAACTTG CAGTGAGACA TCGGGTGACAG TGGGCGACAG TGGGCTCCAG TGGCCTCCAG TGGCCTCCAG TGGCCTCAG CGATGACCAA TCGCATCAG CCATGACCAACTGC CATGACCGA TCGCCTCGG CCAGCTCTCG TCGCTCCGG TCGCTCCGG TCGCTCCGC TGGCCCACCT TGGTCTCCTCT TGGCCCACT TGGTCCAAAAAG CCGCCACCT TGACCCCAAT TGACCCCAAT TGACCCCAAT TGACCCCAACT TGACCCCAAT TGACCCCCAAT TGACCCCCAAT TGACCCCCAAT TGACCCCCAC CAACCTCCCTCC  | AACAACAAA TGTAATCCCA TGGCCGGC TGGGAGCCAG GGTGGCCGGC TGGGAACGGG GAGGTGACT TCGCAACGGG CAAAGTGACT TCCCCTGGGT CTCTCATCT TCGCGGGCCAACGGGC CAAAGTGCCT CTCATCCT CACGGGCTTACCC CAAGTGCCT CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGCAGCTGA AAGTTGCCT CTGCCAGGG TGCCAGCTGA AAGTTGCCT AAGCTGATCC CTGAAGGG GAGGACCATC AACCTCAAAC ACCCTCAAAC ATCGAGTACT TCGCAGAGAAC GTGCGAGAAAC CTCGAAGAAC CTCGAAGAAC CTCGAAGAAC CTCGAAGAAC CTCGAAGAAC CTCGAAGAAC CTCGAAGAAC CTCGAAGAAC CTCGAAGAAAC CTCGAAGAAC CTCGAAGAAAC CTCGAAGAAC CTCGAAAC CTCGAAGAAC CTCGAAC CTCGAAGAAC CTCGAACAAC CTCCAACAAC CTCCAACAACAAC CTCCAACAACAAC CTCCAACAACAACAACAACAACAA | CARAACAAAG GCACTTTCGG AACATGGGAATCC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CACAGTGCTG CAGCTGCAG CAGTGCTG CAGTGCAG CAGTGCTG CAGTGCAG CAGTGCTG CAGTGCAG CAGTGCTG CAGTGCAG CATGTGTCT GGGGCAGCAG TGAGCATCCA ACCAGTGCCT GGCCGACAGT ATCAGTATAC ACAATGAAAA GGCAGCCG TGTACATCGT CACTCTTGA TCACTCTTGA TCACTCTTTGA TCACTCTTTGA TCACTCTTTGA TACATCACCA TAGTACACCA TGTACATCACCA TAGTACACCA TAGACTACCA TACACTACCA TAGACTACCA TAGACTACCA TAGACTACCA TAGACTACCA TAGACTACCA   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560<br>1620<br>1620<br>1630   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>            | CAACACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC ACCCAGTTAA CTCGATTCCC CGTAGGACGG TTATCCAGCT TAGCAGGC TAGCAGGCAC CGGCAGCGCAG CCGGCTTGGC CGGCTTGGC CGGCTTCCC CGTAGGATCC CCTGAAGGAT CCTTCAACGGA CCTTGAAGGAT CCAGGGCCC CAAGGATCCC CAAGGACCGAA AGACCAGCG CAAGATCACC CCAAGATCACC CAAGATCACC CAAGATCACC CCAAGATCACC CAAGATCACC CAAGATCACC CAAGATCACC CAAGATCACC CCAAGATCACC CCAAGATCACC CAAGATCACC CAAGATCACC CAAGATCACC CAAGATCACC CCAAGATCACC CAAGATCACC CAACATCACC CAAGATCACC CAAGATCACC CAAGATCACC CAAGATCACC CAAGATCACC CAACATCACC | AGACCTGTC GGGATGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CCTACGACACA CCTACGCCT CTAGGCCT CTAGGCCT CTAGGGCCT CTAGGGCT TTCTAGGGAG GGGGATCCA AGCCAGAAGC AGCCAGAAGC CCCAGTGTGC CGGGACCGG CCCGGCCCC CAGGCT CAGGTCTCCA GAAATTGGAA CCTACAGGC ATTAGCAGG GTCATTCTAC CGCTCACAG CGTCACCAG CGCTCAGGT CACGTCTCAC CACGTCTCAC CACTCTCAC CACTCTCAC CACTCTCAC CACCTCACC CACCTCAC | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAAATACCT TTGGCAGGT TCGAGTC TGGATGAGGC CCTGCAGGTC CCTGTGAGGC CCTGGAGGC CCTGGAGGC CCTGGAGGC CCCGCAGTC TCACGGTAT AGGCCTGAA AGGCTCTGA AGGCTCTGA AGGCTCTGA AGGCTCTGA AGGCTCTGAGGC CCCGAGGCAC TGTACCAGGA AGGTCCTGA AGGCTCTGAA AGGTCCTGA AGGCCCTGAA TGCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAAACCTTC TGAGCAATGA   | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTTA TGCTTGAACC TGGGGGACAG TCGGGGTGGA GAGAAGCACA TTOGTTTCAC CAGTGAGCA TTOGTTCCC TGGCGCATGC CCAGCATGC CCAGCATGA CCAGCAGCT GGCCAAGCT GGCCAAGCT GGCCAGCT AATTCCAATC GGAGTTCCCAG GAGAGTGCCC AATTCCAAGCG CAACCCCCAAC CAACCCCCAAC CAACCCCCAAC CAACCCCCAAC CAACCCCCAAC ATTCAAAGGC   | AACAAACAAA TGTAATCCCA TGGCGGC GGTGGCCGGC TGGGAGGCAG AGCGGAGCAG TCCCCTGGGT TCCCCTGGGT TCCCCTGGGT CTCTTCCCCG CAAGTGGCT CTCTTCCCCG CAAGTGCCT CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGCAGTTGC CTCTGCAAC TCTGCACCT CTCTGCAAG AGGTACT CTCGCCCGGC GGGACCATC CCTGAAGAAGC CTCAAGAAGC ACCCTCAAAC ACCCTCAAAC ATCAAGAAGC ATCAAGAAC ATCAAGAAGC ATCAAGAACC ATCAAGAAGC ATCAAGAAGC ATCAAGAAGC ATCAAGAAGC ATCAAGAACAC ATCAAGAACAC ATCAAGAAGC ATCAAGAACAC ATCAACAC ATCA | CARAACAAAG GCACTTTCGG ACCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGTGGACCC CACAGTGCTG CAGTGCTG CAGTGCTG CAGTGCTG CAGTGCTG CAGTGCTG CAGTGCTG CAGTGCTC AGGGCACAGT TTGACTCCTC AGGGGTCCCA AGCAGTCCCT GGCCACAGT ATCAGTATAC ACAATGAAAA AGCAGGCCGG CCTGGACAGCT TGACACCCC TGGACACCC TGGACACCC TGGACACCC TGGACACCAC TGGACACCC TGGACACC TGCACCC TGCACC TCCC TGCACC TGCACC TGCACC TCCACC TCCACC TCCACC TGCACC TCCACC TC | 120<br>180<br>340<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>900<br>1080<br>1140<br>1260<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1860   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AAGCCCATCT CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTA ACCCCAGTTAA ACCCCAGTTAA CCTCGATTCCC CGTAGGACGG TTATCCAGCT TAGCCAGCCC CAGCAGCAGCA CCTGGGCATG GGGTGGGCT GGCTTCAC CCTGAAGATT TGACAATACC CTTTCCACGT CAGGGGCCCC CAAGATCCGT AGACCAGGCC CAAGATCACT AGACCAGGCC CAAGATCACT CACGGCCC CAAGATCACT CAACATCACT  | AGACCCTGTC GGGATGAGC GGGATGAGA CTACGAAAAA GGGAGACTGA CTACGACAAAA CCTACGACCT CTAGGCCT TTTTGGCTGT TTCAGGCAGC TTCAGGCACC AGCCAGAACC AGCCAGAACC AGCCAGAACC AGCCAGAACC CCGGCCCC CCGGCCCC CCGGCCCC CAGCTCTCCA CAGATTCCAA AACTAGACAA CCTCCCACAGA ATTGGAA ATTGGAA ATTGGAA ATTGGAA ATTGGAA ATTGCACCACC CCCCTGCCCC CACCTGCCCA ATTTCACC CACCTGCCAC CACCTTGCAC CACCTTGCTC CACCTTGCAC CACCTTCCAC CACCTCCAC C | TGCAGCGAGC TCAAAACAAA CGGGCGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAAATACCA TTGGATGAACCTT TGGATGAGGC CCTGTGAGGC CCTGTGAGGC CCTGTGAGGC TGTGCGTCAC TCAGGTCT TCAGGTCACCTCCAGTC TCAGGTCCTCAGGTC TCTGAGGCTCCTAGGCC TGTGAGGC TGTGCAGCTGA CCCCGCAGTC TCACGGATCA TGAGCTCCTA AGGCTCCTA AGGCTCCTA AGGCTCCTA AGGCTCCTAGGGC TGTACCAGGA AGGTCCTGA AGGCCCTGAT TCAAACCTTC TCAGAATGA TCATGGAATGA TCATGGCACC  | CGTGATCGTG CAAACAAACA GACTACACCC AATTCAAGAT AGCCAAGTAT TGGTGGACAGACAA TCGGGGGACAG TCGGGGGGACAG TCGGTGAACCC CAGGATGACCC CAGGATGACCC CAGGATGAGACA TCGGTTGAGCC CAGGATGAGC CCAGGATGAG CCAGCATGAGC CAGGATGAGC CATGAACGAA TCGCTCGG   | AACAAACAAA TGTAATCCCA TGGGAGCCG GGTGGCCGGC TGGGAGCCG GCTCTCATCG CCCTCGGGT TCCCCTGGGT CTCTTCCCCG CAAGTGGCT CTCTCCCCG CAAGTGGCT CTCTCATCCT CCGGGGTCATC TCGGGGGCA CTCTCATCCT CCGGGTCTT CCGGGTCTT CCGCTGGT TCTCCCCGCC TCTCATCCT CCGCGCTCT CTCCACCCGC CTCTCAACAAG AACTTGACCT CCCGGAGAT AACCTAACAAG ATCGAGTATC ATCGGGAGAAG ATCGAGACC TCTGAGAACCC TCTGAGACCC TCTGAGACCC TCTGAGACCC TCTGAGACCC TCTGAGACCC TCTGAGACCC TCTGAGACCC TCTGAGACCC TCTGAGACCC  | CARAACAAAG GCACTTTCGG AACATGGTGA GCCTGTTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGTGGACCC CACAGTGCTG CAGGTGCCG CATGGACT CAGGCAGCC CACAGTCTC GGGGCAGCAG TGAGCATCCA CTGTGGACT AGGGTCCCA GCCCGTCCCT AGCGGTCCCA GCCCGTCCCT AGCGGTCCCA CTGTACACCC TGACACCC TGACCACCC TGACCACCC TGACCACCC TGACCACCC TGACCACCC TGACCACCC TACACTCTCTCA ATGGGCACAC ATGGGCACACC TACACTCTCTCA TCCCTCTCTCA ATGGGCACAT TCCTTCTCAA GCCAGGCCCT TCACTCTCTCAA TCCCTCTCCAA GCCAGGTCCTT TCCTCTCCAA  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1560<br>1620<br>1620<br>1630   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>            | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AAGCCCAAGCC AACCCCATCT CCAGCTACTC CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTC ACCCAGTTACA CCTGATCACC CGTAGGACGG TTATCCAGCT ATGGGATGC CAGCAGCGAA CCTGGGCATG GCGCTTCGGCATG GCGCTTCACC CCTGACAGGAT TGACAATACC CCTGACAGGAT CCAGGGCCC CAATGTGGTG GTTCGACT GACAATACC CAAGATCACC CACGGGGCC CACGGGGCC CACGGGGCC CACGGGGCC CCTCTCGCGAAG CTCTCGCGAAG CTCTTCGCGAAG CTCTTCGCGAAG CTCTTCGCGAAG CTCTCTCGCGAAG CCTCTCTCGCGAAG CCTCTCTCGCGAAG CCTCTCCAAGGTCC CTCTCGGGAAG CTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCCGGAAG CCTCTCCGGAAG CCTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CTCTCTGGGAAG CTCTCTGGGAAG CCTCTCTGGGAAG CCTCTTGGGAAG CCTCTCTGGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTCTGGAAG CCTCTTCTGGAAG CCTCTCTCTGGAAG CCTCTCTCTGGAAG CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTCA CGCGTCACTG CTACGACCT CTACGACGCT CTACGAGCCT TTCAGGCGGT TTCAGGCGGG CCGGGGATCCA CGCGGCATCCA CGCGGCATCCA CGCGGCATCCA CGCGGCATCCA CGCGGCACCC GCAGCGGGGACC GCAGCGGGGACC GCAGCAGGGGACCGGC GCAGCCGGGGGACCGGCGGGGGACCA ATTGAGCAGA ATTGAGCAG ATTGAGCAG ATTGACCAG GGTTTCTACT CACCGTGACA GACTTTCACT CACCGCGCGC GCCCGCCCGCCC GCGCCCGCCCC GCCCCGCCCC CGCCCCCC   | TGCAGCGAGC TCAAAACAAA CGGGCGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGAG AGAAATACCA TTGGACGGT TTGGCAGGGT CCTCAGGT TGGATGAGC CCTGTAGGC TTGTGTCAC CCTGTAGGC TCACGGT TCAGGTCAC TCACGCT TGGATGAGC TTGTGTCAC CCCGCAGTC TCACGGTAT AGGGCTCCTA TGAAGGTCCT TGAAGGTCT TGAAGGTCT TCAGGGTAT AGGGCTCCTA TGAAGGTCCT TCACGGTAT TCACAGGATCT TCACAGGATCT TCAAACCTTC TGAACATCA TCAAGCACTC TTGAGCAATGA TCATGGCACC TTTGGGCCCA   | CGTGATCGTG CAAACAACAA AGCCAAGTAT TGCTTGAACCC TGGGCGACAG TCGGGGTGGA GAGAAGCACA TATTAACTG CAGGGTGGACAG TCGGGGTGACAG TCGGGGTGACAG TCGGGTGACAC TCGGTGACAC TGGGCTCCAG TGGCCCCAG TGGCCCAG CGAGTGTAG CGATGAC CGAGCTGC TGGCCTCAG TGGCCTCAG TGGCCTCAAAAAG CCGCACGT TGGTCCTCAAAAAG CCGGCAGCT TGGTCCACAAC TGGAAGTGCCAC TGACCCCAAT TGACCCCCAG TCAAAAGGC CAACCTCCTG ATCAAAGGG CAACCTCCTG ATCAAGGGC CAACCTCCTG CGGTTGACAC GGGTGGTCGCC GGGTGTGACA   | AACAAACAAA TGTAATCCCA GGTGGCCGGC TGGGAGGCTG GCTCTCATTG TCGGAACGGG GAGTTGACT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCTTCCCCG CAAAGTGGCT ACATGTCAT CTGGAGCTGAC TCTCATCCT CCGGGTTGAC TCTCATCCT CCGGGTTGAC TCTCATCCT CCGGGTGAGCC TCTCAGCAGG CTGCAGGTGAGCC TCTCAGAGGC TCTCAAGAGC TCTCAGAGACC TCTCAGAGACC TCTCAGAGACC TCTCAGAGCC TCTCAGAGCC TCTTATACTGCT   | CARARCARAG GCACTTTCGG ARCATGCTGA ACCATGCAGA ACCATGCAGA ACCATGCAGA CCTGGAAATCC CTCCTGTCAA CCTGGACATCC CCACAGTGCTG CCACAGTGCTG CCACAGTGCTG CCGCTGCCGC CACAGTGCTG CACAGTGCTG CACAGTGCTC TTGACTCCCA GCCGGCCCCT TGCACACCC TGCACAGCCC TGCACAGCCC TGGACCACCC TGTACATGGT CACTCTCTCA ATGGGCACAT TCCTCTCCAA ATGGGCACAT TCCTCTCCCAA ACGCAGAGATCTT TTCTCTTTTGG  | 120<br>180<br>340<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>900<br>1080<br>1140<br>1260<br>1380<br>1440<br>1500<br>1560<br>1620<br>1680<br>1740<br>1860   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | CAACACAGAG AAAAAAAAAA AGCCCAAGCC AAGCCCAAGCC AACCCCATCT CCAGCTACTC CCAGCTACTC GATCCGAGAT AAGAAAAAAAA TGTGAGTGTC ACCCAGTTACA CCTGATCACC CGTAGGACGG TTATCCAGCT ATGGGATGC CAGCAGCGAA CCTGGGCATG GCGCTTCGGCATG GCGCTTCACC CCTGACAGGAT TGACAATACC CCTGACAGGAT CCAGGGCCC CAATGTGGTG GTTCGACT GACAATACC CAAGATCACC CACGGGGCC CACGGGGCC CACGGGGCC CACGGGGCC CCTCTCGCGAAG CTCTCGCGAAG CTCTTCGCGAAG CTCTTCGCGAAG CTCTTCGCGAAG CTCTCTCGCGAAG CCTCTCTCGCGAAG CCTCTCTCGCGAAG CCTCTCCAAGGTCC CTCTCGGGAAG CTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCCGGAAG CCTCTCCGGAAG CCTCTCTCGGGAAG CCTCTCTCGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CCTCTCTGGGAAG CTCTCTGGGAAG CTCTCTGGGAAG CCTCTCTGGGAAG CCTCTTGGGAAG CCTCTCTGGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTGGAAG CCTCTCTCTGGAAG CCTCTTCTGGAAG CCTCTCTCTGGAAG CCTCTCTCTGGAAG CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC  | AGACCCTGTC GGGAGTGGGG GGGTGGATCA CTACGAAAAA GGGAGACTCA CGCGTCACTG CTACGAGCCT CTACGAGGCT TTCAGGCGGT TTCAGGCGGG CCGGGGTCCA AGCAGTCGC CAGGAGCCT CAGGAGCCT CAGGAGCCT CAGGAGCC CAGGAGCC CAGGAGCC CAGGAGCC CAGGACCGGC CAGCCGGCCC CAGCTCTGC CACGCCTCCA CAGTCTGC CACGCCGGCC CACGCCGGCC CACGCCCGC CACGCCGCC CACGCCTCCA ATTGAGCAG AGCTGTGG GTCACCAT CGCTCCAC CGTTTCACT CACCTGCAC GACTTTCACT CACCTGCCC CCCTCCAC CCCTCCAC CCCCCCCC CCCCCCCC CCCCCCCC   | TGCAGCGAGC TCAAAACAAA CGGGCGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGCG AAAAAGGAG AGAAATACCA TTGGACGGT TTGGCAGGGT CCTCAGGT TGGATGAGC CCTGTAGGC TTGTGTCAC CCTGTAGGC TTGTGTCAC TCACGGT TCACGT TCACGGT TCACGT TCACGT TCACGT TCACGCT TCACCC TCACCC TCACCC TCACCC TCACCC TCACCC | CGTGATCGTG CAAACAACAA AGCCAAGTAT TGCTTGAACCC TGGGCGACAG TCGGGGTGGA GAGAAGCACA TATTAACTG CAGGGTGGACAG TCGGGGTGACAG TCGGGGTGACAG TCGGGTGACAC TCGGTGACAC TGGGCTCCAG TGGCCCCAG TGGCCCAG CGAGTGTAG CGATGAC CGAGCTGC TGGCCTCAG TGGCCTCAG TGGCCTCAAAAAG CCGCACGT TGGTCCTCAAAAAG CCGGCAGCT TGGTCCACAAC TGGAAGTGCCAC TGACCCCAAT TGACCCCCAG TCAAAAGGC CAACCTCCTG ATCAAAGGG CAACCTCCTG ATCAAGGGC CAACCTCCTG CGGTTGACAC GGGTGGTCGCC GGGTGTGACA   | AACAAACAAA TGTAATCCCA GGTGGCCGGC TGGGAGGCTG GCTCTCATTG TCGGAACGGG GAGTTGACT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCCTGGGT TCCTTCCCCG CAAAGTGGCT ACATGTCAT CTGGAGCTGAC TCTCATCCT CCGGGTTGAC TCTCATCCT CCGGGTTGAC TCTCATCCT CCGGGTGAGCC TCTCAGCAGG CTGCAGGTGAGCC TCTCAGAGGC TCTCAAGAGC TCTCAGAGACC TCTCAGAGACC TCTCAGAGACC TCTCAGAGCC TCTCAGAGCC TCTTATACTGCT   | CARAACAAAG GCACTTTCGG AACATGGTGA GCCTGTTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CTCCTGTCAA CGTGGACCC CACAGTGCTG CAGGTGCCG CATGGACT CAGGCAGCC CACAGTCTC GGGGCAGCAG TGAGCATCCA CTGTGGACT AGGGTCCCA GCCCGTCCCT AGCGGTCCCA GCCCGTCCCT AGCGGTCCCA CTGTACACCC TGACACCC TGACCACCC TGACCACCC TGACCACCC TGACCACCC TGACCACCC TGACCACCC TACACTCTCTCA ATGGGCACAC ATGGGCACACC TACACTCTCTCA TCCCTCTCTCA ATGGGCACAT TCCTTCTCAA GCCAGGCCCT TCACTCTCTCAA TCCCTCTCCAA GCCAGGTCCTT TCCTCTCCAA  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1080<br>1140<br>1260<br>1320<br>1380<br>1440<br>1560<br>1560<br>1680<br>1740<br>1880<br>1740<br>1860<br>1920  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | CAACACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC ACCCAGTTAA CTCGATTCCC CGTAGGACGG TTATCCAGCT TAGGCAGGC TAGCAGCCC CAGCAGCACC CGGCATCCC CGGCATCCC CGGCATCCC CGGGTCCCAG GGGTCCCAG GGCTTCCACGT CCTGAAGGAT CCAGTGCCC CAATGTGGT GTTCGACT GAACACCG CAAGATCCC CAAGATCCC CAAGATCCC CAAGATCCCC CAAGATCCCC CAAGATCCCC CAAGATCCCC CACCGTGGGC CCCACTGGGAC CCCAGGGACC CCAGGGCCCC CCAGGGACC CCAGGGACC CCAGGGACC CCAGGGACC CCAGGACCCC CCAGGGACC CCAGGGACC CCAGGGACC CCAGGGACC CCAGTGCCCC CCAGGGCCCC CCAGGCCCCA CCAGGCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCCA CCAGGCCCA CCAGGCCCCA CCAGGCCCA CCAGGCCCCA CCCCCAGCCCCA CCCCCCCC  | AGACCTGTC GGGATGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CCTACGACACA CCTACGCCT CTAGGCCT CTTAGGCGCT TTCTAGGCGGC CCCAGTGTGC AGCCAGAGC AGCCAGAGC CCCAGCCC CCCAGTGTC CCGGCCCC CCAGTCTCCA CCAGCCT CAGCCTCAGCT CACGTCTCCA CACCTCCACA ATTGCAA CGTCTCCAC CACTTCCAC CGCTCCCCC CCCTCAGCT CACCTTCACC CACCTCTCAC CTCACCTCCAC CACTTTCCAC CGCTCTCCAC CACTTTCACC CGCTCTCACC CACCTCTCACC CACCTCTCACC CACCTCTCACC CACTTTCCACC CACCTTCACC CACCTTCACT CACCTTCACT CACCTTCACT CACCTTCACT CACCTTCACT CACCTTCACT CACCTTCACT CACCTTCACT CTCACTTCACT CTCACT | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGGAGAC CACTCCAGGG AAAAAGGGAG AGAAATACCT TTGGCAGGT TGGATGAGGC CCTGCAGGTC CCTGTGAGGC TTGTGGTCAC CCTGGAGGC TCACGGTAT TGACTGGT TGACTGGT TGGATGAGC CCCGCGGTAT TGGACGGTAT TGGACGGTAT TGGACGGTAT TGGACGGTAT TGGACGGTAT TGGACGGTAT TCACGGGATC TTCAGGGATC TTACCAGGT TTCAGGAGCAC TTTACCAGGAT TCCAGGATCT TCAGGATCT TCAGGCACC TTTGGCCCC TTTGGCCCC TTTGGCCCC TTTGGCCCC TTTTGGCCCCT  | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTTA TGCTTGAACC TGGGGGACAG TCGGGGTGGA GAGAAGCACA TTOTTTACTG CAGTGAGAC TGGGTGAGAC TGGGTGAGC TGGGCTGAGC TGGGCTGAGC TGGGCTAGC CAGGATTAG TGCCCAGGT TGGCTCAGAGC CAGGATTAG CAGCCAAGCT TGGCTAGAC TGGCTAGAC TGGCTAGAC TGGCTAGAC GAGTTTAGAC TGCCTCGG GCAGCT ATTCCAAGCG ATCAAAGGC CAACCTCCCAA CAACCCCAAC CAACCTCCCCAACTC CATCAAGGGC CATCAAAGGC CAACCTCCCAACTC CATCAAGGGC CACCTCCAGG CTCAAGGGC CATCAAAGGC CAACCTCCCTC CATCAAGGGC CAACCTCCCAGGTTGACC CAGGTTGACC CAGGTTGACC CGGTTGACAC CGGTTGACAC CGGTTGACAC CGGTTGACAC CGGTTGACAC CGGTTGACAC CGGTTGACAC CGGTTGACAC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CACTTCAACGGC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CACTTCAACGGC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CACTTCAACGGC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CACTTCAACGGC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTGACC CACTTCAACGGC CGGTTGACC CGGTTGACC CGGTTTTACAC CGGTTGACC CACTTCAACGGC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTTTACAC CGGTTGACC CACTTCAACGGC CGGTTGACC CGGTTGACC CGGTTGACC CGGTTTACAC CGGTTGACC CGCTC CGGTTGACC CGGTTCAC CGCTC CGCT CG | AACAACAAA TGTAATCCCA TGGCGGGC GGTGGCCGGC TGGGAGCCGG GGTGGCCGGGCCG  | CARAACAAAG GCACTTTCGG ACCTTTCAGAA GCTCGTTGCAG TCGGAATCCAGAGGCCC CACAGTGCTG CAGTGCAG CACAGTCCAC ACAATGAAAA ACAATGAAAA CACAAG CACAGTCAGC CAGCAGT CACACTCCCAA CACACACAC TCGACACT CACCCCTCCCAA CACAAGATCT TCCTCTCCAA CACAAGACCT TCCACCACAG CACAAGATCT TTCCTCTCCAA CACAAGACCT TCCACCACAGC CACAAGATCT TTCCTCTCCAA CACAAGACCC TGTACACACAC CACAAGATCAT TCCTCTCCCAA CACAAGATCAT TTCCTTCTCCAA CACAAGATCAT TTCCTTCTCCAA CACAAGATCAT TTCCTTCTCCAA CACAAGATCAT TTCCTTCTCCAA CACAAGATCAT TTCCTTCTCCAA CACAAGATCAGCC ACAGTCAGCC CACAGACACT TTCCTCTCCAA CACAAGATCAT TTCCTTCTCCAA CACAAGATCAGCC ACAGTCAGCC ACAGTCAGCC ACAGTCCACAC ACAGTCAGCC ACAGTCACC ACAGTCAGCC ACAGTCAGC ACAGTCAGC ACAGTCAGCC ACAGTCAGCC ACAGTCAGCC ACAGTCAGC ACAGTCAGC ACAGTCAGC ACAGTCAGC ACAGTCAGC ACAGTCAGC ACAGTCAGCC ACAGTCAGC | 120<br>180<br>340<br>360<br>420<br>480<br>540<br>660<br>'720<br>780<br>840<br>900<br>1020<br>1140<br>1260<br>1380<br>1440<br>1500<br>1680<br>1740<br>1680<br>1740<br>1860<br>1980<br>1980<br>1980   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | CAACACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTA CCCAGTTAA CCTCGATTCAC CGTAGGACGA TATCCAGCT TAGCCAGCC CAGCAGCAGCA CCTGGGCATG GGGTTCCCA GGGTTCCCA GGGTTCCCA GGATTCCC CTGAAGGAC CCTGAAGGAC CCTGAAGGAC CCTGAAGGAC CAATGTGGT AGACCAGC CAATGTGGT AGACCAGCC CAAGGCCCC CAAGGCCCC CAAGGCCCC CAAGGCCCC CAAGGCCCC CAAGGCCCC CAAGGCCCC CCAGGGCCCC CCCGGAATTT   | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGAC GGCGTCACTG GGCGTCACTG TTTTGGCTGT TTCAGGCGCT TTCAGGGAGC GGGGATCCACA AGCCAGAAGC AGCCAGAAGC GCCGCCAGAAGC GCAGCCGCC GCAGCCGCC GCAGCCGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGCC GCAGCCGGCC GCAGCCGCC GCAGCCGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCAGCCGGCC GCCGCCGCC CCCGCCCG  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAATACCA TTGGACTCAGGT CCTCCAGGTC ACGCACACTT TTGGCAGGT CCTCAGGTC CCTGAGGGC CCTGTGAGGC CCTGTGAGGC CCTGTGAGGC TTGTGGTCAC CCCGCAGTC TCACGGTAT AGGGCTCTA AGGGCTCTA AGGGCTCTA AGGGCTCTGAGGCACT TCACGGATAT TCACGGATAT TCACGGATAT TCACGGATCT TCACGGATCT TCACGGATCT TCACGGATCT TCACGGATCT TCACGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGCATTG  | CGTGATCGTG CAAACAACA AATCAAGAT AGCCAAGTTA AGCCAAGTTA TGCTTGAACCC TGGGGGACAG TCGGGGTGAA CAGTACACAC CAGTAGACA TCGTTTCTC CAGTGAGACA TCGGTTGACCC CAGGATGAG TCGGCCATCC CAGGATGAG CCTGCCTCAG CGAGTGTAAACGG CCTGCCTCAG GCAGCTTAACCGA TCGCAAGCTG CATGAACGAA CCTGCCTCAG TCGCAAGCTG CTCGAAACAG CCTGCCTCAG TCCAAAAAAG CCGGCCAGCT AATTCCAAC GAACCCAAT GGAACCCAAT GGAACCCACT CATCAAAGGG CAACCTCCTG GTTCAAAGGG CAACCTCCTG GGTTGACG CAACCTCTG CAACCTCAT TGGAACTGC CAACCTCTG CAACCTCCTG CAACCTCTC CAACCTCCTG CAACCTCCTC CAACCTCTC CAACCTCCTC CAACCTCCTC CAACCTCCTC CAACCTCCTC CAACCTCCTC CAACCTCTC CAACCTCCTC CAACCTCCTC CAACCTCCTC CAACCTCCTC CAACCTCCTC CAACCTCTC CAACCTCCTC CAACCTCC CAACCTCC CAACCTCC CAACCTCC CAACCTCC CAACCTCC CAACCTCC CA | AACAAACAAA TGTAATCCCA TGGCGGC GGTGGCCGGC TGGGAGACTC GCTCTCATCT TCGGAACGG GAGATTGACT TCTCCCCG CAAAGTGGCT CTCTTCCCCG CAAAGTGGCT CTCTCATCCT CCGGGTCTCATCCT CCGGGTCTCATCCT CCGGGTCTTCATCCT CCGGGCTCTCATCCT CCGGGCTCTT CCGGGCTCTT CCGGGCTCTT CCGGGCTCTT CCGGGCTCTT CCGGGCTCTT CCGGGCTCTT CTGCCCCGC CTCTCATCAACAACA AACTAACACCTCAACAACACCTCAACAACACCCTAACAAC   | CARAACAAAG GCACTTTCGG AACATGGGA ACCATGCAGA GCCTGTAATC AGGTTGCAGT CTGTTCAGAA GCTCGTTGCA CTGGAAATCCA CTGGACATCC CACAGTGCTG CACAGTGCTG CACAGTGCTG CAGGCACAG CTGGACACC CACAGTCCC CACAGTCCTC CAGGGCACAG CTGGACCC TTGACTCCC AGCGGTCCCA GCCCGTCCCT AGCGGTCCCA GCCGTCCCT AGCACACCC TGACATGAAAA ACAATGAAAA ACAATGAAAA CGCAGGCCGG CCTTCTCTCAA TCACTCTCTCA TACACTACCA TTGACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCCAA GCAAGATCTT TTCCTTCTCCAA GCAAGATCTT TTCCTTCTCCAA TCACTCTCTCAA TCACTCTCTCCAA TCACTCTCTCCAA TCACTCTCTCCAA TCACTCTCTCCAA TCACTCTCTCCAA TCACTCTCTCCAA TCACCCGTAT TCCTCTCCCAA TCACCCGTAT   | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1080<br>1140<br>1260<br>1320<br>1380<br>1560<br>1560<br>1680<br>1740<br>1880<br>1740<br>1890<br>1990<br>1990<br>1990<br>1990<br>1990<br>1990<br>199               |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | CAACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CCAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC CCTGAGCAGC CGTAGGACGA ATGCCAGCTACTC CGTAGGACGA ATGCCAGCCC CAGCAGCCC CAGCAGCCATCAC CGGGTCCCAG GGGTCCCAG GGGTCCCAG GGGTCCCAG GGAGATCTCAC CCTGAAGAAT TGACAATACC CTTTCCACGT CAGGGGCCCC CAAGATCATCA GTTCGACTG GTCGAACTG AGACCAGCCC GAAGATCATC CCAGGGGCCCC CCAGTGCCCA CCTGGGAAC CCAGTGCCCA CCTGGGAAC CCTGGAACTG CCCTGGGAAC CCTGGGAACT CCCTGGGAAC CCTGGGAAC CCTGGGAAC CCTGGGAAC CCTGGGAAC CCTGGGAAC CCTGGGAAC CCTGGGACAG CCTGGGACAAG CCTGGGACAAG CCTGGGACAAG CCTGGGACAAG CCTGGGACAAG CCTGGGACAAG CCTGGACAAG CCTGGGACAAG CCTGGGACAAG CCTGGGACAAG CCTGGACAAG CCTGCAAC CCTGGACAAG CCTGCAAC CCTCCAAC CCTCCCAAC CCTCCCAAC CCCCAC CCCCCCCC  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGCTCACTG CTACGACCT CTACGACGCT TTCAGGCGCT TTCAGGCGCT TTCAGGCGGCT TTCAGGCAGCCT TTCAGGCAGCC GCAGTGTGCA GCCAGAAGC GAGTCTCCA GCCAGAAGC GAGTCTCCT CACGTCAGC GCAGCTCAGCC GCAGCTCAGCT  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT TGGCAGGGT CCTCCAGGG AAAAAGGAG AGAAACCA TTGAACCTT TTGGCAGGGT CCTCCAGGT CCTGTAGGC CCTGTAGGC TTGTGTCAC GCACCTT TGGATGAGG TTGTGTCAC TGGATCAC TGGATCAC TGGATCAC TGGATCAC TGGATCAC TGTGCTCAC TGTGCTCAC TGTGCTCAC TGTACCAGGAT TGAAGCTTT TCCAGGATCT TCAACCTT TGACAATGA TCTTGGCACT TTTGGCACC TTTTGGCACT TCAACCTT CCAGGATCT TCAACCTT CCAGGATCT TCAACCTT CCAGGATCT TCAACCTT CCACACATAGC CCACATAGC CCACATAGC CCACATAGC CCACATAGC CCACATAGC CCACATAGC CCACATAGC CCACATAGC CCGACGATCAT  | CGTGATCGTG CAAACAACAA AGCCAACTAACACACAACAACAACAACAACAACAACAACAAC   | AACAAACAAA TGTAAATCCCA TAGCCTGGAC GGTGGCCGGC TGGGAGGCTG GCTCTCATTG TCGGAACGG GAGTTGACT TCCCCTGGGT TCCCCTGGGT TCCCCTGGGT TCTCCCCG CAAGTGGCT ACATGCT TCTGGAGCTC TCTTCCCCG TCTTCCCCG TCTTCCCCG TCTTCCCCG TCTGGTGTAT TCTGGAGCTTGAT TCTGCAAG TCTGCATCCT TCTGCAAG TCTGCAAGATGCCT TCTGCAAG TCTGCAAGATGCCT TCTGCAAGATGCCT TCTGCAAGATGCCT TCTGCAAGATGCCT TCTGCAAGATGCCT TCTAGAAGACCT TCAAGAAGC TCTAAGATACT TCTGAGAGCCC TCTAAGATCA TCTAACTCA TCTAAC | CARAACAAAG GCACTTTCGG AACATGGTGA GCTGTTAATC AGGTTGCAGT CGTTTCAGAA CCTGGAAATCC CTCCTGTCAA CGTGGACCC CACAGTGCTG CCGCTGCCG GCGCCACAGTCCCC AGCGGTCCCC AGCGGTCCCC AGCGGTCCCC AGCGGTCCCC AGCGGTCCCC AGCGGTCCCC AGCCGTCCCT ACATGAAAA CGCAGCCC TGGACCACCC TGGACCACCC TGGACCACCC TGGACCACCC TGTACATGGA TACACTACCCA ATGGGCACAT TCCTCTCTCGA CCCTTCTCGA CCCCTTCTCGA TCCCTCTCTGA TCCCTCTCTGA TCCCTCTCTGA TCCCCCTGTA TCCCTCTCTGA AGGGACCCC TTGACATGGT TCCTCTCCCA ATGGGCACAT TCCTTCTCCCA ATGGCCACTTTTGG AGAGTCAGC TTGCCTTTTGG AGAGTCAGCT TCCCCCGGTT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500<br>1500<br>1680<br>1740<br>1800<br>1920<br>1980<br>2040<br>2160                                |
| 50<br>55<br>60<br>65<br>70                                       | CACACAGAG ANANANAN AGCCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC GATCCGAGAT AGANANAN TGTGAGTGTC ACCCAGTTAA CTCGATTCCC CGTAGGAGG TTATCCAGCT TAGGCAGCT AGGCAGCAG CCGGCTTGGCAGC GGGTCCCAG GGGTCCCAG GGGTCCCAG GGGTCCCAG GGGTCCCAG GGGTCCCAG GCCTACTCA CCTGAAGGAT TGACATAC CCTGAAGGAT CAGGGCCC CAATGTGGG GTCGACTG CAGGGCCC CAGGGCCC CAGGGCCC CAGGGCCC CCTGGAAGTCGC CCCGGGAGC CCCTGGAACTC CCCGGAGGCAC   | AGACCTITIC GGGATGGGC GGGTGGATCA CTACGAAAA GGGAGACTGA AGAAAAAAAAA CTACGCCT CTAGGCCT CTAGGGCT TTTTTGGCTT TTCAGGGAG GGGGGATCCA AGCCAGAGCC AGCCAGAGCC CCCAGTGTGC AGCCAGAGC CCCGCCCC CCGGCCCC CCGGCCCC CCGGCCCC AGCTCAGC AACTTCAAC AGCTAGCAGAGC AACTTCAAC AGCTGCCAC AACTTCCAC AAGTTTCAAC CGTCAGCAGAGC CGCTCAGCT CACCTGCCAC CACCTCCAC CACCTCACC CACCTGACA CGCTCTGACA CGCTCTGACA CGCTCTGACA CCCTCCAC CCCTCGACA CCCCGCCT CCCTTGGATG CCCACCAGC CCCACCAGC CCCACCAGC CCCACCAGC CCCACCAC CCCCCACCAC CCCCCACCAC CCCCCCACC CCCCCC  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGAAG AGAATACCA TTGGACAGGT TTGGCAGGT TTGGCAGGT TTGGCAGGT TTGGATGAGC CCTGTGAGGC TTGTGGTCAC CCCTGAGGC TTGTGGTCAC CCCTGAGGC TTGTGGTCAC CCCGAGGTC TCACGGGT TCACGGGTAT TGAAGCTGCT TGAAGCTCTCAGG AGCCCTGGA GCCCCCC TGTACAGGC TCACGGGAGC CCCGAGGTCC TGAAGCTCTC TGAAGCTCT TGAAGCTCT TGAAGCTCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT TCAGGATCT CCGACATAGC CCGACATAGC CCGACATAGC CCGACATAGC CCGACATCGT CCGACATCGC CCGACATCGT CCCACACT CCCCACACC CCCCACACC CCCCACACC CCCCCACC CCCCCC  | CGTGATCGTG CAAACAACAA AGCCAACACA AATTCAAGAT AGCCAAGTTA TGCTTGAACCC TGGGGGACAG TCGGGGTGGA GAGAAGCACA TATTTAACTG CAGTGAGCA TGCGTGAGCA TGCGCATGC CCAGGTTGACCC CAGGATTAG TGCTCAGAGCT TGCGCAAGCTG CCAGGATTAG CCAAGCTCCAG GCAGCTCAAACAGC CCACCCAACTC GATCAACAGC CCACCTCCTCAAACAGC CAACCTCCTCAACAGC CAACCTCCTCAACTG CAACCTCCTCCAACTG CAACCTCCTCCAACTG CAACCTCCTCCAACTG CAACCTCCTCCAACTG CAACCTCCTCCAACTGC CAACCTCCTCCAACTGC CAACCTCCTCCTCAACTGC CAACCTCCTCCTCCAACTGCACCTCCTCCAACTGCACCTCCTCCTCCAACTGCCCACCTCCTCTCCAACTGCACCTCCTCTCCTCCTCTCCTCTCCTCTCCTCTCCTCTCCTCT  | AACAAACAAA TGTAATCCCA TGGCGGGC GGTGGCCGGC TGGGAGCCGG GGTGGCCGGGCCG   | CARAACARAG GCACTITICGS ARCATGGTGA ACCATGGTGA GCCTGTTAATC AGGTTGCAGT CTGTTCAGAA GCTCGTTGCA CTGGAAATCC CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTC GGGGCAGCAG TGAGCATCCA ACCAGTCCC AGCAGTCCCC AGCAGTCCCC AGCAGTCCCC TCGACCACT TTGACTCCCC GGCCACAGT ATCAGTATTAC ACAATGAAAA AGGCAGGCCGG GCATCCAGCC TGGACACCC TGGACACCC TGGACACCC TGGACACCC TGTACATGCAA ATCGGACACT TTCCTCTCCAA GCAAGATCTT TCCTCTCCAA GCAAGATCTT TTCTTTTGG TACACCGTTT TACCCCTGGT ACACCGCTTT ACCCCTGGT ACACCCTGGT ACACCCTGGT TACCCCTGGT ACACCCTGGT ACACCCCTGGT ACACCCCTGGT ACACCCCTGGT ACCCCTGGGT TCCCCCTGGGT TACCCCTGGGT   | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>900<br>1080<br>1140<br>1260<br>1380<br>1440<br>1500<br>1620<br>1680<br>1740<br>1860<br>1920<br>1980<br>2040<br>2160<br>2160<br>2220                               |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul> | CAACACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC GATCOGAGAT AAGAAAAAAA TGTGAGTGTA CCCAGTTAA CTCGATTCAC CGTAGGACG TTATCCAGCT TAGCCAGCC CAGCAGCAGCA CCTGGGCATG GGGTCCCAG GGGTCCCAG GGGTCCCAG GCCTTACTCAC CCTGAAGGAC CTTGAAGGAC CTTTCACCC CAATGTGGT GGTCCAACGC CAATGTGGT GGTCCACG CAAGGCCCC CAATGTGGT CTCACCGC CAAGTCCCT CACGGGCCCC CAAGGGCCCC CAAGGGCCCC CCAGGGCCCC CCCGGAATTT GCTGGACAGG CCAGGGCCCC CCTGGAATTT GCTGGACAGG CCAGGGCCCC CCTGGAATTT GCTGGACAGG CCAGGGCCCA CCTGGACAGGCCCC CACGAGGCCCC CCTGGACAGGCCCC CCTGGACAGGCCCC CCTGGACAGGCCCC CCTGGACAGGCCCC CCTGGACAGGCCCC CCTGGACAGGCCCCC CCTGGACAGGCCCCC CACGAGGCCCCC CCTGGACTGCCCACCCCCCCCCC  | AGACCCTGTC GGGAGTGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGAC GGCGTCACTG AAAAAAAAAA  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGGAG AGAATACCA TTGGACTCAGGT ACGCACACTT TTGGCAGGT CCTCCAGGTC ACGCACACTT TGGATGAGC CCTGTGAGGC CTTGTGGTCAC CCCTGGAGGC CCCTGGAGGC TCACGGTAT ACGGCTCTA ACGCTCTGAGGT TCACGGTAT TCAGGATCT CCGACATAGC CGACATAGC CGACATAGC CGACATAGC CGACATAGC CGACATCAG CCTCAGTCCT ACTCAGTTCA  | CGTGATCGTG CAAACAACA AATTCAAGAT AGCCAAGTTA TGCTTGAACCC TGGGGGACAG TCGGGGTGGA CAGGAGCACA TTCATAACTG CAGTGAGACA TTCGTTTCTC AAGGCTCCAG TGGGCGATGA CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGGATGAG CCAGCAAGCTG CAGGATGAG CCAGCAGCTG CAGGACTGT CGCCCCGG GCAGCTTAACAGAA CCGGCCAGCT AATTCCCATC CGACTCGC GATCAAAGGC CAACCTCCTG GATCAAAGGC CAACCTCCTG ATTCAAGGGC CCAACCTCTG CGAGTTGACC CAACCTCTG CGAGTTGACGAC CTGACCCCAT TGAGGACTTCC CGGTTTGACAC CTGAGCTTG CGAGTCGCTC CGGTTTGACAC TGAGGACTTG CGGGTTGACAC CTGAGCCTCG GGGTGGCCTC CGGTTGACAC CTGAGGACTTG CGGGTGGCCGGAA CGGGCAGAC CTGAGGCCTCG GGGTGGCCGGAA CGGGCCGGAA CGGGCCGGAA CGGGCCTGG CGGGTGGCCC CGGGGAAGAGGATGAC ACACATTCCC  | AACAACAAA TGTAATCCCA TGGCGGGC GGTGGCCGGC TGGGAGACTC GCTCTCATCT TCGGAACGGG GAGGTTGACT TCTCCCCG CAAGTGGCT TCTCCCCG CAAGTGGCT CTCTCATCCT CCGGGTCTCATCCT CCGGGTCTCATCCT CCGGGTCTTC CCGGGCTCT CCGGGTCTTC CCGGGCTCT CCGGGCTCT CCGGGCTCT CCGGGCTCT CCGGGCTCT CCGGGCTCT CCGGGCTCT CCGGAGACC TCTCACCAC AACTGCACC CTCGAGACC CTCAGAACAC ATCGAGACC TCTGAGACC TCTGAGACC TCTGAGACC TCTGAGACC TCTGAGACC TCTGAGACC TCTGAGACC TCTGAGACC TCTGAGACC TCTAGACC TCTAGAC TCTA | CARAACAAAG GCACTTTCGG AACATGGGA ACCATGCAGA GCCTGTAATC AGGTTGCAGT CTGTTCAGAA CCTCGTTGCA CTGGAAATCCA CCGCTGCCGG CACAGTGCTG CACAGTGCTG GCGGCAGCAG CTGGACACCC ACAGTGCCC CACAGTCCCA CCGTCCCCA CCGTCCCCA CCGCGCCCC TTGACTCCCA GCCCGTCCCT AGCGGCACAGT ATCAGTATAC ACAATGAAAA AGCACACCC TGTACATCGC TGTACATGGT TACACTGCT TTCCTTCTCAA GCAGGCCCGTCCCT TTCACTCTCTCAA TCAGTATAC TCCTCTCTCAA TCACTCTCTCAA TCCCTCTCCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCCCTCTCCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCCCTTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCAA TCACTCTCTCT  | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1080<br>1140<br>1260<br>1320<br>1380<br>1560<br>1560<br>1680<br>1740<br>1860<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>1920<br>192                |
| 50<br>55<br>60<br>65<br>70                                       | CAACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CCAGCTACTC GATCCGAGAT AAGAAAAAAA TGTGAGTGTC CCAGTTACCC CGTAGGACGA TTATCCAGCT TTATCCAGCT TTAGCCAGCCC CAGCAGCCAAC CCTGGGCATGCC CGGCTTGGCAT CGGCTTGGCAT CGGCTTGCCAG GGGTGCCAG GGGTGCCAG GGAGTCCCAG GGAGTCCCAG GGAGTCCCAG GGAGTCCCAG CCTGAAGGAT TGACAATACC CCTTGAAGAT CCTGAACTG AGACCAGCC CAAGATCATCC CAGGGGCCCC CAAGATCACTC CCAGGGGCCCC CCAGTGCCCA CCCTGGGAACTG CCCTGGGAACTG CCCTGGGAACTG CCCTGGGAACTG CCCTGGGAACTG CCCTGGGAACTG CCCTGGGAACTG CCCTGGGAACTG CCCTGGGAACTG CCCTGGAACTG CCCTGGAACAC CCCTGAACAC CCCTGGAACAC CCCTGAACAC CCCTGAACAC CCCTGAACAC CCCTGAACAC CCCTGAACAC CCCTGAACAC CCCTGCAAC CCCTGCAAC CCCTGCAAC CCCTGCAAC CCCTGCAAC CCCCTGCAAC CCCCTCCAAC CCCCTCCCAAC CCCCCCCCC CCCCCCCC  | AGACCCTGTC GGGATGAGC GGGATGAGC GGGTGGATCA GGGAGCATCAGC GGAGACTCACTG TTCAGGCGCT TTCAGGCGCT TTCAGGCAGCT TTCAGGCAGCT TTCAGGCAGCCT CCAGTGCAGC CCCAGTGCAGC GGGACCAGC GCAGCAGCAGC GCAGCAGCAGC GCAGCAGCAGC GCAGCAGCAGC GCAGCAGCAGC GCAGCTCCCA ATGAGCAGC ATTGAGCAGC GCAGTTCTCACT CACCTTGCAC ATTGAGCAGC GCTTCCAC ATTGAGCAGC GCTTCCAC ATTGAGCAGC GCTTTCACT CACCTTGACC ACCTTGAGCT CCCCTTGAGCT CCCCTTGAGCT CCCCTTGAGCT CCCCTTGAGCT CCCCTTGAGCT CCCCTTGAGCT CCCCTTGAGCT CCCCTGACCAGC GCCCTTGGAGC GCCCTTGGAGC ACCCCGGCT GCCTTGGAGC ACCCCGGCT ACCCCGCT ACCCCCGCT ACCCCGCT ACCCCGCT ACCCCGCT ACCCCGCT ACCCCGCT ACCCCGCT ACCCCGCT ACCCCGCT ACCCCGCT ACCCCCGCT ACCCCCCC ACCCCCCC ACCCCCCC ACCCCCCC ACCCCCC  | TGCAGCGAGC TCAAAACAAA CGGGCGGGT CGAGGTCAGG TACAAAAATT TGGCAGGGAAC CACTCCAGCG AAAAAGGAGA AGAAATACCA TTGAACCTT TTGGCAGGGT CCTCCAGGT CCTCCAGGT CCTGAGGC CCCTGTAGGC TTGGATGAGC TTGTGTCAC GCACCTT TGGATGAGGC TTGTGGTCAC TGAACCTT TGAACCTT TGAACCTT TGAACCTT TGAACCTGA AGGCTCCTA TGAACCTT TCAACCTT TCACGACT TCCAGGATCAT AGCGATCAT AGCGATCAT ACCTCCT ACTCACTCAA AACCCTC ACTCACTC   | CGTGATCGTG CAAACAACAA AGCCAACTTCAAGAT TGCTTGAACCC TGGGCGACAG TCGGGGTGGA GAGAAGCACA TATTTAACTG CAGTGAGAC TGGGCTCAGC TGGGCTCAGC TGGGCTCAGC TGGGCTCAGC TGGGCTCAGC TGGGCTCAGC TGGGCTCAGC TGGGCTCAGC TGGGCTCAGC CATGAACGAC TCGCAAAAGG TCGCAAAAGG TCGCAAAAGG TGGCAACTCCC TGACCCACAC TGGGATCAGC TGGGATCAGC TGGTGTCCTCG TCAAAAAG TCGCAAAAG TCGCAAAAG TGGCAACTCCC TGACCCCAGC TGGTGTCAACAAG TTAAAGGC CAGCTCCTG TGACCCCAAT TGACCCCAAT TGACCCCAAT TGACCCCAAT TGACCCCAAT TTAAGGGC TGGTTTACAC TGGGACTGCT TGAGGCTGGC TGGGACGACT TGGGACCACT TGAGGCCGAAC TGGGACCACT TGAGGCCGGAAC TGGGACCACT TGGGACCCACT TGGGAACCACTCCC TGGGAACCCACT TCGGGAACCCAC TTCGGAACCCAC TCGGAACCCAC TCGCACAC TCGGAACCCAC TCGCACAC TCGCACAC TCGCACAC TCGCACAC TCGCACAC TCGCACAC TCCCTCAC TCGCACAC TCCCTCAC TCCCTCAC TCCCCCAC TCCCTCAC TCCCCCCAC TCCCCCCC TCCCCCC TCCCCCCC TCCCCCCC TCCCCCC  | AACAACAAA TGTAATCCCA TGGCAGCCGG GGTGGCCGGC TGGCAGCCGG TGGCAGCCGG GAGATTGACT TCCCCTGGGT TCCCCTGGGT TCCCCTGGGT TCCCCTGGGT TCTCCCCG CAAGTGGCT TCTCATCCT CCGGGGCAG CCTCATCCT TCGGAGCGC TCTCATCCT TCGGGGCAGCT TCTCATCCT TCGCGGGTATCCT TCTGCAGG TGCAGCTCATCCT TCTCGCAGGCT TCTCACCGC TCTCACCGC TCTCACCCG TCTCACCCC TCTACCCC TCTACCCC TCTACCCC AACCCCACAC AACCCCCACAC AACCCCCACAC AACCCCCC   | CARAACAAAG GCACTTTCGG AACATGCTGA GCTGTTAATC AGGTTGCAGT CGTTTCAGAA CCTGGAAATCC CTCCTGTCAA CGTGGACCC CACAGTGCTG CGGCGAGCAG TGAGCATCCA GCGGGCAGCAG TGAGCATCCA GCCGGTCCCT AGCGGTCCCA GCCGGTCCCT GGCCGACAGT ATCAGTATAC ACAATGAAAA GGCAGCCGC TGGACCACCC TGTACATGGACT TCACTCTCAA TGGGCTCCA TCACTCTCAA TCAGTATAC TCCTCTCAA TCAGTATAC TCCTCTCAA TCAGTATAC TCCTCTCAA TCAGTATAC TCCTCTCTGA TACACTACTAC TTCTCTCCAA TCCTCTCTCAA TCCTCTCTCAA TCCTCTCTCAA TCCTCTCTCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCCCAA TCCCTCTCTCCAA TCCTCTCCCAA TCCCTCTCTCCAA TCCCTCTCCTCCAA TCCCTCTCTCCCAA TCCCTCTCCCAA TCCCTCTCCTCCAA TCCCTCTCCTCCAA TCCCTCTCTCCCAA TCCCTCTCCTCCCAC TTCACCCGTTAT CCCTCTGGTCTCCCCGCGGGGAA CCCCTGGATCCCCCCGCGGGGAA CCCCTGGGTCCCCCCCCCC   | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500<br>1500<br>1620<br>1620<br>1740<br>1800<br>1900<br>1900<br>1900<br>2000<br>2000<br>2000<br>2000<br>20 |
| 50<br>55<br>60<br>65<br>70                                       | CAACACAGAGE AAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC CCAGCTACTC CCAGCTACTC CATCCAGATACAC ACCCAGTTACACC CGTAGGAGGC TTATCCAGCT TAGCCAGCT TAGCCAGCT TAGCCAGCC CAGCTAGCAC CGGCTCCCAG GGGTTCCAC GGAGTCCCAC CCTCAAGGAC CCTCAAGGAC CCTCAAGGAC CCAGCCC CAATGTGGTG GGACCCC CAATGTGGTG CCACCTGAACTC CAAGATCCC CTCGAATTC CAAGGCCCC CCTCGGAATTC CACCGTGGCCC CCTCGGAATTC CACCGTGGCCC CCTCGGAATTC CACGTGCCCA CCTCGGAATTC CCTCGGAATTC CCTCGGAATTC CCTCGGAATTC CCTCGGAATCCC CCTGGAATTC CCTCGGAATCCC CCTGGAATCCC CCTGGAATCCC CCTGGAATCCC CCTGGAACCCCC CCGGAAGCCCC CCGGAAGCCCCC CCGGAACCCTCA   | AGACCTICTIC GGGAGTGGGG GGGTGGATCA CTACGAAAAA GGGAGACTGAA CCTACGGACTCA AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CAGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGAG AGAAATACCA TTGAACTTT TTGGCAGGT CCTCCAGGTC CCTGTAGGC CTTGTGTCAC CCTGTAGGC TTGTGTCAC CCTGTAGGC TTGTGTCAC CCTGTAGGC TTGTGTCAC CCCGCGAGTC TCACGGTAT AGGGCTCCTA TGAAGGTCCTA TGAAGGTCCTA TGAAGGTCCTA TGAAGCTCTA TGAAGCTCTA TGAAGCTCTA TGAAGTCTT CCAGGATTA TCAGGATTA TCAGGATCT TCAGAATCT CCGACATTAG CCGACATCGT CCGACATCGT CCGACATCGT CCGACATCGT CCTGGAAACTT CTGGAAACTT  | CGTGATCGTG CAAACAACAA AGCCAAGTAT AGCCAAGTAT TGCTTGAACC TGGGGGACAG TCGGGGTGAA CAGGACTCACAC TATTTAACTTG CAGTGAGACA TCGGTGAGACA TCGGTGAGACA TCGGATGAG CCTGGGGGCCAGTT TCGTTTCTC CAGTGAGACA TGGCTCAG TGGCCAAGTGGC CAAGTGGCCAA TGGCTCAG GCAGGCTCGG GCAGGCTGC GCAGGACTGC GCAGGACTGT TGGTCCTCAAAAAG CCGGCAGCT TGGTCCAACAG GAAACTGCCC ATTCAAGGG CAACCTCCTG ATTCAAGGG CAACCTCTCG TGGTTTACAC TGAGCACTGT TGAGCACTGA TGAGGACTGAC TGAGCACTGA TGAGGACTGAC TGAGCACTGA TGAGGACTGAC TGAGCACTGA TGAGCACTGAC GGTGTTTACAC GGTGTTTACAC TGAGGACTGAC TGAGCACTCAC TGAGCACTCAC TGAGCACTCAC TGAGCACTCAC TGAGCACTCAC TGAGCACCAC TGAGCACCAC TGGGAACCCA TGGCACCACAAC GCTCACCAACA  | AACAAACAAA TGTAATCCCA TGGCGGGC GGTGGCCGGC TGGGAGCAGG GGTGGCCGGG TGGGAGCAGG GGTGGCCGG TCTCATCT TCGGAACGGG CCTCTCATCT TCGCAGTGGAC CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGAGGCT CTGGAGGCT CTGGAGGCT CTGAAAACACACACACACACACACA AACAGCACCAC AACTGCACGC AACTGCACGC AACTGCACGC AACTGCACCA AACACCACAACACA   | CARAACARAG GCACTTTCGG AACATGGAG ACCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CACAGTGCTG CCGCTGCAG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTC CACAGTGCTC CACAGTGCTC CACAGTGCTC CACAGTCCC CACAGTGCCC TGACCACC TGACCC TGACCACC TCTCTCCAA CACAGTCCT ACCGGTACT TTCCTCTCGA TCCCTCTGA TCCCGTAT TCCCTGGGGC TCACCGGTT CCCTGGGGGA CCCTGTGACTCT CCCTGGATCTT CCCCTGGATCT CCCTGGATCTT CCCTGGGGGA CCGGGGGGA CGGGAAGTTGA  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500<br>1500<br>1620<br>1620<br>1740<br>1800<br>1900<br>1900<br>1900<br>2000<br>2000<br>2000<br>2000<br>20 |
| 50<br>55<br>60<br>65<br>70                                       | CAACACAGAGE AAAAAAAAA AGCCCAAGCC AACCCCATCT CCAGCTACTC CCAGCTACTC CCAGCTACTC CATCCAGATACAC ACCCAGTTACACC CGTAGGAGGC TTATCCAGCT TAGCCAGCT TAGCCAGCT TAGCCAGCC CAGCTAGCAC CGGCTCCCAG GGGTTCCAC GGAGTCCCAC CCTCAAGGAC CCTCAAGGAC CCTCAAGGAC CCAGCCC CAATGTGGTG GGACCCC CAATGTGGTG CCACCTGAACTC CAAGATCCC CTCGAATTC CAAGGCCCC CCTCGGAATTC CACCGTGGCCC CCTCGGAATTC CACCGTGGCCC CCTCGGAATTC CACGTGCCCA CCTCGGAATTC CCTCGGAATTC CCTCGGAATTC CCTCGGAATTC CCTCGGAATCCC CCTGGAATTC CCTCGGAATCCC CCTGGAATCCC CCTGGAATCCC CCTGGAATCCC CCTGGAACCCCC CCGGAAGCCCC CCGGAAGCCCCC CCGGAACCCTCA   | AGACCTICTIC GGGAGTGGGG GGGTGGATCA CTACGAAAAA GGGAGACTGAA CCTACGGACTCA AAAAAAAAAA   | TGCAGCGAGC TCAAAACAAA CAGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGAGAAC CACTCCAGGG AAAAAGGAG AGAAATACCA TTGAACTTT TTGGCAGGT CCTCCAGGTC CCTGTAGGC CTTGTGTCAC CCTGTAGGC TTGTGTCAC CCTGTAGGC TTGTGTCAC CCTGTAGGC TTGTGTCAC CCCGCGAGTC TCACGGTAT AGGGCTCCTA TGAAGGTCCTA TGAAGGTCCTA TGAAGGTCCTA TGAAGCTCTA TGAAGCTCTA TGAAGCTCTA TGAAGTCTT CCAGGATTA TCAGGATTA TCAGGATCT TCAGAATCT CCGACATTAG CCGACATCGT CCGACATCGT CCGACATCGT CCGACATCGT CCTGGAAACTT CTGGAAACTT  | CGTGATCGTG CAAACAACAA AGCCAAGTAT AGCCAAGTAT TGCTTGAACC TGGGGGACAG TCGGGGTGAA CAGGACTCACAC TATTTAACTTG CAGTGAGACA TCGGTGAGACA TCGGTGAGACA TCGGATGAG CCTGGGGGCCAGTT TCGTTTCTC CAGTGAGACA TGGCTCAG TGGCCAAGTGGC CAAGTGGCCAA TGGCTCAG GCAGGCTCGG GCAGGCTGC GCAGGACTGC GCAGGACTGT TGGTCCTCAAAAAG CCGGCAGCT TGGTCCAACAG GAAACTGCCC ATTCAAGGG CAACCTCCTG ATTCAAGGG CAACCTCTCG TGGTTTACAC TGAGCACTGT TGAGCACTGA TGAGGACTGAC TGAGCACTGA TGAGGACTGAC TGAGCACTGA TGAGGACTGAC TGAGCACTGA TGAGCACTGAC GGTGTTTACAC GGTGTTTACAC TGAGGACTGAC TGAGCACTCAC TGAGCACTCAC TGAGCACTCAC TGAGCACTCAC TGAGCACTCAC TGAGCACCAC TGAGCACCAC TGGGAACCCA TGGCACCACAAC GCTCACCAACA  | AACAAACAAA TGTAATCCCA TGGCGGGC GGTGGCCGGC TGGGAGCAGG GGTGGCCGGG TGGGAGCAGG GGTGGCCGG TCTCATCT TCGGAACGGG CCTCTCATCT TCGCAGTGGAC CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGAGGCT CTGGAGGCT CTGGAGGCT CTGAAAACACACACACACACACACA AACAGCACCAC AACTGCACGC AACTGCACGC AACTGCACGC AACTGCACCA AACACCACAACACA   | CARAACAAAG GCACTTTCGG AACATGCTGA GCTGTTAATC AGGTTGCAGT CGTTTCAGAA CCTGGAAATCC CTCCTGTCAA CGTGGACCC CACAGTGCTG CGGCGAGCAG TGAGCATCCA GCGGGCAGCAG TGAGCATCCA GCCGGTCCCT AGCGGTCCCA GCCGGTCCCT GGCCGACAGT ATCAGTATAC ACAATGAAAA GGCAGCCGC TGGACCACCC TGTACATGGACT TCACTCTCAA TGGGCTCCA TCACTCTCAA TCAGTATAC TCCTCTCAA TCAGTATAC TCCTCTCAA TCAGTATAC TCCTCTCAA TCAGTATAC TCCTCTCTGA TACACTACTAC TTCTCTCCAA TCCTCTCTCAA TCCTCTCTCAA TCCTCTCTCAA TCCTCTCTCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCTCCAA TCCTCTCCCAA TCCCTCTCTCCAA TCCTCTCCCAA TCCCTCTCTCCAA TCCCTCTCCTCCAA TCCCTCTCTCCCAA TCCCTCTCCCAA TCCCTCTCCTCCAA TCCCTCTCCTCCAA TCCCTCTCTCCCAA TCCCTCTCCTCCCAC TTCACCCGTTAT CCCTCTGGTCTCCCCGCGGGGAA CCCCTGGATCCCCCCGCGGGGAA CCCCTGGGTCCCCCCCCCC   | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1500<br>1500<br>1620<br>1620<br>1740<br>1800<br>1900<br>1900<br>2010<br>2010<br>2010<br>2010<br>2010<br>20 |
| 50<br>55<br>60<br>65<br>70                                       | CAACACAGAG AAAAAAAAA AGCCCAAGC AACCCCATCT CCAGCTACTC CAGCTACTC GATCCAGAGAC AACACAGAGAC AACACAGAGAC AACACAGATCAC CGATCAGACAC CGTAGGACAGG TTATCCAGCT TAGGCAGGC TAGCCAGCAC CAGCAGCAC CGGCTTGGCA GGGTTCCAC GGGTTCCAC GGAGTCCCAG GCCTTACTCA CCTGAAGGAT TGACAATACC CAATGTGGTG GTTCGACAGG GTTCGACAG CCAGGGCCC CAAGATCGCT CACGTGGGC CAGGGCCC CAAGATCGCT CACGTGGGAC CCTGGACATT GCTGGACAGA CCTGGACAGAC CCTGGACATC CCTGGACAGAC CCTGGACATC CCTGGACAGAC CCTGGACAGAC CCTGGACACC CCTGGACACT CCTGGACAGAC CCTGGACACC CCTCGCACACC CCTCGCCACC CCTCGCCC CCTCGCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC  | AGACCTGTC GGGATGGGC GGGTGGATCA CTACGAAAAA GGGAGACTGA CCTACGAACAA CCTACGCCT CTAGGCCT CTAGGGCCT TTCTAGGCGGC GGGGGATCCAC AGCCAGAGCC AGCCAGAGCC CCCGGCCCC GCAGCCGGCCC GAGCCTCAGG GCTCAGGT GCAGCCGGCCC GCAGCCGCCC GCCCCGCCCC  | TGCAGCGAGC TCAAAACAAA CGGGGGGGT CGAGGTCAGG TACAAAAATT GGCAGGAGC CACTCCAGGG AAAAAGGGAG AGAATACCA TTGGACGGT TGGCAGGT TGGATGAGC CCTGTGAGGC TTGTGGTCAC CCTGGAGGC CCTGGAGGC TCACGGATC TGAAGCTGT TGGCAGGT TCACGGGT TCACGGTAT TGGAGGCACCC CCTGGAGGC CCCGCGAGTC TCACGGTAT TGAAGCTGT TCACGGTAT TGAAGCTGCT TGAGGCACC CCGAGGCAC CCGAGGCAC TGTACCAGGA AGGTCCTGA AGGCCGTGAT TCCAGGATCAT TCAGGAATCAT TCAGGCACC TTTGGCCCT TGAGCATCAT TCAGGCATCAT TCAGGAATCAT CCGAGGATCAT CCGAGGATCAT CCGACATAGC CGACATAGC C | CGTGATCGTG CAAACAACAA AGCCAAGTTA AGCCAAGTTA TGCTTGAACCC TGGGGGACAG TCGGGGTGAA CAGGATCAAC AGTCAAGAT TATTAACTG CAGTGAGAC TCGGTGAGCA TCGGTTAT TCCTTGTTCCC CAGGATCAG CCGAGCTGA CCGAGCTGA CCGAGCTGA CTCGCCCCG GCTCAAACGC CAACCCCAAC CAACCCCCAC CAACCCCCCCC  | AACAACAAA TGTAATCCCA TGGGGGGCGG TGGGAGGCAG AGGGGTGGCGGG TGGGAGCAG AGGGTGACTG CCCTCCATTG TCGCAACGGG CAAAGTGGCT CTCTCCCG CAAAGTGCCT CTCTCATCCT CTGGGGCACAG ACCATGCATC CTGCCCGGGT CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA CTCTCATCCT CTGGGGGCA TCTGGCACTGA AAGTTGCCT CTCAGAGAGC CTCAAGAAGC CTCAAGAAGC TCTGAGAGCAC ACCTCAAAC ACCTCAAAC ACTGAGACCAC ACTGAGCCC AGTAAGCTGC AACTGCACCG ACTGAGGCC ACCTCACGGCC ACCTCACGGCC ACCTCACGGCC CCTCCAGGCC CCTCCAGCC CCTCCAGCC CCTCCAGGCC CCTCCAGCC CCTCCAGGCC CCTCCAGCC CCCACC CCCACC CCCCACC CCCCACC CCCCCACC CCCCACC CCCCCACC CCCCCC   | CARAACARAG GCACTTTCGG AACATGGAG ACCTGTAATC AGGTTGCAGT CGTTTCAGAA GCTCGTTGCA CTGGAAATCC CACAGTGCTG CCGCTGCAG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTG CACAGTGCTC CACAGTGCTC CACAGTGCTC CACAGTGCTC CACAGTCCC CACAGTGCCC TGACCACC TGACCC TGACCACC TCTCTCCAA CACAGTCCT ACCGGTACT TTCCTCTCGA TCCCTCTGA TCCCGTAT TCCCTGGGGC TCACCGGTT CCCTGGGGGA CCCTGTGACTCT CCCTGGATCTT CCCCTGGATCT CCCTGGATCTT CCCTGGGGGA CCGGGGGGA CGGGAAGTTGA  | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>900<br>1020<br>1140<br>1260<br>1320<br>1440<br>1500<br>1620<br>1680<br>1740<br>1560<br>1620<br>1680<br>1740<br>2040<br>2160<br>2260<br>2280<br>2280<br>2240       |

2580

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                                                                                           1800
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         CATCCTCATG AGTGAGTGGA GGAGCTCGGG GGAGCAGGCG GGCCGGGGCT GGGGCTCCCC
                                                                                            480
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40
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         ATGAGGACAG ACCAGCTGAA ATTGGGTGGA GGACCGTTCT CTGTCCCCAG GTCCTGTCTC
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         TGCACAGAAA CTTGAACTCC AGGATGGAAT TCTTCCTCCT CTGCTGGGAC TCCTTTGCAT
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         GGCAGGGCCT CATCTCACCT CTCGCAAGAG GGTCTCTTTG TTCAATTTTT TTTAATCTAA
                                                                                            780
45
         AATGATTGTG CCTCTGCCCA AGCAGCCTGG AGACTTCCTA TGTGTGCATT GGGGTGGGGC
          TTGGGGCACC ATGAGAAGGT TGGCGTGCCC TGGAGGCTGA CACAGAGGCT GGCACTGAGC
                                                                                            900
         CTGCTTGTTG GGAAAAGCCC ACAGGCCTGT TCCCTTGTGG CTTGGGACAT GGCACAGGCC CGCCCTCTGC CTCCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTTAC TAGTAGCCAA
                                                                                            960
                                                                                            1020
         AAGGAATGAA AGAGAGCTCT AACCAGATGG AACACTGGAA CATTCCAGTG GACCCTGGAC
                                                                                            1080
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         CATTCCAGGA AAACTGGGAC ATAGGATCGT CCCGCTATGA TGGAAGTGTT CAGACAGTTT
                                                                                            1140
                                                                                            1200
         ATAATAGTAA GCCCCTGTGA CCCTCTCACT TACCCCGAGA CCTCACTTA TTACAAGATC TTTCCAAATA CCCAAATATC CCTGCAAGCC CGTTAAATAA TTCCCTATGC TACCCTTAAT
                                                                                            1260
         AACATACAAT GACCACATAG TGTGAGAACT TCCAACAAGC CTCAAAGTCC CTTGAGACTC
                                                                                            1320
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                                                                                            1380
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                                                                                            1440
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         Nucleic Acid Accession #: NM_005971.2
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          Coding sequence: 176..439
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GAAGGTGACC CTGGGCCTGC TTGTGTTCCT GGCAGGCTTT CCTGTCCTGG ACGCCAATGA
                                                                                            120
                                                                                             240
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                                                                                             300
          CATCTGCGCT GGGGTTCTGT GCGCCATGGG CATCATCATC GTCATGAGTG CAAAATGCAA
ATGCAAGTTT GGCCAGAAGT CCGGTCACCA TCCAGGGGAG ACTCCACCTC TCATCACCCC
                                                                                             360
 70
          AGGCTCAGCC CAAAGCTGAT GAGGACAGAC CAGCTGAAAT TGGGTGGAGG ACCGTTCTCT
                                                                                             480
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                                                                                             540
                                                                                             600
                                                                                             660
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          CAGAGGCTGG CACTGAGCCT GCTTGTTGGG AAAAGCCCAC AGGCCTGTTC CCTTGTGGCT
                                                                                             780
          TGGGACATGG CACAGGCCCG CCCTCTGCCT CCTCAGCCAT GGGACCTCAT ATGCAATTTG
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          GGATTTACTA GTAGCCAAAA GGAATGAAAG AGAGCTCTAA CCAGATGGAA CACTGGAACA
          TTCCAGTGGA CCCTGGACCA TTCCAGGAAA ACTGGGACAT AGGATCGTCC CGCTATGATG
                                                                                             960
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          GAAGTGTTCA GACAGTTTAT AATAGTAAGC CCCTGTGACC CTCTCACTTA CCCCGAGACC
TCACTTTATT ACAAGATCTT TCCAAATACC CAAATATCCC TGCAAGCCCG TTAAATAATT
                                                                                             1020
                                                                                             1080
          CCCTATGCTA CCCTTAATAA CATACAATGA CCACATAGTG TGAGAACTTC CAACAAGCCT
                                                                                             1140
          CAAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTTCT CATGAACTAC CCCACAACAC GCCTAAAACT CAAAACACCC AAAAATATCT CCTCCAATGT CCTGAGACAT
                                                                                             1200
                                                                                             1260
```

|     | GAACCCAAAA  | AGAGACCCAC                              | DOTDARATAR   | TGACTTGTCC   | CCTC         |                          | 1304         |
|-----|-------------|---|--------------|--------------|--------------|--------------------------|--------------|
| 5   | Nucleic Aci | C196 DNA Se<br>d Accession<br>ence: 551 | #: NM_0049   | 61.2         |              |                          |              |
|     | 1<br>       | Í.                                      | 1            | 1            | Ī            | 51<br>                   |              |
| 10  |             | GAGCCGCGAC<br>TTCCAGTCCT                |              |              |              |                          | 60<br>120    |
|     | CCTCAGACTG  | AATCAAAGAA                              | TGAAGCCTCT   | TCCCGTGATG   | TTGTCTATGG   | CCCCCAGCCC               | 180          |
|     |             | AAAATCAGCT<br>GCAAACTGCC                |              |              |              |                          | 240<br>300   |
|     |             | TGCGCCCTGG                              |              |              |              |                          | 360          |
| 15  | GTCAACAGCC  | TTGGTCCTCT                              | CTCTATCCTA   | GACATGGAAT   | ACACCATTGA   | CATCATCTTC               | 420          |
|     |             | GGTACGACGA<br>TGGTGAGCCA                |              |              |              |                          | 480<br>.540  |
|     |             | ATGAGATCAC                              |              |              |              |                          | 600          |
| 20  |             | CAATTAGGAT                              |              |              |              |                          | 660          |
| 20  |             | CTCACTCTTG<br>AGTGGGAAAA                |              |              |              |                          | 720<br>780   |
|     | TTCCAGTTTG  | ATTTTACAGG                              | AGTGAGCAAC   | AAAACTGAAA   | TAATCACAAC   | CCCAGTTGGT               | 840          |
|     |             | TCATGACGAT                              |              |              |              |                          | 900<br>960   |
| 25  |             | TCCCTTCTTC                              |              |              |              |                          | 1020         |
| -   | TTGGGCACCT  | TTTCTCGTAA                              | GAATTTCCCG   | CGTGTCTCCT   | ATATCACAGC   | CTTGGATTTC               | 1080         |
|     | TATATCGCCA  | TCTGCTTCGT<br>ACAACCAGAC                | CTTCTGCTTC   | TGCGCTCTGT   | TGGAGTTTGC   | TOTOCTCAAC               | 1140<br>1200 |
| ••  |             | CCCATGCCCG                              |              |              |              |                          | 1260         |
| 30  |             | TGTGCCAGAT                              |              |              |              |                          | 1320         |
|     |             | AGCAGCCCCC<br>GCTGTGAGTG                |              |              |              |                          | 1380<br>1440 |
|     | TGTGAGGGCA  | GTACCTGGCA                              | GCAGGGCCGC   | CTCTGCATCC   | ATGTCTACCG   | CCTGGATAAC               | 1500         |
| 35  |             | TTGTTTTCCC                              |              |              |              |                          | 1560<br>1620 |
| 55  | GGTCCAAGCC  | CCTTGCCAAG                              | GGAGTTGGGG   | GAAAGCAGCA   | GCAGCAGCAG   | GAGCGACTAG               | 1680         |
|     |             | GCCCCATTCC                              |              |              |              |                          | 1740         |
|     |             | TGGCCCATTC                              |              |              |              |                          | 1800<br>1860 |
| 40  | ACTTAGTGAT  | CAGCTCCCTA                              | AAACCATGCC   | TAAGTACAGG   | CGGATTAGCT   | ATCTTCCAAC               | 1920         |
|     |             | ACCAGACAAT<br>AGTTCTGGCC                |              |              |              |                          | 1980<br>2040 |
|     |             | TAAGATGCTG                              |              |              |              |                          | 2100         |
| 45  |             | ATGTTCTCAG                              |              |              |              |                          | 2160         |
| 43  |             | ATCCCTTTAG<br>TCTGCTGCTG                |              |              |              |                          | 2220<br>2280 |
|     | ACTACCAATT  | CAATGCCCTT                              | CATCCAATGG   | GTATCTATTT   | TTGTGTGTGA   | TTATAGTAAC               | 2340         |
|     |             | TTTATATGCC                              |              |              |              |                          | 2400<br>2460 |
| 50  |             | TAAGGAAACT                              |              |              |              |                          | 2520         |
|     |             | CACTGTCGGA                              |              |              |              |                          | 2580         |
|     |             | CCCGGGGCAC                              |              |              |              |                          | 2640<br>2700 |
| 55  | GATAGCCTTG  | TGACATCTTT                              | AGGGCAGGAT   | TCTTATCCCC   | ATTTTGCAGA   | TGAAAACCCT               | 2760         |
| 55  |             | TTTCTGTGGG                              |              |              |              | CTTCTGTCAC               | 2820<br>2880 |
|     | CTCTGCTGGC  | : ACACCAGTGG                            | CAAGGCCCAG   | AATGGCGACC   | TCTCTTTAGC   | TCAATTTCTG               | 2940         |
|     |             |   |              |              |              | TAACCCAGTG               | 3000<br>3060 |
| 60  |             |   |              |              |              | TCTGAAATGG               | 3120         |
|     | GGAAATATGI  | IATAAATAAA 1                            | * ATCAGCAAAG | CAAAAAGAAA   | AAAAAAA A    |                          | 3168         |
|     |             | : C197 DNA S                            |              | 984.1        |              |                          |              |
| 65  |             | quence: 572                             |              |              |              |                          |              |
|     | 1           | 11                                      | 21           | 31           | 41           | 51                       |              |
|     | GCCAGAGCG   | <br>r gagccgcgag                        | CTCCGCGCAC   | <br>         | CGGTCTCCGC   | GGAAATGTTG               | 60           |
| 70  | TCCAAAGTT   | TTCCAGTCCT                              | CCTAGGCATO   | TTATTGATCO   | TCCAGTCGAG   | AACATGTATA               | 120          |
|     |             |   |              |              |              | GACCACAGCG<br>CCCCCTTTGT | 180<br>240   |
|     |             |   |              |              |              | TCGAGGGACC               | 300          |
| 75  | TCAGACTGA   | A TCAAAGAAT                             | AAGCCTCTT    | COGTGATGT    | r grctatggc  | CCCAGCCCCA               | 360          |
| 13  |             |   |              |              |              | G AGACTGGGAG             | 420<br>480   |
|     | CCACAAACT   | G CGCCCTGGC                             | A TTGGAGAGA  | A GCCCACTGTY | G GTCACTGTTC | AGATCTCCGT               | 540          |
|     | CAACAGCCT   | T GGTCCTCTC                             | r CTATCCTAG  | A CATGGAATA  | C ACCATTGAC  | TCATCTTCTC               | 600          |
| 80  |             |   |              |              |              | TTGTTCTGAA<br>CTAAGAGGAC | 660<br>720   |
| -   | CCACGAGCA   | T GAGATCACC                             | A TGCCCAACC  | A GATGGTCCG  | C ATCTACAAGO | ATGGCAAGGT               | 780          |
|     |             |   |              |              |              | TCAGATTTCC<br>AGAATGAGAT | 840<br>900   |
| • • |             |   |              |              |              | r GGAAGCTCTT             | 960          |
|     |             |   |              |              |              |                          |              |

```
CCAGTTGGAT TTTACAGGAG TGAGCAACAA AACTGAAATA ATCACAACCC CAGTTGGTGA
        CTTCATGGTC ATGACGATTT TCTTCAATGT GAGCAGGCGG TTTGGCTATG TTGCCTTTCA
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                                                                                         1200
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                                                                                         1620
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                                                                                          1740
        CCTTAACTTG TAGGTACCAG CTGGTACCCT GTGGGGCAAC CTCTCCAGTT CCCCAGGAGG
                                                                                          1800
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        TCCAAGCCCC TTGCCAAGGG AGTTGGGGGA AAGCAGCAGC AGCAGCAGGA GCGACTAGAG
                                                                                          1860
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                                                                                          1920
                                                                                          1980
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                                                                                          2100
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TTCGGCCCAG TTCTGGCCTC AGCCTCAAAG TGCACCGACT AGTTGCTTGC CTATACCTGG
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                                                                                          2340
         CTGGCATTAT CCCTTTAGGA AGAGGGGGGG GCAGCAAGAG AGCCTATTTG GGACAGCATT
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                                                                                          2520
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                                                                                          2640
         CAAGAAACTA AGGAAACTCG GCTTTGCAAC AGGCATTACT CGCCATTGAT TGGTGCCCAC
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                                                                                          2880
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         CCTGAGGTGC TCAGACTGCC CCCAAGATCA AATCTCTCCT GGCTGTAGTA ACCCAGTGGA
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         Coding sequence: 572..1657
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                                                                                          120
50
                                                                                          180
         CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC
                                                                                           300
         TCAGACTGAA TCAAAGAATG AAGCCTCTTC CCGTGATGTT GTCTATGGCC CCCAGCCCCA
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG
                                                                                          360
                                                                                           420
55
         CAGAGTTGGC AAACTGCCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA
         CCACAAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTTG AGATCTCCGT
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         CAACAGCCTT GGTCCTCTCT CTATCCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC
                                                                                           600
         CCAGACCTGG AATTCTAAGA GGACCCACGA GCATGAGATC ACCATGCCCA ACCAGATGGT
         CCGCATCTAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATTG ATGCCGGATG
                                                                                           720
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         CTCACTCCAC ATGCTCAGAT TTCCAATGGA TTCTCACTCT TGCCCTCTAT CTTTCTCTAG
                                                                                           780
         CTTTTCCTAT CCTGAGAATG AGATGATCTA CAAGTGGGAA AATTTCAAGC TTGAAATCAA
                                                                                           840
         TGAGAAGAAC TCCTGGAAGC TCTTCCAGTT TGATTTTACA GGAGTGAGCA ACAAAACTGA
         AATAATCACA ACCCCAGTTG GTGACTTCAT GGTCATGACG ATTTTCTTCA ATGTGAGCAG
                                                                                           960
         GCGGTTTGGC TATGTTGCCT TTCAAAACTA TGTCCCTTCT TCCGTGACCA CGATGCTCTC CTGGGTTTCC TTTTGGATCA AGACAGAGTC TGCTCCAGCC CGGACCTCTC TAGGGATCAC
                                                                                           1020
 65
                                                                                           1080
          CTCTGTTCTG ACCATGACCA CGTTGGGCAC CTTTTCTCGT AAGAATTTCC CGCGTGTCTC
                                                                                           1140
         CTATATCACA GCCTTGGATT TCTATATCGC CATCTGCTTC GTCTTCTGCT TCTGCGCTCT
GTTGGAGTTT GCTGTGCTCA ACTTCCTGAT CTACAACCAG ACAAAAGCCC ATGCTTCTCC
                                                                                           1200
                                                                                           1260
          TARACTCCGC CATCCTCGTA TCARTAGCCG TGCCCATGCC CGTACCCGTG CACGTTCCCG
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          AGCCTGTGCC CGCCAACATC AGGAAGCTTT TGTGTGCCAG ATTGTCACCA CTGAGGGAAG
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          GGGTCCCCGC AGCCTCTGCT CCAAGCTGGC CTGCTGTGAG TGGTGCAAGC GTTTTAAGAA
                                                                                           1500
          GTACTTCTGC ATGGTCCCCG ATTGTGAGGG CAGTACCTGG CAGCAGGGCC GCCTCTGCAT
          CCATGTCTAC CGCCTGGATA ACTACTCGAG AGTTGTTTTC CCAGTGACTT TCTTCTTCTT
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          CAATGTGCTC TACTGGCTTG TTTGCCTTAA CTTGTAGGTA CCAGCTGGTA CCCTGTGGGG
CAACCTCTCC AGTTCCCCAG GAGGTCCAAG CCCCTTGCCA AGGGAGTTGG GGGAAAGCAG
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                                                                                           1740
          CAGCAGCAGC AGGAGCGACT AGAGTTTTTC CTGCCCCATT CCCCAAACAG AAGCTTGCAG
          AGGGTTTGTC TTTGCTGCCC CTCTCCCCTA CCTGGCCCAT TCACTGAGTT TTCTCAGCAG ACCATTTCAA ATTATTAATA AATGGGCCAC CTCCCTCTTC TTCAAGGAGC ATCCGTGATG
                                                                                           1860
                                                                                           1920
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                                                                                           1980
          GGCGGATTAG CTATCTTCCA ACAATGCTGA CCACCAGACA ATTACTGCAT TTTTCCAGAA
                                                                                           2040
          GCCCACTATT GCCTTTGCAG TGCTTTCGGC CCAGTTCTGG CCTCAGCCTC AAAGTGCACC
GACTAGTTGC TTGCCTATAC CTGGCACCTC ATTAAGATGC TGGGCAGCAG TATAACAGGA
                                                                                           2100
                                                                                           2160
          GGAAGAGATC CCTCTCCTTT GGTCAGATTA TTATGTTCTC AGTTCTCTCT CCCTGCTACC
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|         | CCTTTCTCTG (   | CAGATAGATA     | GACACTGGCA    | TTATCCCTTT     | aggaagaggg             | GGGGCAGCA    | 2280 |
|---------|--|----------------|---------------|----------------|------------------------|--------------|------|
|         | AGAGAGCCTA S   | TTTGGGACAG     | CATTCCTCTC    | TCTCTGCTGC     | TGTGACATCT             | CCCTCTCCTT   | 2340 |
|         | GCTGGCTCCA '   | TCTTTCGTCT     | GCACTACCAA    | TTCAATGCCC     | TTCATCCAAT             | GGGTATCTAT   | 2400 |
| _       | TTTTGTGTGT (   | GATTATAGTA     | ACTACTCCCT    | GCTTTATATG     | CCACCCTCTT             | CCTTCTCTTT   | 2460 |
| 5       | GACCCCTGTG   | ACTCTTTCTG     | TAACTTTCCC    | AGTGACTTCC     | CCTAGCCCTG             | ACCAGGCACT   | 2520 |
| _       | AGGCCTTGGT   | CACTTCCTCC     | GGCCAAGAAA    | CTAAGGAAAC     | TOGGOTTTGC             | AACAGGCATT   | 2580 |
|         | ACTCGCCATT   |                |               |                |                        |              | 2640 |
|         |  |                |               |                |                        |              | 2700 |
|         | CCCTGGACCC   | ATAAACCAGT     | CCACIGITAT    | ACCUGGGGCA     | CTCTAACCAT             | CHCHAICHAI   |      |
| 10      | CAATCAAATT   | CCCTTAAATT     | TGTATGGCAC    | TGGAACTTTG     | GCAAAGCACT             | TTTGACAAGT   | 2760 |
| 10      | TGTGTCTGAT   | TGGAGCTTCA     | TGATAGCCTT    | GTGACATCTT     | TAGGGCAGGA             | TTCTTATCCC   | 2820 |
|         | CATTTTGCAG .   | ATGAAAACCC     | TGAGTCACAG    | ATTTCTGTGG     | GACTGTGGAT             | CTCACTGGAA   | 2880 |
|         | GCTATCCAAG .   | ACCCCACTGT     | CACCTTCTAG    | ACCACATGAT     | AGGGCTAGAC             | AGCTCAGTTC   | 2940 |
|         | ACCATGATTC   | TOTTOTOTO      | CONCUCATION   | CACACCACTG     | GCA AGGCCCCA           | GAATGGCGAC   | 3000 |
|         |  |                |               |                |                        |              | 3060 |
| 15      | CTCTCTTTAG   |                |               |                |                        |              |      |
| 15      | CCTGGCTGTA   |                |               |                |                        |              | 3120 |
|         | GTGAAATCTG   | TGTCTGTAAT     | TTGTTGGGGG    | GTGGATAGGG     | TGGGGTCTCC             | ATCTACTTTT   | 3180 |
|         | TGTCACCATC   | ATCTGAAATG     | GGGAAATATG    | ATAAATAAAT     | TATCAGCAAA             | GC .         | 3232 |
|         |  |                |               |                |                        |              |      |
|         | Seq ID NO:   | C199 DNA Se    | quence        |                |                        |              |      |
| 20      | Nucleic Aci  |                |               | 90.1           |                        |              |      |
|         | Coding sequ  |                |               |                |                        |              |      |
|         | couring sequ   | lence. 1303.   | .2450         |                |                        |              |      |
|         | _  |                |               |                | 4.5                    |              |      |
|         | 1  | 11             | 21            | 31             | 41                     | 51           |      |
| 0.5     | 1  |                | 1             |                |                        |              |      |
| 25      | GCCAGAGCGT   | GAGCCGCGAC     | CTCCGCGCAG    | GTGGTCGCGC     | CGGTCTCCGC             | GGAAATGTTG   | 60   |
|         | TCCAAAGTTC   | TTCCAGTCCT     | CCTAGGCATC    | TTATTGATCC     | TCCAGTCGAG             | AACATGTATA   | 120  |
|         |  |                | AAGTGTACAG    |                |                        |              | 180  |
|         |  |                | AGGACCCGAA    |                |                        |              | 240  |
|         | GIGIAAAGAA   | AGCCAAAICA     | AGGACCCGAA    | TOTOMOCHOO     | ACCI CHOISIO           | CACHERCATA   | 300  |
| 20      |  |                | AGCACTATCC    |                |                        |              |      |
| 30      | CCTTGGCAGA   | TGGCCTTTAA     | CATTTTTGTT    | TAATTCAATT     | ATTCTTACTA             | ATCTTCTTCT   | 360  |
|         |  |                | GGCTGTGGAG    |                |                        |              | 420  |
|         | TCCTGGATGG   | CTGTCTGTGG     | GTGGAGGACT    | CCTGCCTTTC     | CTGTTTAGAC             | ACCCACAAAG   | 480  |
|         |  |                | CCTTCATCCC    |                |                        |              | 540  |
|         |  |                | AATATTCCCA    |                |                        |              | 600  |
| 35      |  |                | CCTGGCCCTC    |                |                        |              | 660  |
| 55      |  |                |               |                |                        |              |      |
|         |  |                | GGCGACCAAC    |                |                        |              | 720  |
|         |  |                |               |                |                        | GTTTTGTTGA   | 780  |
|         | TTTTTTTTTA   | AATAAAAGAG     | TGATCATAAA    | AGAGGGACAG     | CATAGAAAGT             | CCCCAAAGAG   | 840  |
|         | CAGCAAGGTT   | TTAAAGAAAT     | TCACAAGCCT    | AATCTGTCAC     | TGTCTTATAA             | TTTGCTATTA   | 900  |
| 40      |  |                |               |                |                        | TCTGTCCCAA   | 960  |
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|         |  |                |               |                |                        |              | 1080 |
|         |  |                |               |                |                        | TGATGTTGTC   |      |
|         |  |                |               |                |                        | AAAGTCAACT   | 1140 |
|         |  |                |               |                |                        | CCTGAACACT   | 1200 |
| 45      | ATCCTGAGTA   | ATTATGACCA     | CAAACTGCGC    | CCTGGCATTG     | GAGAGAAGCC             | CACTGTGGTC   | 1260 |
|         | ACTGTTGAGA   | TCTCCGTCAA     | CAGCCTTGGT    | CCTCTCTCTA     | TCCTAGACAT             | GGAATACACC   | 1320 |
|         |  |                |               |                |                        | CGACACCTTT   | 1380 |
|         |  |                |               |                |                        | CACCTTTTTT   | 1440 |
|         | GAGICICITO   | 11CIGAAIGG     | CARIGIGGIG    | AUCCOLOCIAL    | CARCACAG               | GGTCCGCATC   | 1500 |
| 50      |  |                |               |                |                        |              |      |
| 30      | TACAAGGATG   | GCAAGGTGTT     | GTACACAATT    | AGGATGACCA     | TIGATGUEGG             | ATGCTCACTC   | 1560 |
|         | CACATGCTCA   | GATTTCCAAT     | GGATTCTCAC    | TCTTGCCCTC     | TATCTTTCTC             | TAGCTTTTCC   | 1620 |
|         |  |                |               |                |                        | CAATGAGAAG   | 1680 |
|         | AACTCCTGGA   | AGCTCTTCCA     | GTTTGATTTT    | ACAGGAGTGA     | GCAACAAAAC             | TGAAATAATC   | 1740 |
|         | ACAACCCCAG   | TTGGTGACTT     | CATGGTCATG    | ACGATTTTCI     | TCAATGTGAG             | CAGGCGGTTT   | 1800 |
| 55      | CCCTATCTTC   | CCTTTCAAA      | CTATCTCCCT    | TCTTCCGTGA     | CCACGATGCT             | CTCCTGGGTT   | 1860 |
| • •     |  |                |               |                |                        | CACCTCTGTT   | 1920 |
|         |  |                |               |                |                        | CTCCTATATC   | 1980 |
|         |  |                |               |                |                        |              | 2040 |
|         |  |                |               |                |                        | TCTGTTGGAG   |      |
| 60      |  |                |               |                |                        | TCCTAAACTC   | 2100 |
| 60      |  |                |               |                |                        | CCGAGCCTGT   | 2160 |
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|         | CGCAGCCTCT   | GCTCCAAGCT     | GCCTCCTGT     | GAGTGGTGC      | AGCGTTTTA              | GAAGTACTTC   | 2340 |
|         | TGCATCCTCC   | CCGATTGTG      | GGGCAGTACO    | TGGCAGCAGC     | GCCGCCTCTC             | CATCCATGTC   | 2400 |
| 65      | T3 CCC CCTCC   |                |               | THE COUNTY     |                        | CTTCAATGTG   | 2460 |
| 05      | ances cross  | MINACIACIO     | . ununuiigi   | 11CCCMSIG      |                        | GGGCAACCTC   | 2520 |
|         | CTCTACTGGC   | TIGITIGCC      | TAACTIGIA     | GIACCAGCIC     | GIACCCIGIO             | GGGCAACCIC   | 2520 |
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| 70      | CAAATTATTA   | ATAAATGGG      | CACCTCCCT     | C TTCTTCAAGC   | AGCATCCGT              | ATGCTCAGTG   | 2760 |
|         | TTCAAAACCA   | CAGCCACTT      | GTGATCAGC     | CCCTAAAAC      | ATGCCTAAG              | r ACAGGCGGAT | 2820 |
|         | TACCTATION   | CONTRACTOR     | TGACCACCAC    | ייייעיייעמייע  | CATTTTTCC              | A GAAGCCCACT | 2880 |
|         |  |                |               |                |                        | CACCGACTAGT  |      |
|         | ATTGCCTTTC   | CAGIGCTIT      | - GGCCCAGTT   | TOUCCICAGO     | CICHANGIO              | · wordering: | 3000 |
| 75      | TGCTTGCCT  | A PACCTGGCA    | CICATTAAG     | A TGCTGGGCA    | CAGTATAAC              | A GGAGGAAGAG | 3000 |
| 75      | ATCCCTCTCC   | TTTGGTCAG      | A TTATTATGT   | r ctcagttct    | C TCTCCCTGC            | r ACCCCTTTCT | 3060 |
|         | CTGCAGATAC   | ATAGACACTO     | GCATTATCO     | C TTTAGGAAG    | A GGGGGGGC             | A GCAAGAGAGC | 3120 |
|         | CTATTTGGG  | CAGCATTCC      | CTCTCTCTG     | C TGCTGTGAC    | A TCTCCCTCT            | CTTGCTGGCT   | 3180 |
|         | CCAmmint   | י דריונים ביים | CAATTCAAT     | G CCCTTCATO    | CANTGGGTAT             | C TATTTTTGTG | 3240 |
|         | DOMESTICAL PROPERTY OF THE PRO | Catal Catal    | - Chalcharder | T PAGE CONTROL | th Calabate Adalah ala | C TTTGACCCCT | 3300 |
| 80      | TOTGATTAT/   | GIAACIACT      | r conscilla   | * WIGGONE      |                        | C YOUNGGOOD  | 3360 |
| UU      | GTGACTCTT  | CIGTAACIT      | LCCLAGTGAC    | TUCCUTAGE      | CIGACCAGG              | CACTAGGCCTT  | 3360 |
|         | GGTGACTTC  | C TGGGGCCAA    | G AAACTAAGG   | A AACTCGGCT    | T TGCAACAGG            | C ATTACTCGCC | 3420 |
|         | ATTGATTGG:   | r gcccaccca    | G GGCACACTG   | T CGGAGTTCT    | A TCACTTGCT            | T GACCCCTGGA | 3480 |
|         |  |                |               |                |                        | C AATCAATCAA |      |
|         | ATTCCCTTA  | A ATTTTTATO    | G CACTGGAAC   | T TTGGCAAAG    | C ACTITICAC            | A AGTTGTGTCT | 3600 |
|         |  | . ALLIGINIO    |               |                |                        |              |      |
|         |  |                |               |                | 4                      | 205          |      |

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|     | 211222222               |                          |                  | mmacaamman                              | OCT COMMON CT C  | TOTO CO CO  |      |
| _   | GAATCATTGG C            | SATGCAACIG               | ATCACAAGTC       | TIGGCCTTCA                              | GGAGIIIGAC       | AT TOCCAGGA | 1800 |
| 5   | ACGTTCTAGA A            | CTGATCTAT                | GCACAAACTC       | TGGTGTGGAT                              | TGGCATCTTC '     | TTCTGCCCCC  | 1860 |
|     | TGCTGCCCTT T            |                          |                  |   |                  |             | 1920 |
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|     |                         |                          |                  |   |                  |             |      |
|     | TCCATGAGCA (            | GATCATTAAT               | GAGGGCAAAG       | ATAAAATGTT                              | CCTGATAGAA       | AAATTGATCA  | 2340 |
|     | AGCTGCAGGA S            | PATCCACAAC               | AAACCAAACC       | CCACCTCACT                              | теттетела в      | ACCAGAGAGG  | 2400 |
| 15  |                         |                          |                  |   |                  |             |      |
| 13  | TGGAGCAACA A            | AGGCTTTTTG               | CATTTGGGGG       | AACATGATGG                              | CAGTCTTGAC       | TTGCGATCTA  | 2460 |
|     | GAAGATCAGT T            | TODACDACCT               | DOMASTICA        | CCTGATGACT                              | CTTTTTCCTT A A   | CCAGACACCA  | 2520 |
|     |                         |                          |                  |   |                  |             |      |
|     | ATCAAATAAG (            | GGGAGGAGAY               | GAAAATGGAA       | TGATTTCTTC                              | CATGCCACCT       | GTGCCTTTAG  | 2580 |
|     | GAACTGCCCA (            | TEAGAGOAG                | CARCICITITA      | CCCACCACCA                              | GAAACTGACT       | ACCATGTAAT  | 2640 |
|     |                         |                          |                  |   |                  |             |      |
| 20  | TATCAAAGTA A            |                          |                  |   |                  |             | 2700 |
| 20  | GACAAAATAC :            | TTCCCCTTTT               | CCAATAAAGA       | TTGTTGTAAT                              | ATTGAAAWRA       | RMMWAMAAAA  | 2760 |
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|     | ACCTAGGAAG              |                          |                  |   |                  |             | 2820 |
|     | GATTGGTTCT '            | TAGAAATCTC               | TCCTGCCAGA       | CTTCCCAGAC                              | CTGGCAAAGG       | TTTAGAAACT  | 2880 |
|     | GTTGCTAAGA              |                          |                  |   |                  |             | 2940 |
|     |                         |                          |                  |   |                  |             |      |
|     | CCTCTGAATT (            | GTAGAACCTG               | CATTTATTTG       | TGACTTTGAA                              | CTAAAGACAT       | CCCCCATGTC  | 3000 |
| 25  | CCAAAGGTGG              |                          |                  |   |                  |             | 3060 |
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|     | AGTCTTTGGA              | GTCGGGGATG               | GAGGAGGTTC       | TGCCCCTGTG                              | AGGTGTTATA       | CATGACCATC  | 3120 |
|     | AAAGTCCTAC              | CTCN NCCTNC              | CTTTCCACTC       | CCACTACCCT                              | ACCCAATCAC       | ATTTATOOGA  | 3180 |
|     |                         |                          |                  |   |                  |             |      |
|     | GACGCGATTA '            | TTGCTAATTG               | GAAATTTTCC       | CAATACCCCA                              | CCGTGATGAC       | TTGAAATATA  | 3240 |
|     | ATCAGCGCTG              | באושושות מיום            | ACACTCTCTA       | CCCACACTCA                              | ATABC            |             | 3285 |
| 20  | ATCAGCGCIG              | GCMIIIIIG                | ACAGICICIA       | COGNONCION                              | AIAAG            |             | 3203 |
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|     | Sea ID NO:              | COAS DATA SA             | mience           |   |                  |             |      |
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| 25  |                         |                          |                  |   |                  |             |      |
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|     |                         |                          |                  | GTCTTTATCC                              |                  |             | 120  |
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| 40  |                         |                          |                  | CCTCCCCGCC                              |                  |             | 240  |
| 70  |                         |                          |                  |   |                  |             |      |
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|     |                         |                          |                  | CTGTGCGTGC                              |                  |             | 360  |
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|     |                         |                          |                  | TTCCTGGTTA                              |                  |             | 600  |
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|     | ACCTTCTTAC              | TCCTCTGCCT               | CATCGTGGCC       | TTTCATGCCA                              | AAGAGGTCCA       | GCTGTTCATG  | 660  |
|     | ACCCACAACC              | CONTRACTOR               | CTCCCCCCTC       | GCGCTGACCG                              | CCCCCCACCC       | CCCCCACATC  | 720  |
|     |                         |                          |                  |   |                  |             |      |
|     | GTGCTGGAGC              | TGGTGGTGTG               | TGGGCTGCAC       | CCGGCGCCCG                              | TGCGGGGCCC       | GCCGTGCGTG  | 780  |
| 50  | CACCATTAC               | CCCCCCCCC                | CACCTCCCCC       | CAGCCCTGGC                              | CCCCATTCCT       | CCCCCAACCC  | 840  |
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|     | GAAGCGCTGC              | TGTCCCTGGC               | CATGCTGCTG       | CGTCTCTACC                              | TGGTGCCCCG       | CGCCGTGCTC  | 900  |
|     | CIRCUSCINGOS.           | COURTONICA               | CARCECTOCC       | TACCGCAGCA                              | THEOLOGICAL      | CAATCAAGTC  | 960  |
|     |                         |                          |                  |   |                  |             |      |
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|     |                         |                          |                  | CGGAAGCTCC                              |                  |             | 1500 |
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|     | CACCGGGGCCC             | TGGAGAAACA               | GATTCACACC       | CTGGCGGGGA                              | AGCTGGATGC       | CCTGACTGAG  | 1620 |
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| 65  | CTGGACCCAC              | GAGGAGGAAC               | CAGGCTACTT       | TCCCCAGTAC                              | TGAGGTGGTY       | GACATCGTCT  | 1740 |
|     |                         | man accorda              | 00011011         | 0100000                                 |                  | **********  |      |
|     |                         |                          |                  |   |                  | AAGGGGCCC   | 1800 |
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|     |                         |                          |                  |   |                  | TCCAGAGCTG  | 2160 |
|     |                         |                          |                  |   |                  | TTATCTTTGT  | 2220 |
|     |                         |                          | COLLIGION        | , ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, |                  |             |      |
| 75  | AATAAATGTT              | AAAGCCAG                 |                  |   |                  |             | 2238 |
| ·75 | **                      |                          |                  |   |                  |             |      |
|     |                         |                          |                  |   |                  |             |      |
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|     |                         |                          |                  |   |                  |             |      |
| 80  | _                       |                          |                  |   |                  |             |      |
| 90  |                         | 11                       | 21               | 31                                      | 41               | 51          |      |
|     | 1                       |                          |                  |   |                  |             |      |
|     | •                       | ī                        | 1                | 1                                       | 1                |             |      |
|     | Ĺ                       | 1                        | L                | _ <u> </u>                              | . <u> </u>       |             |      |
|     | Ĺ                       | 1                        | <br>  CGAGGATGAG |   | <br>  GGAAGCCAGT | CAAATACGAC  | 60   |
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|                                  | GTGCGAGTG TGGCAGCGGG CCGGCGGGGGG AGGACCTTAC TCCTCTTCCT TCTATCTCGA GTTTACCCAA ACGAAGTGGG GCTCGAGGG GTGCCACAGC GGACACGCT GACTCACCTC  | GCGAGTGTCA<br>CTCGGACCCA<br>CAGATGCCC<br>GCAGCCAACG<br>CTTCCTCTCG<br>TCACCCAGAC<br>TCTGCACTGAC<br>GCAGTTCAGC<br>CCACGCCACAG<br>ACAGGTCCAG<br>CAACCCCCTC  | GGGGGCGGC GGCGCGCGC GGGCGCGCG TTTGACTTCA TACACCGGGG GAGCTCACCG AAGGACAGCG AACTCCATGA AACACCACG GAGTTGCTCG AACACCACG  | CGGCGGGGC CGGCCCGCT GGAGGTTTAAAC CATTATCTC GATTTATAAC GTGGCAAGAT AGATCCCGCT TCCCCGGCAA TGACGCATGT GGCTTTAAA ACTACATCCT   | GGGCGGCCG<br>GGCCTGCAGG<br>CATCTACAGG<br>CATCTGCTGC<br>GACAGAAGTT<br>CGACGTCAGT<br>GAACAATGGG<br>CTTCCACGTG<br>CATCCACAAG<br>TGCTCTCGGG<br>GAAGATTGTG  | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA TGCCTCTTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CTCTCCTTTG GGAGCAGCA CCCACGGTTT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600  |
| 50                               | GTGGCGAGTG TGGCAGCGGG CCGGCGGGGG AGGACCTTAC TCTCTTCTT TCTATGTCGA GTTTACCCAA ACGAAGTGGG GCTCCACAGC GGGACACGCT GACTCACCTC ATGAGGACACA  | GCGAGTGTCA CTCGGACCCA CACGATGCCC CTCCTCTCG TGACCCAGAC TCTGCACTGC CCACATCGAC GCAGTTCAGC CCAGCACAC ACAGGTCCAC GAACTCCCCTG GAACTGCCACAC GAACCCCCTG GAGTGGCACAC  | GGGGGCGGC GGGGCGCGC GGGGCGCGG TTTGACTTCA TACACCGGGG GAGCTCACCG AAGGACAGCG AACTCCATGA AACACCCAGACA AACATCCACG GGCTCCCCCGG   | CGGCGGGGC CGGCCCSCT GGAGGTTTGA CCATTATCTC GATTTATAAC GTGGCAAGAT GGCTTGACAC AGATCCCGCT TCCCCGCAA TGACGCATGT GAGCTTTCAC ACTACATCCT CCTACCAGTA  | GGGCGGCCG GGCCTGCAGG CATCTACAGG CATCTGCTGC GACAGAAGTT CGACATCAGT GACAATGAG GACAATGAG CTTCCACGTG CATCCACAAG TGCTCTCCGCG GACAATGGG CATCCACAAG CACGCTGCACAAG CACGCTGCCCCCCACAAG CACGCTGCCCCCCCCCC   | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA ATGGTCTTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CTCTCTTTG GGAGCAGACA CTCTCCTTTG CCCACGGTTT AACAAGGAAT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840  |
| 50                               | GTGGCGAGTG TGGCAGCGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGG GTGCCACAGG GGGACACGCT ATGAGGACA ACGAGTCACCTA  | GCGAGTGTCA CTOGGACCCA CAGGATGGCC GCAGCCAACG CTTCCTCTCC TGACCCAGAC TCTGCACTGC CCACATGGAC GCAGTTCAGC CCAGCCACAC ACAGGTCCAC CAACCCCTTC GAGTGGCAAC CAGCCACACC CAGCCACACC CAGCCACACC CAGCCACACC CAGCCACACC CAGCCACACC CAGCCACACC  | GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCGCCT GGAGGTTTGA CCATTATCTC GATTTATAAC GTGGCAAGAT GGCTTGACAT AGATCCGGCT TCCCCGGCAA TGACGCATGT GAGCTTTCAA ACTACCATGT CCTACCAGTA TCCCTGCAAT   | GGGGGGGCG<br>GGCCTGCAGC<br>CATCTACAGG<br>CATCTGCTGC<br>GACAGAAGTT<br>TCAGGATGAG<br>GAACAATGG<br>CATCCACAAG<br>TGCTCTCGGG<br>GAAGATTGTG<br>CAGGGGGCC<br>CATGGTTCGCC   | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACAC CTCTCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAT TACGACCTCA  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900   |
| 50                               | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGG AGGACCTTAC TCCTCTTCCT TCTATCTCA ACGAAGTGGG GCTTCGAGGG GCTCCACAGC GGGACACGCT GACTCACCTC ATGAGGACAA ACGTCGCCTA ACGTCGCCTA ACGTCGCCTA   | GCGAGTGTCA CTOGGACCCA CAGGATGCCC GCAGCCAACG CTTCCTCTCG TGACCCAGAC CCACATGAC GCAGTTCAG CCAGCCACAC ACAGGTCCAG ACAGGTCCAG CAACCCCCC GAGTGGCAAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG GGGTGAAG CAGCCACAG GGTGAAGTAG  | GGGGGCGGC GGGGCGCGC GGGGCGCGGG TTTGACTTCA TACACCGGGG GAGCTCACCG AAGGACAGCG AACTCCATGA AACTCCATGA AACCCAGAGG AACCCAGGGGGGGGGG   | CGGCGGGGGC CGGCCGCTTGA CCATTATCTC GATTTATAAC GTGGCAAGAT GGCTTGACAT AGATCCCGCT TCCCCGGCAA TGACGCATGT GAGCTTCAA ACTACATCCT CCTACCAGTA TCCCTGCAAT CGGCAGCCCCCT  | GGGGCGGCCG GGCCTGCAGC CATCTACAGG CATCTACTGC GACAGAAGTT TCAGGATGAGG GAACAATGGG CATCCACAGAG TGCTCTCGGG GAAGATTGTG CACGTTGGGG GAAGATTGTG CACGTTGGCG GTACAGATTCGGGG GTACAGATTCGGGG   | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA ATGGTCTTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CTCTCTTTG GGAGCAGACA CTCTCCTTTG CCCACGGTTT AACAAGGAAT   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840  |
| 50                               | GTGGCGAGTG TGGCAGCGGG CCGGCGGGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGG GGGACACGCT GACTCACCT ATGAGGACA ACGTGGCCTA ACGACCT CCCCTACCT CCCCTACCCT CCCCTACCCT CCCCCTACCCT CCCCCTACCCCT CCCCCTACCCCT CCCCCTACCCCT CCCCCTCT  | GCGAGTGTCA CTOGGACCCA CAGGATGCCC GCAGCCAAGG CTTCCTCTCC TGACCCAGAC TCTGCACTGC CCACATGGAC GCAGTTCAGC CCAGCCACAG ACAGGTCCAG ACAGGTCCAG GAGTGCAGC GAGCCACAC GGTCAAGTAC GGTCAAGTAC GGTCAAGTAC GGTCAAGTAC GGTCAAGTAC GGTCAAGTAC GGCCTGGAAC GGCCTGGAAC GGCCTGGAAC GGCCTGGAAC GGCCTGGAAC GGCCTGGAAC  | GGGGGCGGC GGGGCGCGC TTTGACTTCA TACACCGGGG GAGCTCACCG GAGTTGGTTG AACTCCATGA AACTCCATGA AACATCCACGG GAGTTCGTTG AACATCCACGG AACATCCACGG GAGCTCCACGG AACATCCACGG CAGCGGTACT CACAGAGAGAGA AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACCG   | CGGCGGGGGC CGGCCCCCT CGGAGGTTTGA CCATTATCTC GATTTATAAC GTGGCAAGAT GGCTTGACAT AGATCCGGT TCCCCGGCAA TGACGCATGT CCTACCAGTA TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCCTGCAAT TCCCTGCAAT  | GGGGGGGCG<br>GGCCTGCAGC<br>CATCTACAGG<br>CATCTGCTGC<br>GACAGAAGTT<br>TCAGGATGAG<br>GAACAATGG<br>CATCCACAG<br>GAAGATTGTG<br>GAAGATTGTG<br>CATGGTGGCC<br>CTGGTTCGGG<br>GTACAGATTC<br>CCTGGACTCA  | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACAC CTCTCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAT TACGACCTCA ATCACCACGA TTCACCACGAC TTCACCACGAC TCCACGGTTT TACAAGGAT TACGACCTCA TACACCACGA TGCATCTTCA CACACCCAGGC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080   |
| 50                               | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTTCGAGGG GTGCCACAGC GGGACACGCT ATGAGGACA ACGTCGCCTA ACGAGCTCAC TCTGTGCCAT CCACCTCTGAGCGCCTCAC CCTATCACCCCTC   | GCGAGTGTCA CTOGGACCCA CACGATGCCC GCAGCCAACG CTCCTCTCC TGACCCAGAC CCACATCGAC GCAGTTCAGC CCACATCGAC GCAGTTCAGC CACATCGAC GCAGTTCAGC CACCCCTC GAGTGCCACAC CAGCCACAC GGGCTGCAAC AGGACCCTGGAAC AGGACCCTGCAAC AGGACCCTGCAAC AGGACCCTCGAAC AGGACCCTCGAAC AGGACCCTCGAAC AGGACCCTCGAAC AGGACCCTCGAAC AGGACCCTCGAAC AGGACCCTCC   | GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCCGCTT GGAGGTTTGA CCATTIATCTC GATTTATAAC GGCTTGACAT GGCTTGACAT AGATCCCGCT TCCCCGGCAA TGACGCATGT GAGCTTCAA ACTACATCCT CTACCAGTA TCCCTGCAAT CTGCCGGCAAT CGGCAGGCAT CTGCCGGCAAT CGGCAGGAT CTGCCGGCAAT CTGCCGGCAAT  | GGGGCGGCCG GGCCTGCAGC CATCTACAGG CATCTACAGG GACAGAAGTT TCAGGATGAGG GAACAATGGG CTTCCACAGT GATCTCCACAGG GAAGATTGT CACGTCGCC CATCGACGTCGCC CTGGTTCCGCG GTACAGATTCCCCTGGGCTCCCC CTGGTTCCGCC CTGGTTCCGCC CTGGACTCCACACC AGTGCCCTGGCC AGTGCCCTGGCC AGTGCCCTGGTCCCCC AGTGCCCTGGTCCCCC AGTGCCCTGGT   | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA CCCACGGTTT AACAAGGAAT TACGACCTCA TACACCCACG TTCACCCCGC CCCACTCCCCCCCCCC  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140  |
| 50                               | GTGCGAGTG TGGCAGCGGG CCGCGCGGCGGCGGCGGCGGCGGCGGCGGGGGCGGGGGCGGGG   | GCGAGTGTCA CTCGGACCCA GCAGCCAACA CTTCCTCTCG CTCGCCTCG CCACATCGAC CCACATCGAC GCAGTTCAGC CCACATCGAC GCAGTTCAGC GCAGTTCAGC GCAGTTCAGC CCACATCGAC GCAGTTCAGC GAGTGCAAA CAGCCACCAC GGCCACAG GGCCACAG GGTCAAGTAC AGGCACAC GGTCAAGTAC AGGACCCTCG GGCTGGAAA AGGACCTCGAAAT AGGACCACAC GGCTGGAAA AGGACCTCAAAT AGGACCTCAAAT AGGACCTCAAAT GTCCCAAAT  | GGGGGCGGC GGCGCGCGC GGGCGCGCG TTTGACTTCA TACACCGGGG GAGCTCACCG AAGGACAGCG AACCCCAGAG AACCCACAGG CAGCGGTACG CAGCGGGACT CAGCGGGACT CAGCGGGACG ACCTCCACG ACGAGAGAGAG ACCTTCACCG ACGAGAGAGAC ACCTCCACG ACGAGAGAGAC ACCTCACCG ACGAGAGAGAC TGGCTGCCACC   | CGGCGGGGGC CGGCCGCTTGA CCATTATCTC GATTTATAAC GTGGCAAGAT AGATCCCGCTA TCCCCGGCAA ACACCCATCCATCACAC CCTACCAGTA ACTACATCCT CCTACCAGTA GGCAGCCGCT TCCCTCCAAT CGGCAGCCGCT TCCCTCCAAT CGGCAGCCGCT CCTCCACCAGTA CGCCTCCCTCCACCACT CCTCCCTCCAAT CGCCAGCCCCCCCCCC  | GGGCGGCCG GGCCTGCAGC CATCTACAGG CATCTACAGG GACAGAAGTT CGACGTCAGT GAACATCAGGA GAACATCGG CTTCCACGTG CATCCACAGG GAAGATTGTG CACGGTGGCC CTGGTTCCGC GTACAGATTC CCTGGACTCA GCATTGACGG GAACATTGACGG GAACATTGACGG GAACATTGACGG AGTGCCCTGG TGTGCCCGGG TGTGCCCGGG TGTGGGAAGATT  | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA TGCCTCTTCA GTGAACATCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CTCTCCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAAT TTACGACCTCA ATCACCACGA TGCATCTTCA CCACACCAGC CCACCGGTT CACACCAGA TGCACCTCCACCAGC CCCCCGGCCAGCCCGCCCCGC   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1080   |
| 50<br>55<br>60                   | GTGGCGAGTG TGGCAGCGGG CCGGCGGGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GACTCACAGC GACTCACCTC ATGAGGACA ACGTCGCCTA ACGACCTCACCTC   | GCGAGTGTCA CTOGGACCCA CACGATGCCC GCAGCCAACG CTTCCTCTCC TGACCCAGAC CCACATGAC CCACATGAC CCACATGAC CCACCCCTC GAGTCCAG CAACCCCTC GAGTGCACAC GGCTGAAGTAC CATTGGCGAC GGCTGGAAC ACGACCCTGGAAC ACGACCTGGAAC ACGACCCTGGAAC ACGACCCTGGAAC ACGACCCTGGAAC ACGACCCTGGAAC ACGACCCTGGAAC ACGACCTGGAAC ACGACCTGGAAC ACGACCTGGAAC ACGACCTGGAAC CTCCCAAATTC CCACATGTTGCAC CTCCCAATTCC  | GGGGGCGGC GGGGCGCGC GGGGCGCGG TTTGACTTCA TACACCGGGG GAGCTCACCG GAGTTGGTTG AACTCCATGA AACACCAGACA AACATCCACGG GCGCGCATCA CGGCGCATCA CGGCGGATCACCG ACAGAGAGAGA ACCTTCACCG GCATCACCG GCATCACCG GCATCACCG GCATCACCG TGGCGGATCA   | CGGCGGGGGC CGGCCCGCT GGAGGTTTGA CCATTIATACAC GATTTATACAC GGTGCAAGAT GGCTTGACAT AGATCCGGT TCCCCGGCAA ACTACATCCT CCTACCAGTA ACTACCAGTA TCCCTGCAAT CGCGGCAAG TCGCGGGAAGAT CCTTGCCTCC CCAAAGGGTG TCTTTTCCCC CCTGGGGAGGC  | GGGGCGGCCG GGCCTGCAGG CATCTACAGG CATCTACTGC GACAGAAGTT TCAGGATGAG GACAATAGG CATCCACAG GACAATAGG CATCCACAG TGCTCCCCGG GAAGATTGTG CACGGTGGCC CTGGATCAG GCATTGAGC AGTGCCCTGGACTA TGCTGGACTA TGTGGGAAGT TGTGGGAAGT TGTGGGAAGACA  | GAGGAGGCGT GCTCCCACCC AAGGTGCCCA TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA CCCACGGTT AACAAGGAAT TACGACCCAC TTCACCCAC CTCACCCAC TTCACCCAC TTCACCCACACA TTACACCACAC TTCACCCACG TTCACCCACGC TTCACCCACGC TTCACCCACGC TTCACCCACGC TTCACCCACGC TTACACACAAT AGCACACAAT AGCACACAAT AGCACACACAAT AGCACACACCACCCACC TTACACCACGC TTACACCACGC TTACACCACCACCCACCC TTACACCACCACCCACCCCCC TTACACCACCACCCAC                                   | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1200<br>1320   |
| 50                               | GTGCGAGTG TGGCAGCGGG CCGCGCGGCGG AGGACCTTAC TCCTCTTCCT TCTATTCCA ACGAAGTGGG GCTTCGAGGG GCTCCACAGC GGGACACGCT ATGAGGACAA ACGTCGCCTA ACGCCTCA TCTGTGCCACAG CCATCAC TCTGTGCCAT CAGCCTCAGC CTAATCTC TAGAGGATGG TAGAGGATGG CCTCAATCTC TAGAGGATGGC TAGAGGATGGC TAGAGGATGGC TAGAGGATGGC TAGAGGATGG  | GCGAGTGTCA CTOGGACCCA CACGATGCCC GCAGCCAACG CTTCCTCTCG CTCCCCTCG CCACATCGAC GCAGTCCAG ACAGCCACAG ACAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG GGTCAAGTA CATTGGCGG GTCAAGTA GAGACCTTG GTCCAAAT GCGAGTTTT GAGATGTTT GAGATTGCAG AATTCCAGGGG AATTCCAGGGG AATTCCAAGGGG AATTCCAAGGGG AATTCCAAGGGG AATTCCAGGGG AATTCCAGGGG AATTCCAGGGG AATTCCAGGGG AATTCCAGGGG  | GGGGGCGGC GGGGCGCGC GGGGCGCGG TTTGACTTCA TACACCGGGG GAGCTCACCG AAGGACACAG AACCCAGAGA AACCCAGAG AACCCAGGGGTACT GGCGCATCA CGGCGCATCA CGGCTACCCAC CGCATCACCCAC CTGCCCACC CTGCCCTTTC   | CGGCGGGGGC CGGCCGCTTGA CGATTTATAAC GTGGCAAGAT GGGCTTGACAT AGATCCCGCT TCCCCGGCAA AGATCCCGCT CCCTGCAAT ACTACATCCT CCTACCAGTA TCCCGCAT CGGCAAGGCAT CCTGCCAT CCTGCGCAAGGTG CCTTTTCCCC CCAAAGGGTG CCTTGGCGAAG ATGCATATC  | GGGGCGGCCG GGCCTGCAGC CATCTACAGG CATCTACAGG GACAGAAGTT TCAGGATGAGG GAACAATGGG CATCCACAGA TGCTCTCGGG GAAGATTGTG CACGGTGGCC CTGGTTCGGG GTACAGATTCC CTGGACTCA GGATTGCCC AGTGCCCTGGT TGTGGGAAGA TGCCCTGGT TGTGGGAAGA GGATTGTTCGCG AGTGCCCTGT CCCAAGAAGA GGATAGACTC   | GAGGAGGCGT GCTCCCACCC ARGGTGCCCA ARGGTGCCCA TGCCTCTTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CTCTCCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAAT TAGGACCTCA ATCACCACGA TGCATCTTGC CTCCTTTTGCC GGGGGGAAAG TGCACCTCAC CTCCTTTGCC CTCCTTTGGC CTCCTTTGGC CTCCTTTGGC CGGGGGAAAG TTAGACAAAT CGAGCCAAGCC CTCCTTTGGC  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1240<br>1320<br>1380                                  |
| 50<br>55<br>60                   | GTGGCGAGTG TGGCAGCGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GGGACAGCCT ATGAGGACAA ACGTCACCTA ACGAAGTGGG GGCCCATCAC CTCGGCCTA CAGCCCATCAC CTAATGGCCG TAGAGGATGG TAGAGGATGG TACACTGCCT AGGGGTGGGGT  | GCGAGTGTCA CTCGGACCCA CACGATGCCC GCAGCCAACG CTTCCTCTCG TGACCCAGAC TCTCCCATGC TCACCAGAC CCACCAGCAC CCACCACAGA ACAGGTCCAG CAGCCACAG ACAGGTCCAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG CAGCCACAG CATGGGGG GCCTGGAAC CTCGAGTTC CTCGATGTT CAGAGTTCAG CAGCCCCC CGCACACC CGCCACACC CCCCCC CCCCCC CCCCCCC CCCCCCC CCCCCC  | GGGGGCGGC GGGGCGCGC GGGGCGCGG TTTGACTACA TACACCGGGG GAGCTCACCG GAGTTGGTTG AACTCCATGA AACATCCACG GAGTTGGTTG AACATCCACG AACATCCACG ACATCACACG ACAGAGAGACA ACATCCACG ACAGAGAGACA CAGAGAGACA CAGAGAGACA CTGCCTGGTTC TGCAGCTACC TGCAGCTACC AACATCCACG TGCAGCTACC AACATCCACC AACATCCACC AACATCCACC AACATCCACC AACATCCACC AACATCCACC AACATCCCACC AACATCCACC AACATCCCACC AACATCCACC AACATCCACCACC AACATCCACCACC AACATCCACCACC AACATCCACCACC AACATCCACCACC AACATCCACCACC AACATCCACCACC AACATCCACCACC AACATCCACCACC AACATCCACCACCACC AACATCCACCACCACC AACATCCACCACCACCACCACC AACATCCACCACCACCACCACCACCACCACCACCACCACC  | CGGCGGGGGC CGGCCGCCT CGGAGGTTTGA CCATTATATAC GATTTATAAC GGCTGAAGAT GGCTTGACAT AGATCCCGCAA TGACGCATGT CCTACCAGTA TCCCTGCAAT TCCCTCCCCC CCAAAGGGTG TCTTTTCCCC CCAAAGGTG AATGCATAATG ACACTTAATG   | GGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGGGT GCTCCCACCC AGGCTCCCACC TGCCTCTCA TGCCTCTCA TGCAATCA ATGGGCAGGC CCAACACAC TCCACACAC TCCACACAC TCCACACAC TCCACACAC TCACACACA   | 120<br>180<br>240<br>360<br>420<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1140<br>1260<br>1320<br>1440   |
| 50<br>55<br>60                   | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GGGACACGCT ATGAGGACAA ACGTGGCCTA ACGACTCAC CTCATCTGCCTA TCTGTGCCAT CTGACTAC TAGAGGATGG TAGAGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGGGTGGCCT AGGCAACCTC AGCCAACCTC   | GCGAGTGTCA CTOGGACCCA CAGGATGCC GCAGCCAAGG TTCCTCTCC TCAGCCAGAC TCTCCACTGC CCACATGGAC CCAGCCACAG ACAGGTCCAG ACAGGTCCAG CCAGCCACAG ACAGGTCCAG CCAGCCACAG CCAGCCACAG CCAGCCACAG CATTGGAG GGCTGGAAG AGGACCCCTG GTCCAAATT CCGGAGG AGGACCCCCC GTCCAAATT CCGGAGGCCCCG CCCCAGAGGGCCCCG CCCCAGAGGGC  | GGGGGCGGC GGGGCGCGC GGGGCGCGG TTTGACTTCA TACACCGGGG GAGCTCACCG GAGTTGGTTG AACTCCATGA AACATCCACGG GAGTTGGTTG AACATCCACGG AACATCCACGG AACATCCACGG CAGGGGTACT CACGGGGTACT CACGGGTACT CACGGTACT CACGGTAC | CGGCGGGGGC CGGCCGCCT GGAGGTTTGA CGATTATATAC GATTTATAAC GGTGGCAGAT GGGCTTGACAT AGATCCGGCT TCCCCGCAA TGACGCATGT CCTACCAGTA TCCCTGCAAT CCTACCAGTA TCCCTGCAAT CCTACCAGTA TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCGCGGCAGT TCGGGAAGAT CCTACCGGAAGAT CCTTGCCTCC CCAAAGGGT TCTTTTCCCC CCTGGGGAGC AATGCATAATG GGCTTTCAGC   | GGGGCGGCCG GGCCTGCAGC CATCTACAGG CATCTGCTGC GACAGAAGTT TCAGGATGAG GACAATGGG CATCCACAGA TGCTCCACGG GAAGATTGTG GAAGATTGTG CATCCACAGA TGCTCTCGGG GAAGATTGTG GATCAGAT GCATTGACGC CTGGTTCCGC TGGTTCGCGC TTGGACATGA TGCTCTTGACTGA TGCGAAGATCA GCATTGACGC AGTGCCCTGT TTTGGGAACA TTTTGGTACC TATTGGTTTC TTTGGGACCC  | GAGGAGGCGT GCTCCCACCC ARGGTGCCCA ARGGTGCCCA TGCCTCTTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CTCTCCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAAT TAGGACCTCA ATCACCACGA TGCATCTTGC CTCCTTTTGCC GGGGGGAAAG TGCACCTCAC CTCCTTTGCC CTCCTTTGGC CTCCTTTGGC CTCCTTTGGC CGGGGGAAAG TTAGACAAAT CGAGCCAAGCC CTCCTTTGGC  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1140<br>1200<br>1240<br>1320<br>1380                                  |
| 50<br>55<br>60<br>65             | GTGGCAGTG TGGCAGCGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GGGACACGCT ATGAGGACAA ACGTCGCCTA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGTGGCCTA ACGTCGCCTA CAGCCTCTGA CCTAATGGCCG TAGAGGATGG TACACTCCT AGGGTGGCGAACTCC TCGACAACTCC AGGCAACTCC AGGCAACTCC TAGGCAACTCCT AGGCAACTCCT AGGCAACTCCT AGGCAACTCCT AGGCAACTCCT AGGCAACTCCT AGGCAACTCCT AGGCAACTCCT TATGATTTCTT  | GCGAGTGTCA CTCGGACCCA CAGGATGCCC GCAGCCAACG CTTCCTCTCC GCAGCCAGC TCTCCCACGC TCACCAGCA CAGCACCAGC CCACCCACCA CAGGTCCAC CAGCCACCA CAGCCACCA CAGCCACCA CAGCCACCA CAGCCACCA CAGCCACCA CAGCCACCC GCCCAACA CAGCCCCCC CCCCAACAGC CCCCCAGAGGG CCCCCCCAGAGGG CCCCCCAGAGGG CCCCCCAGAGGG CCCCCCAGAGGG CCCCCCAGAGGG CCCCCCAGAGGG CCCCCAGAGGG CTTATACACCC CACTATAGACC CACATATAGACC CACATATAGACCC CACATATAGACC CACATATAGACCC CACATATAGACC CACATATAGACC CACATATAGACC CACATATAGACC CACATATAGACC CACATATAGACCC CACATATAGACCC CACATATAGACACC CACATATAGACC CACATATAGACACC CACATATAGACC CACATATAGACC CACATATAGACC CACATATAGACC CACATATAGACCC CACATATAGACC CACATATATATACACC CACATATAGACC CACATATAGACC CACATATATATATATATATATATATACACC CACATATATAT   | GGGGGCGGC GGGGCGCGC GGGGCGCGC TTTGACTTCA TACACCGGGG GAGCTCACCG GAGTTGGTTG AACTCCATGA AACATCCACG GGCTCCACG GGCTCCACG GCCTCCACG ACAGAGAGA ACATCCACG ACAGAGAGA ACATCCACG ACAGAGAGAGA ACTTCACCC ACAGAGAGAGA TGCCTGTGTT TGCAGCTACC ACTAGGTGGT ACAGGGGCTCC TGCCTGTGT TGCAGCTACC ACTAGGTGGC ACGAGCCTTC GGGAACTTC GGGAACTTC GGAACTTC GGAACTTC GGAACTTC GGAACTTC GGAACTTC GGAACTTC GGAAATGTGC  | CGGCGGGGGC CGGCCCCCC CGGCGCCCCCC GGAGGTTTATAAC CGATTATATAC GGTGGAAGAT GGCTTGACAT AGATCCGGCA TGACGCAT TCCCCGGCA TGACATCCT CCTACCAGTA TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCGCAGCAC TCGCAAGAT CCCTACCTCCACT CCCACAGGGGCC CCCAAAGGGTG TCTTTTCCCC CCTGGGGAGC AATGCATAT ACACTTAATC CGCATTCAAC CACATTAATC GGCATTCAAC CACAAAGATC CACAAAGATC CACAAAGATC CACAAAGATC CACAAAGATC CACAAAGATC CACAAAGATC   | GGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGGGT GCTCCCACC GCTCCCACC TGCCTCTCA TGCCTCTCA TGCATCA TGCCTCTTCA GTGAACCAGC CCCACCACACA CTCCCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAAT TGCATCTCA TGCACCACG TTCCTTTGGC GGGGGGAAAG TTAGACAAAT GGATCAGGAT TTAGACACAG TTAGACACAG TTAGACACAG TTAGACACAG TTAGACACAG TTAGACACAG TTAGACACAG TTAGACAAAT AGCAGCTC TCCCTTGGC AGCGGGGAAAG TTCCCTTGGC TCCCTTGGC AGCGTGCCCAA AGCAAGCCCC ATCTTTTATG   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1120<br>1260<br>1380<br>1440<br>1560<br>1620                   |
| 50<br>55<br>60                   | GTGGCGAGTG TGGCAGCGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGG GGGACACGCT ATGAGGACAA ACGTCGCCTA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGGACACACCTC ATGAGGACAA TCTGTGCCAT CAGCCTCAATCTG TACACTGCCT AGGGGTGGGCT AGGGGTGGGCT AGGGGTGGGCT AGGGTGGCCT AGGGTTGACTCTCTATTCTTCCTCCTCATCTCTCTCCCTCATCACCTCCT  | GCGAGTGTCA CTCGGACCCA CACGATGCC GCAGCCAACG CTTCCTCTCG GCAGCCACAC TCTGCACTGC CCACATCGAC CCACATCGAC CCAGCCACAC ACAGGTCCAC ACAGGTCCAC CGACCACAC CGAGCCACAC GGTCAGTGAC GGTCAGTGAC GGTCAGTGAC GTCCCACTGGAC GTCCCACTGGAC GTCCCACTGGAC GTCCCACTGGAC CTCGAGTGTTC GCAGCCCC CCCCAGAGGC CCCCAGAGGG TTATACACC CCCACTACGAC AGAGTACCAC CCCCAGAGGG CCCCAGAAGGG CCCCAGAAGGG CCCCCAGAAGGG CCCCCAGAAGAAAAAAAA   | GGGGGCGGC GGGGCGCGC GGGGCGCGC TTTGACTTCA TACACCGGGG GAGCTCACCG GAGTTGGTTG AACACAAGAC AACACCACACACACACACACACACACA   | CGGCGGGGGC CGGCCGCCT CGGCGCGCT GGAGGTTTGA CCATTATCTC GATTTATACAC GTGGCAAGAT GGCTTGACAT AGATCCGCT TCCCGGCAA TGACGCATGT CCTACCAGTA TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCGGCAAGAT CCTACCAGTA TCGGCAAGAT CCTACCAGTA GCAAAGGTG CAAAGGTG CAAAGGTG CACATTAATG GGCTTTCAGC CAGAAAGAT GGCATTCAGC CACAGAAAGAT GGCATTCAGC CAGGAAAGAT TGGCATCACC CAGGAAAGAT TGGCATCACC CTCGGAGACC CTCTGAGGACC   | GGGGGGGCGGCGGGCGGCGGCGGCGGCGGCGGCGGGGCGC   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGCAGGC GCAGGCTGCC TCCACACACA CTCTCCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAT ATACACACACA CCCACGGTTT ACAAGGAT TACACACACA CCCACGGTTT ACAAGGAT TTACACACAGA TTCACTTGGC CTCCTTTGGC GGGGGAAAG TTAGACAAGT CAGCCAGGCT CCCTTTGGC TGCCCAGGCT CTCCTTTGGC TGCCCAGGCT TTCCTTTTATG CAGCAGCCCAGCT TTCCTTTTATG CAGCAGCCCAC TTCCTTTTATG  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1020<br>1080<br>1140<br>1220<br>1320<br>1340<br>1500<br>1500<br>1620<br>1620         |
| 50<br>55<br>60<br>65             | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGG AGGACCTTAC TCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GACTCACACC GACTCACCTA ACGAGGCGA ACGAGCCT ACGAGCCTA CCGCCTACCCTA CCGCCTACCCTA CCGCCTACCCTA TCGGCCAT TAGAGGATGG CTAATCGCC TAGAGGATGG TACACCTC AGGGTGGCGT AGGGTGGCCT AGGGTACCCT AGCCAACCTC AGGGTGCGCT TAGACTCCT AGCCAACCTC AGGTACTCCT TAGACTTCCT TAGACTTCCT TAGACTACCTC AGCTACTCCT TAGACTACCTC TCACATTTTTTCC TCATATTTTTTC CATTTTTTTT  | GCGAGTGTCA CTOGGACCCA GCAGCCACAC GCAGCCACAC CTCCTCTCC TGACCCAGAC CTCCTCTCC TGACCCAGAC CCACATCGAC CCACATCGAC CCACCTCC GAGTTCAGC CAACCCCTC GAGTGCACAC GGCTGAAGTAC AGGACCCTC GGCCTGGAAC AGGACCCTC GGCCTGGAAC AGGACCCCCC CCCCAGATTCAGC TCCCCAATTGCAGC CTCCCAATTGCAGC CTCCCAATTGCAGC TCCCCAATTGCAGC TCCCCAATTAGAC TCCCCCAATTAGAC TCCCCCCAATTAGAC TCCCCCAATTAGAC TCC | GGGGGCGGC GGGGCGCGC GGGGCGCGC GGGGCTACCG GAGTTGGTTG AACACAGG GAGTTCACAG AACACACAG AACATCCACG GAGTTCACCG GAGTTCACCG GAGTTCACCG GAGTTCACCG AACATCCACG ACAGAGAGAGA ACATCCACG GGCGCATCAC ACAGAGGAGAC ACAGAGGGGACT TGCGTGTGTT TGCAGCTAC ACAGAGGGGAC TGCGCTACT GGCAGCCTCC GGCACTTCCCC GGCACTTCCCCC GGCACTTCCCCCCC GGCACTTCCCCCCCC GGCACTTCCCCCCCCCC  | CGGCGGGGGC CGGCCGCT CGGCGGGTTTGA CGATTIATACA GGTTTGAGA GGCTTGAGAT GGCTTGACAT GGCTTGACAT GGCTTCACAT CCTACCAGTA TCCCGGGAA TCCCGCAAT CCTACCAGTA CCTACCAGTA CCTACCAGTA TCCTGCAGAT CCTACCAGTA TCCTGCAAT CCTACCAGTA TCCTGCAGAT CCTTGCCGGGAGC AATGCATATATCAC CCTGGGGAGC AATGCATTAATCAC CGCTTTTCCCC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGAGGAAGAT CGCTTTCAGC CTTGAGGAAGAT CGCTTTCAGC CTTGAGGAAGAT CGCTTTCAGC CTTGAGGAAGAT CTGAGGAGCC CTTGAGGACC CTTGAGACC CTTGAGGACC CTTGAGACC CTTGAGGACC CTTGAGACC CTTGAGACC CTTGAGACC CTTGAGACC CTTGAGACC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGACC CTTGA | GGGGCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA GGAGCAGACA CCCACGGTT AACAAGGAAT TACGACACA TTACACACGA TTACACACGA CCCACGGTT GACATCTCA TTACACACGA TGCATCTTGGC GGGGGAAAG TTACACACGA TTACACACGA TTACACACGA TTACACACGC CTCCTTTGGC GGGGGGAAAG TTACACACGA TTACACACAC TTCTTTTATG GGCTGCCCAA AGCAAGCCCC TTCTTTTATTG CAGTATTCCTTA AAAAAATGTT  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1740         |
| 50<br>55<br>60<br>65             | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGGG AGGACCTTAC TCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GACTCACACC GACTCACCTA ACGAGGCGA ACGACCTA ACGAGCCT ATGGGCAT CTGTGCCAT TCAGCGCT TAATGCCG TAATGCCG TAATGCCT AGGGACACCCT AGGGTGGCGT TACACTCCT AGGGATGGCT AGGGTTCCCT AGGGATGGCT TACACTCCT AGCCAACCTC AGGGTTCCCT AGCTACTCCT AGCTACTCCT AGCTACTCCT AGCTACTCCT AGCTACTCCT AGCTACTCCT AGCTACTCCT AGCTACTCCT TATGATTTTTT CATTTTTTTTC TGGAAAGAGAA  | GCGAGTGTCA CTOGGACCCA GCAGCCACAC GCAGCCACAC CTCCTCTCC TGACCCAGAC CTCCTCTCC TGACCCAGAC CCACATCGAC CCACATCGAC CCACCTCC GAGTTCAGC CAACCCCTC GAGTGCACAC GGCTGAAGTAC AGGACCCTC GGCCTGGAAC AGGACCCTC GGCCTGGAAC AGGACCCCCC CCCCAGATTCAGC TCCCCAATTGCAGC CTCCCAATTGCAGC CTCCCAATTGCAGC TCCCCAATTGCAGC TCCCCAATTAGAC TCCCCCAATTAGAC TCCCCCCAATTAGAC TCCCCCAATTAGAC TCC | GGGGGCGGC GGGGCGCGC GGGGCGCGC TTTGACTTCA TACACCGGGG GAGCTCACCG GAGTTGGTTG AACACAAGAC AACACCACACACACACACACACACACA   | CGGCGGGGGC CGGCCGCT CGGCGGGTTTGA CGATTIATACA GGTTTGAGA GGCTTGAGAT GGCTTGACAT GGCTTGACAT GGCTTCACAT CCTACCAGTA TCCCGGGAA TCCCGCAAT CCTACCAGTA CCTACCAGTA CCTACCAGTA TCCTGCAGAT CCTACCAGTA TCCTGCAAT CCTACCAGTA TCCTGCAGAT CCTTGCCGGGAGC AATGCATATATCAC CCTGGGGAGC AATGCATTAATCAC CGCTTTTCCCC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGTCAGC CTTGAGGAAGAT CGCTTTCAGC CTTGAGGAAGAT CGCTTTCAGC CTTGAGGAAGAT CGCTTTCAGC CTTGAGGAAGAT CTGAGGAGCC CTTGAGGACC CTTGAGACC CTTGAGGACC CTTGAGACC CTTGAGGACC CTTGAGACC CTTGAGACC CTTGAGACC CTTGAGACC CTTGAGACC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGAGCAC CTTGACC CTTGA | GGGGCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA GGAGCAGACA CCCACGGTT AACAAGGAAT TACGACACA TTACACACGA TTACACACGA CCCACGGTT GACATCTCA TTACACACGA TGCATCTTGGC GGGGGAAAG TTACACACGA TTACACACGA TTACACACGA TTACACACGC CTCCTTTGGC GGGGGGAAAG TTACACACGA TTACACACAC TTCTTTTATG GGCTGCCCAA AGCAAGCCCC TTCTTTTATTG CAGTATTCCTTA AAAAAATGTT  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1020<br>1080<br>1140<br>1220<br>1320<br>1340<br>1500<br>1500<br>1620<br>1620         |
| 50<br>55<br>60<br>65<br>70       | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGG AGGACCTTAC TCCTCTTCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GGGACACGCT ATGAGGACA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGCTCGCCTA ACGAGCTCGCCTA ACGAGCTCGCCTA ACGAGCTCTGA CTAATGGCCC TAATGGCCC TAGAGGATGG TGACAATCT AGCCAACCTC TAGAGTATCCT TAGATTCTTCT CCATTTTTTTC TGGAAGAGAC TTAGATTCTT CATTTTTTTTC TGGAAGAGAC TTAGTTCTT TGGAAGAGAC TTAGTTCTTT Seq ID NO:  | GCGAGTGTCA CTCGGACCCA GCAGCAACG CTTCCTCTCC GCAGCCAACG TCTCCCACTCG CCACATCGAC CCACATCGAC CCACCACACC CACATCGAC CCACCACACC GGCCACACC GGCCACACC GGCCACACC GGCCACACC GGCCTGGAAC AGGACCCCTG CCACACCC GGCCTGGAAC AGGACCCCTG CCCCAATTCAGC CCCCAATTCAGC CCCCACTCG   | GGGGGGCGGC GGGGCGCGC GGGGCGCGG GGGCTCACCG GGGTTGGTTG AACTCCATGA AACATCCACGG GAGTTCGTCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCACGG AACATCCCACGG AACATCCCACGGCGCG AACATCCCACGGCCTTCCGGAAATGTCT AACAAAACAA  | CGGCGGGGGC CGGCCGCCT CGGCGGCTTGA CGAGGTTTGA CCATTATCTC GATTTATAAC GGTGCAGAT GGCTTGACAT GGCTTGACAT GGCTTCAA TGACGCATGT CCTACCAGTA TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCGCGGGAGC CCAAAGGGT CTGGCAGCA TTGGCAGCA TTGGCAAT CTTGCCTGCAT CCTACAGTA CCTTGCAAT CCTGCAAT CCTTGCAAT CCTTGGGAAC CCTTGGGGAC CACATTAAT CCTTGAGGAC CTTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGTAAA CTTAGATTAAAA CTTAGATTAAAA   | GGGGCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA GGAGCAGACA CCCACGGTT AACAAGGAAT TACGACACA TTACACACGA TTACACACGA CCCACGGTT GACATCTCA TTACACACGA TGCATCTTGGC GGGGGAAAG TTACACACGA TTACACACGA TTACACACGA TTACACACGC CTCCTTTGGC GGGGGGAAAG TTACACACGA TTACACACAC TTCTTTTATG GGCTGCCCAA AGCAAGCCCC TTCTTTTATTG CAGTATTCCTTA AAAAAATGTT  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1740         |
| 50<br>55<br>60<br>65             | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCAAGC GACTCACCTC ATGAGGACA ACGTGGCCTA ACGAGCTGGCCTA ACGAGCTGCACCTC ATGAGGACA CCTCAATCTG TAGAGGATGG TACACCTC AGGGTGCCT AGGGTGCCT TAGAGGATGG TACACTCCT AGGGTGCCT TAGAGGATGG TCGACAATCTC TAGAGATTGC TCGACAATCTC TAGAGTACTCCT TAGAGTACTCCT TAGAGTACTCCT TATGATTTTTTC CATTTTTTTTTT  | GCGAGTGTCA CTCGGACCCA GCAGCCACAC GCAGCCACAC GCAGTCACC CCACACACAC GCAGTTCAGC CCACACACAC GCAGTTCAGC CAACCCCTC GAGTGCACAC GAGTCCAGC GGCTGAAGTAC GGCTGAAGTAC AGGACCCTG GGCTGAAGTAC AGGACCTGC GGCTGAAGTAC AGGACCCTG GGCTGAAGT CTCCAATTC CATCAGAGC CTCAAGTATAC CCCCAAGGC CTCAAGTAC CCCCAAGGC CCCCCACTGGC CCCCAAGGC CCCCACTCG CCCCACTCC CCCCCCC CCCCCCC CCCCC CCCCCC CCCCCC   | GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCGCCT CGGCGGCTTGA CGAGGTTTGA CCATTATCTC GATTTATAAC GGTGCAGAT GGCTTGACAT GGCTTGACAT GGCTTCAA TGACGCATGT CCTACCAGTA TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCGCGGGAGC CCAAAGGGT CTGGCAGCA TTGGCAGCA TTGGCAAT CTTGCCTGCAT CCTACAGTA CCTTGCAAT CCTGCAAT CCTTGCAAT CCTTGGGAAC CCTTGGGGAC CACATTAAT CCTTGAGGAC CTTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGTAAA CTTAGATTAAAA CTTAGATTAAAA   | GGGGCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA GGAGCAGACA CCCACGGTT AACAAGGAAT TACGACACA TTACACACGA TTACACACGA CCCACGGTT GACATCTCA TTACACACGA TGCATCTTGGC GGGGGAAAG TTACACACGA TTACACACGA TTACACACGA TTACACACGC CTCCTTTGGC GGGGGGAAAG TTACACACGA TTACACACAC TTCTTTTATG GGCTGCCCAA AGCAAGCCCC TTCTTTTATTG CAGTATTCCTTA AAAAAATGTT  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1740         |
| 50<br>55<br>60<br>65<br>70       | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCAAGC GACTCACCTC ATGAGGACA ACGTGGCCTA ACGAGCTGGCCTA ACGAGCTGCACCTC ATGAGGACA CCTCAATCTG TAGAGGATGG TACACCTC AGGGTGCCT AGGGTGCCT TAGAGGATGG TACACTCCT AGGGTGCCT TAGAGGATGG TCGACAATCTC TAGAGATTGC TCGACAATCTC TAGAGTACTCCT TAGAGTACTCCT TAGAGTACTCCT TATGATTTTTTC CATTTTTTTTTT  | GCGAGTGTCA CTCGGACCCA GCAGCAACG CTTCCTCTCC GCAGCCAACG TCTCCCACTCG CCACATCGAC CCACATCGAC CCACCACACC CACATCGAC CCACCACACC GGCCACACC GGCCACACC GGCCACACC GGCCACACC GGCCTGGAAC AGGACCCCTG CCACACCC GGCCTGGAAC AGGACCCCTG CCCCAATTCAGC CCCCAATTCAGC CCCCACTCG   | GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCGCCT CGGCGGCTTGA CGAGGTTTGA CCATTATCTC GATTTATAAC GGTGCAGAT GGCTTGACAT GGCTTGACAT GGCTTCAA TGACGCATGT CCTACCAGTA TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCGCGGGAGC CCAAAGGGT CTGGCAGCA TTGGCAGCA TTGGCAAT CTTGCCTGCAT CCTACAGTA CCTTGCAAT CCTGCAAT CCTTGCAAT CCTTGGGAAC CCTTGGGGAC CACATTAAT CCTTGAGGAC CTTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGTAAA CTTAGATTAAAA CTTAGATTAAAA   | GGGGCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA GGAGCAGACA CCCACGGTT AACAAGGAAT TACGACACA TTACACACGA TTACACACGA CCCACGGTT GACATCTCA TTACACACGA TGCATCTTGGC GGGGGAAAG TTACACACGA TTACACACGA TTACACACGA TTACACACGC CTCCTTTGGC GGGGGGAAAG TTACACACGA TTACACACAC TTCTTTTATG GGCTGCCCAA AGCAAGCCCC TTCTTTTATTG CAGTATTCCTTA AAAAAATGTT  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1740         |
| 50<br>55<br>60<br>65<br>70       | GTGGCGAGTG TGGCAGCGGG CCGGCGGCGGG AGGACCTTAC TCCTCTTCCT TCTATGTCGA ACGAAGTGGG GTGCCAAGC GACTCACCTC ATGAGGACA ACGTGGCCTA ACGAGCTGGCCTA ACGAGCTGCACCTC ATGAGGACA CCTCAATCTG TAGAGGATGG TACACCTC AGGGTGCCT AGGGTGCCT TAGAGGATGG TACACTCCT AGGGTGCCT TAGAGGATGG TCGACAATCTC TAGAGATTGC TCGACAATCTC TAGAGTACTCCT TAGAGTACTCCT TAGAGTACTCCT TATGATTTTTTC CATTTTTTTTTT  | GCGAGTGTCA CTCGGACCCA GCAGCCACAC GCAGCCACAC GCAGTCACC CCACACACAC GCAGTTCAGC CCACACACAC GCAGTTCAGC CAACCCCTC GAGTGCACAC GAGTCCAGC GGCTGAAGTAC GGCTGAAGTAC AGGACCCTG GGCTGAAGTAC AGGACCTGC GGCTGAAGTAC AGGACCCTG GGCTGAAGT CTCCAATTC CATCAGAGC CTCAAGTATAC CCCCAAGGC CTCAAGTAC CCCCAAGGC CCCCCACTGGC CCCCAAGGC CCCCACTCG CCCCACTCC CCCCCCC CCCCCCC CCCCC CCCCCC CCCCCC   | GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCGCCT CGGCGGCTTGA CGAGGTTTGA CCATTATCTC GATTTATAAC GGTGCAGAT GGCTTGACAT GGCTTGACAT GGCTTCAA TGACGCATGT CCTACCAGTA TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCGCGGGAGC CCAAAGGGT CTGGCAGCA TTGGCAGCA TTGGCAAT CTTGCCTGCAT CCTACAGTA CCTTGCAAT CCTGCAAT CCTTGCAAT CCTTGGGAAC CCTTGGGGAC CACATTAAT CCTTGAGGAC CTTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGGAC CTTGAGTAAA CTTAGATTAAAA CTTAGATTAAAA   | GGGGCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC TCCACACACA CCTCACACACA GGAGCAGACA CCCACGGTT AACAAGGAAT TACGACACA TTACACACGA TTACACACGA CCCACGGTT GACATCTCA TTACACACGA TGCATCTTGGC GGGGGAAAG TTACACACGA TTACACACGA TTACACACGA TTACACACGC CTCCTTTGGC GGGGGGAAAG TTACACACGA TTACACACAC TTCTTTTATG GGCTGCCCAA AGCAAGCCCC TTCTTTTATTG CAGTATTCCTTA AAAAAATGTT  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1740         |
| 50<br>55<br>60<br>65<br>70<br>75 | GTGGCGAGTG TGGCAGCGGG AGGACCTTAC TCCTCTTCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GGACCACCC ATGAGGACAA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGTCACCTA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGTACCCTA ACGAGTACCCTA ACGCTCTGA CTAATGGCCG CTCAATCTGCTCAC TAATGGCCG TACACTGCT TACACTGCTT AGGGTACTCCT TATGATTCTT CATTTTTTC TGGAGAGATCT TATGATTCTT CATTTTTTTC TGGAGAGACTA TTAGTTCTTT Seq ID NO Nucleic AC Coding sec   | GCGAGTGTCA CTCGGACCCA CACGATGGCC GCAGCCAACG CTTCCTCTCG TGACCCAGCA TCTGCACTGC CCACCACGGCACAG ACAGGTCCAG CAGCCACAG ACAGGTCCAG CAGCCACAG ACAGGTCCAG CAGCCACAG CAGTCCAGC GGTCAAGTAG AGGACCTGGAAC GTCCAAATTGAC GTCCAAATTGAC CCCCCCCGG CCCACAGGG CTCAAGTAGA AGAAAAAAA ACCCCACTCG CCCACCCCC CCCCCCCCG CCCCCCCCC CCCCCCCC  | GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCCGCT CGGCGGTTTGA CGATTATATAC GATTTATAAC GGTGCAAGAT GGCTTGACAT AGATCCGGTA TGACGCATGT CCTACCAGTA TCCCTGCAAT CCTACCAGTA TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TGGCGGAGT TTGGGCAAGAT CCAATTAATC CACATTAATC ACACATTAATC ACACATTAATC GGCATGCACT TTTTCCCC TTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTGAGGAC TTTTAATCAAAA TTAGATTAAAA  | GGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | GAGGAGGGGT GCTCCCACCC ARGCTGCCCA TGCCTCTCA TGCATCCA TGCATCCA TGCATCCA TGCATCCA TGCATCCA TGCATCCA TGCATCCA ATGGCAGC CCCACCACCA TCCACCACA ATCACACACA CCCACGGTTT AACAAGGAAT TACGACCTCA TTACCCACGG TTACACCACGC TCCTTTGGC CTCCTTTGGC CTCCTTTGGC TTAGACAAAT GAGTACACACA TTAGACAAAT CAGCCAGGCT TCCCTTGGC TCCCTTGGC TCCCTTGGC TCCCTTGGC TCCCTTGGC TCCCTTGGC TCCCTTGGC TCCCTTGGC TCCCTTGGC TCCCTGGC TCCTTTTATG CAGTTCCTA AAAAAATGTT CAG  51                    | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1020<br>1140<br>1260<br>1320<br>1320<br>1440<br>1500<br>1560<br>1740<br>1793         |
| 50<br>55<br>60<br>65<br>70       | GTGGCGAGTG TGGCGCGGG AGGACCTTAC TCCTCTTCT TCTATGTCGA GTTTACCCAA ACGAAGTGGG GTGCCACAGG GGGACACGCT ATGAGGACAA ACGTCGCCTA GCCCATCAC CTATTCGAGGACAA ACGAGTGGCCTA ACGAGGTGGGCTA TCAGGCTCAATCTGTCCAT TAGAGGATGGCTA AGGGGTGGGGT   | GCGAGTGTCA CTCGGACCCA CACGATGGCC GCAGCCAACG CTTCCTCTCG GCAGCCAACG TCTCCCACTCG CCACATCGAC CCACCTCACACC CCACCACCACAC ACAGGTCCACAC ACAGGTCCAC CCACCACCC GGTCAGTAG AGGCCCTCG GCCTGGAAC GGTCCACACC GTCCACACC CCCCACACCG CCCCAGAGGC CCCCAGAGGC CCCCAGAGGC CCCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCACTCG CCCCACTCG CCCCACTCG CCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCACTCG CCCCACTCG CCCCACTCG CCCCACTCG CCCACTCG CCCCACTCG CCCCCCCCCC   | GGGGGGCGGC GGGGCGCGC GGGGCGCGCG GGGGCTACCG GGGGTCACCG GAGTTGGTTG AACACAGAG AACATCCACGG GACTCCACG GAGTCGCACG AACATCCACG AACATCCACG AACATCCACG AACATCCACG AACATCCACG AACATCCACG AACATCCACG AACATCCCACG AACATCCCACG AACATCCCAC GGCACTTCC TGCCGTACT TGCCGTACT TTGCCTTTCC AACATCCCAC ACAGGGGGC ACCAGACCTT TGCGCTTATCT TGGGTTCAAC CGTAATCT TGGGTTCAAC CCCTACCTG AACCCCTACCTG AACCCTACCTG AACCTACCTG AACCCTACCTG AACCTACCTACCTG AACCCTACCTG AACCTACCTACCTG AACCCTACCTG AACCCTACCTG AACCCTACCTACCTG AACCCTACCTG AACCTACCTACCTG AACCTACCTACCTG AACCTACCTACCTG AACCCTACCTACCTG AACCCTACCTACCT | CGGCGGGGGC CGGCCCCCC CGGCGCCGCCT GGAGGTTTGA CGATTATATAC GGATTATATAC GGTGCACATT GGCTTGACAT GGCTTGACAT GGCTTCAA TCCCCGCAA TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT TCGGCAAGAT TCGGCAAGAT TCCTTGCCTCC CCAAAGGGTG TCTTTTCCCC CCTGGGGAGC TATATCAAT GGCATTAAT GGCATTCAGC TCTGAGGACT TAGATTAAAT TAGATTAAAT TAGATTAAAT TAGATTAAAT TAGATTAAAT TAGATTAAAT   | GGGGGGGCGGCGGGCCGGGCCTGCAGGCCTGCAGGCCAGAAGTTTCAGGGGATGAGGGACATCTGCAGGGGACATCAGAGACATTCACGGGGACACAGAACATTGAGGATGAGAGATTCTGGACTGACTTCCCTTTTGGGACCACACACACACACACACACACACACACACACACACACA   | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC TGCCTCTCA GTGAACATCA ATGGCAGGC GCAGGCTGCC TCCACACACA CTCTCCTTTG GGAGCAGACA CCCACGGTTT AACAAGGAT TACGACCTCA ATGGCAGACA CCCACGGTTT AACAAGGAAT TACGACCTCA CTCTCTTGGC CTCCTTTGGC CTCCTTTGGC CTCCTTTGGC TACGACAGAC TTCCTTTGGC TACGCAGGCT CTCCTTTGGC TACGCAGGCT CTCCTTTGGC TACGCAGGCT CTCCTTTGGC TTCCTTTGGC TCCCTGGGC TTCCTTTATG CAGCAGGCTC TTCCTTTATG CAGTTTCCTA AAAAAATGTT CAG 51   CCTGGCCTAGC                        | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1560<br>1620<br>1740         |
| 50<br>55<br>60<br>65<br>70<br>75 | GTGGCGAGTG TGGCAGCGGG AGGACCTTAC TCCTCTTCT TCTATGTCGA ACGAAGTGGG GTGCCACAGC GGGACAGCTA ACGAAGTGGG GGACCCATCA ACGAGTGGCCTA ACGAGCGGGACAGCTA ACGAGCGCCATCA TCTGTGCCAT CAGCCTCTAATGGCCG TAGAGGATGGCT TAGAGGACTA AGGCAACCTG TAGAGCACTG TAGAGTACTCCT TATGATTTTT TCGAAGAACTT CATTTTTTTC CATTTTTTTC TGAAGGACT TAGAGTACTCCT TAGAGCCCGAC TCGAGCCCGAC TCGAGCCCGAC TGCCCAGGCCCACC TGCCCAGGCCCACC TGCCCAGGCCCACC TGCCCAGGCCCACC TCCCCAGGCCCACC TCCCCAGGCCCACC TCCCCAGGCCCACC TCCCCAGGCCCCACC TCCCCAGGCCCCACC TCCCCCAGGCCCCACC TCCCCCAGGCCCCACC TCCCCCAGCCCCACC TCCCCCACC TCCCCAGCCCCACC TCCCCAGCCCCACC TCCCCAGCCCCACC TCCCCAGCCCCACC TCCCCCAGCCCCACC TCCCCCAGCCCCACC TCCCCCAGCCCCACC TCCCCCAGCCCCACC TCCCCCAGCCCCACC TCCCCCAGCCCCACC TCCCCCACC TCCCCAGCCCCACC TCCCCCACC TCCCCAGCCCCACC TCCCCCACC TCCCCCACC TCCCCACC TCCCACC TCCCCACC TCCCCCCCC | GCGAGTGTCA CTCGGACCCA CACGATGGCC GCAGCCAACG CTTCCTCTCC GCAGCCAACG TCTCCCACGC TCACCAGCA CAGCATCAGA CAGCACCACA CAGCACCACA CAGCCCACAC CAGCCACAC CAGCCACAC CAGCCACAC CAGCCACAC CAGCCACAC CAGCCACAC CACCACAC CACCACAC CACCACAC CCCCACAGGG CCCCACAGGG CCCCACAGGG CCCCACACGCC CCCCACACGG CCCCACACGC CCCCCCCC  | GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCGCCC CGGCGGCGC CGGCGGCGC CGGCGG  | GGGGCGGCCG GGCCTGCAGC CATCTACAGG CATCTACAGG CATCTACAGG CATCTACAGG CATCTACAGG CATCTACAGG TCACGATGAG GAACAATGGG GAACAATGGG GAACAATGGG GAAGATTGTG CACGTGGCC CTGGTTCCACGG CATCACAAG TGCTCTAGGG CACGTGCCC CTGGTTCACG CACGTGCCC CTGGTTCACG CCTGGACTCA GCATTGACGC CTGGTTCACG TTTTGCACAGT TTTTGGACCT TTTTGGACCT TTTTGGACCT TTTTGGACCA TTTGGTTTCC TTTTGGACCA TTTGGTTTCC TTTTGGACCA TTTGGTTTCC TTTGGACCA TTTGGTTTCC TTTGAAGGCAC TTGAAGGCAC TTGAAGCAC TTGAAGGCAC TTGAAGGCAC TTGAAGGCAC TTGAAGGCAC TTGAAGGCAC TTGAAGCAC TTGAAC TTGAAC TTGAAC TTGAAC TTGAAC TTGAAC TTGAAC TTGAAC TTGAAC TTGA | GAGGAGGGGT GCTCCCACCC GCTCCCACCC TGCCTCTCA TGCCTCTCA TGCCTCTTCA TGCAACCACC CTCAACAATCA ATGGGCAGGC TCCACCACA CCCACGGTTT AACAAGGAAT TGCATCTCA TGCACCACG TTCACCACGA TTCACCACGA TTCACCACGA TTAGACAAAT CACACCGG TTCCTTTGC CGCGGGGAAAG TTAGACAAAT CGACTCCTCA CGGGGGAAAG TTAGACAAAT CAGCACGGCT CTCTTTTATG CAGCTCCCACGC TTCCTTTATG CAGCTCCCACGC TTCCTTTATG CAGGTTCCTA CAGGTTCCTA CAGTTCCTA CAGTTTCCTA CAAAAAATGTT CAG  51  CCGGGCCTAGC CACCATGCTCC CCCCACCTGC | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>1020<br>1140<br>1200<br>1320<br>1380<br>1440<br>1500<br>1620<br>1620<br>1740<br>1793 |
| 50<br>55<br>60<br>65<br>70<br>75 | GTGGCGAGTG TGGCAGCGGG AGGACCTTAC TCCTCTTCT TCTATGTCGA ACGAGTGGGGGG GTGCCACAGG GGGACACGCT ATGAGGACAA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGTGGCCTA ACGAGTACCAT CTGTGCCAT CAGCCTCGA CTAATGGCCG TAATGGCCG TAAGAGTACTC TAGAGTACTC TAGAGTATCT TAGACTACTC TATGATTCTT CATTTTTTC TGGAGAGAGA TTAGTTCTTT Seq ID NO: Nucleic Ac Coding sec  1 1 1 TCGAGCCCGC AGGCCCCAC TGCACCCCAC TGCACCCCAC TGCCCAGGCCCCAC TGCCCCAGGCCCCAC TGCCCCAGGCCCCAC TGCCCCAGGCCCCAC TGCACCCCAC TGCCCCAGGCCCCAC TGCACCCCAC TGCACCCCAC TGCACCCCAC TCCCCAGGCCCCAC TCCCCAGGCCCCAC TCCCCAGGCCCCAC TCCCCAGGCCCCAC TCCCCAGGCCCCAC TCCCCAGGCCCCAC TCCCCAGGCCCCAC TCCCCAGCCCCAC TCCCCAGCCCCAC TCCCCAC TCCCCAGCCCCAC TCCCCAC TCCCCAC TCCCCAC TCCCCAC TCCCCAC TCCCCACCCA   | GCGAGTGTCA CTCGGACCCA CACGATGGCC GCAGCCAACG CTTCCTCTCG GCAGCCAACG CTTCCTCTCG GCAGCCACAG TCGCACTCG CCAGCCACAG ACAGGTCCAG ACAGGTCCAG CCAGCCACAG ACAGGTCCAG CCATCGGAC CCATCGGAC CCATCGGAC AGGCCCTGG GCCTGGAAC GCCCCTGGAC AGGCCCCC CCCCAGAGGG TTATACACCC CCCCACTCG CCCCACTCGC CCCCACTCG CCCCCCCCCC   | GGGGGGCGGC GGGGGGGGGGGGGGGGGGGGGGGGGGG   | CGGCGGGGGC CGGCCGCCT CGGCGCGCCT CGGCGCGCCT CGGCGCGCT CGGCGGCT CGGCGGCGCGCT CGGCGGCGCGCT CGGCGGCGCGCT CGGCGGCGCGCT CGGCGGCGCGCT CGGCGGCGCGCGC   | GGGGCGGCCG GGCCTGCAGC CATCTACAGG CATCTACAGG CATCTGCTGC GACAGAAGTT TCAGGATGAG GAACAATGGG CATCTCACAGG GAACAATGGG CATCTCACAGG CATCTCACAGG CATCTCACAGG GAACAATGGC CATGGTGGCC CATGGACTCA GCATTGACGC GATCACAGATTC CATGGAACAT GCATTGACGC AGTGCCCTGT TTTGGGAACAT TTTGGATTCCC TTTTGGACCA ATTGGTTCACG GATCACCTCT TTTTGGACCA ATTGGTTCACGC GGATCACCCT TTTTGGACCA ATTGGATTCAA ATTGGTTCAAGGGATGA ATTGGATCACC GGATCACCCT GGTACTCCCC GGAGCTCCGC GGAGCTCCGC GGAGCCTCCGC GGAGCCCCGC GGAGCTCCCGC GGAGCCTCCGC GGAACACTT GGAGCCCCCCC GGAGCCTCCGC GGAACACTT GGAGCCTCCGC GGAACACT GGACCTCCCCCC GGAACACT GGACCTCCCCC GGAACACT GGACCTCCCCC GGAACACT GGACCTCCCCC GGAACACT GGACCTCCCCC GGAACACT GCACCCCCCC GGAACACT GCACCCCCCCC GGAACACT GCACCCCCCCCC GCACCCCCCCC GGAACACT GCACCCCCCC GCACCCCCCCC GCACCCCCCCCC GCACCCCCCCC  | GAGGAGGCGT GCTCCCACCC AGGCTCCCACCC AGGCTCCCACCC ATGCCTCTCA GTGAACATCA ATGGGCAGGC GCAGGCTGCC CCCACGGTTT AACAAGGAACA CCCACGGTTT AACAAGGAACA CCCACGGTT CACACCCAC CTCCCTTGGC GGGGGAAAG CCACACCACA   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1380<br>1140<br>1500<br>1560<br>1560<br>1680<br>1740<br>1793   |

|                | CAGCTCTCAC               | TGCGGGGACC           | CTGCTACTTC      | TGACAGCCAT              | CGGGGCGCA                               | TOTTCCCCCA    | 360  |
|----------------|--------------------------|----------------------|-----------------|-------------------------|---|---------------|------|
|                | THETECHTET               | TCTCCTCACC           | AGTGACCAGG      | ACCCCCTCTA              | CCCACTCCAC                              | CECTOOOCCA    |      |
|                | 0001000000               |                      | MOTOACCAGG      | MOCCOCTOIN              | CCCMG1GCMG                              | GICAGCICIO    | 420  |
|                | CGGACGCTCG               | GCTCATGGTC           | TTTGACAAGA      | CGGAAGGGAC              | GTGGCGGCTG                              | CTGTGCTCCT    | 480  |
| -              | CGCGCTCCAA               | CGCCAGGGTA           | GCCGGACTCA      | GCTGCGAGGA              | GATGGGCTTC                              | CTCAGGGCAC    | 540  |
| 5              | TGACCCACTC               | CCACCTCCAC           | GTGCGAACGG      | CCCCCCCAA               | TOCONOCTOO                              | CCCOMO        |      |
| -              | Conconcio                | CONSCISSAC           | GIGCGAACGG      | COGGCCCAA               | IGGCACGICG                              | GGCIICIICI    | 600  |
|                | GIGIGGACGA               | GGGGAGGCTG           | CCCCACACCC      | AGAGGCTGCT              | GGAGGTCATC                              | TCCGTGTGTG    | 660  |
|                | ATTGCCCCAG               | AGGCCGTTTC           | TTGGCCGCCA      | TCTGCCAAGA              | CTGTGGCCGC                              | AGGAAGCTGC    | 720  |
|                |                          |                      | GGCCGGGACA      |                         |   |               |      |
|                |                          |                      |                 |                         |   |               | 780  |
| 10             | GCCTTCGCTA               | TGATGGAGCA           | CACCTCTGTG      | GGGGATCCCT              | GCTCTCCGGG                              | GACTGGGTGC    | 840  |
| 10             | TGACAGCCGC               | CCACTGCTTC           | CCGGAGCGGA      | ACCGGGTCCT              | GTCCCGATGG                              | CCACTCTTTC    | 900  |
|                | COCCTCCCCT               | CCCCCACCCC           | TCTCCCCACG      | 0000000000              | 000000000000000000000000000000000000000 |               |      |
|                | CCOGIGCCGI               | GGCCCAGGCC           | TCTCCCCACG      | GICIGCAGCI              | GGGGGTGCAG                              | GCTGTGGTCT    | 960  |
|                | ACCACGGGGG               | CTATCTTCCC           | TTTCGGGACC      | CCAACAGCGA              | GGAGAACAGC                              | AACGATATTG    | 1020 |
|                | CCCTGGTCCA               | CCTCTCCAGT           | CCCCTGCCCC      | TCACAGAATA              | CATCCAGCCT                              | CTCTCCCTCC    | 1080 |
|                |                          |                      |                 |                         |   |               |      |
| 15             |                          |                      | GTGGATGGCA      |                         |   |               | 1140 |
| 13             | CGCAGTACTA               | TGGCCAACAG           | GCCGGGGTAC      | TCCAGGAGGC              | TCGAGTCCCC                              | ATAATCAGCA    | 1200 |
|                | ATGATGTCTG               | CAATGGCGCT           | GACTTCTATG      | CALACCACAT              | CANCCCCANG                              | ATTENTOTY     | 1260 |
|                | CTCCCTLCCC               | 003000000            | * WHO THE COMP  | 0.001.000.001           | Chroccoro                               | AIGIICIGIG    |      |
|                | CIGGCINCCC               | CONGOCIOC            | ATTGATGCCT      | GCCAGGGCGA              | CAGCGGTGGT                              | CCCTTTGTGT    | 1320 |
|                | GTGAGGACAG               | CATCTCTCGG           | ACGCCACGTT      | GGCGGCTGTG              | TGGCATTGTG                              | AGTTGGGGCA    | 1380 |
|                | CTGGCTGTGC               | CCTGGCCCAG           | AAGCCAGGCG      | TCTACACCAA              | ACTUACTUAC                              | TTCCCCCACT    | 1440 |
| 20             |                          |                      |                 |                         |   |               |      |
| 20             |                          |                      | ACTCACTCCG      |                         |   |               | 1500 |
|                | CGGTGGCTTC               | TCGCTGCGCA           | GCCTCCAGGG      | CCCGAGGTGA              | TCCCGGTGGT                              | GGGATCCACG    | 1560 |
|                |                          |                      | TTTTCTTCTT      |                         |   |               | 1620 |
|                |                          |                      |                 |                         |   |               |      |
|                | CCCICCAGGG               | recretere            | CACAGTGGCG      | GGCCCACTCA              | GCCCCGAGAC                              | CACCCAACCT    | 1680 |
| 0.5            | CACCCTCCTG               | ACCCCCATGT           | AAATATTGTT      | CTGCTGTCTG              | GGACTCCTGT                              | CTAGGTGCCC    | 1740 |
| 25             |                          |                      | AAATAATAAA      |                         |   |               | 1783 |
|                |                          |                      | ***********     | un10011110              |   |               | 1103 |
|                |                          |                      |                 |                         |   |               |      |
|                | Seq ID NO:               | C215 DNA Se          | equence         |                         |   |               |      |
|                |                          |                      | #: AB03774      | 15.1                    |   |               |      |
|                |                          |                      |                 |                         |   |               |      |
| 30             | couring aedi             | ence: 26             | 1/44            |                         |   |               |      |
| <b>3</b> 0     |                          |                      |                 |                         |   |               |      |
|                | 1                        | 11                   | 21              | 31                      | 41                                      | 51            |      |
|                | Ī                        | 1                    | ī               | ī                       | ī                                       | 1             |      |
|                |                          | 1                    | 1               | 1                       | 1                                       |               |      |
|                | ATGGTGGAAC               | ACGCTGCCCA           | CAAACATGGA      | AACGACCGTT              | CTCAGTGGGA                              | TCAACTTCGA    | 60   |
|                | GTACAAGGGC               | ATGACAGGCT           | GGGAGGTGGC      | TGGTGATCAC              | ATTTACACAG                              | CTGCTGGAGC    | 120  |
| 35             |                          |                      |                 |                         |   |               |      |
| 33             |                          |                      | TTCTCACTCT      |                         |   |               | 180  |
|                | GGTGATGGCA               | GACACAGAGA           | ATAAAGAGGT      | GGCCAGAATC              | ACATTTGTCT                              | TTGAGACCCT    | 240  |
|                |                          |                      | TCTACTTCAT      |                         |   |               | 300  |
|                |                          |                      |                 |                         |   |               |      |
|                |                          |                      | CCAAAGGCAA      |                         |   |               | 360  |
| 40             | CACTACCACG               | AGCTTCACCT           | GGGCCTTCCA      | GAGGACCACT              | TTTCATGAGG                              | CAAGCAGGAA    | 420  |
| 40             | GTACACCAAT               | CACCTTCCCA           | AGATCTACTC      | CATCAATCTC              | ACCAATCTTA                              | TYPE A TOTOTT | 480  |
|                |                          |                      |                 |                         |   |               |      |
|                |                          |                      | GTGCCCTAGA      |                         |   |               | 540  |
|                | TTGTCCTGCT               | GGTTACTATA           | TTGACCGAGA      | TTCAGGAACC              | TGCCACTCCT                              | GCCCCCCTAA    | 600  |
|                | CACAATTCTG               | AAAGCCCACC           | AGCCTTATGG      | TOTOCAGGGG              | TOTOTOTOTO                              | CTCCTCCACC    | 660  |
|                | Charante                 | *************        | ACCCITATOO      | TOI COMOCCE             | 1010100001                              | GIGGICCAGG    |      |
| 45             | GACCAAGAAC               | AACAAGATCC           | ACTCTCTGTG      | CTACAATGAT              | TGCACCTTCT                              | CACGCAACAC    | 720  |
| 43             | TCCAACCAGG               | ACTTTCAACT           | ACAACTTCTC      | CGCTTTGGCA              | AACACCGTCA                              | CTCTTGCTGG    | 780  |
|                | AGGGCCAAGC               | TTCACTTCCA           | AAGGGTTGAA      | ATACTTCCAT              | CACALATACOC                             | TOROTOTO      | 840  |
|                |                          |                      |                 |                         |   |               |      |
|                |                          |                      | TGTCTGTGTG      |                         |   |               | 900  |
|                | TGAGGGTGAG               | TCAGGGTTCT           | CCAAATCTAT      | CACAGCCTAC              | GTCTGCCAGG                              | CAGTCATCAT    | 960  |
|                | CCCCCCAGAG               | CTCACACCCT           | ACAAGGCCGG      | CC Transport            | CACCCTICACA                             | CCCMACCANCA   |      |
| 50             | B000000000000            | oranomout.           | ACANOGECOG      | GGITICCICA              | CAGCCIGICA                              | GCCIIGCIGA    | 1020 |
| 50             | TOGACTTATT               | GGGGTGACAA           | CAGATATGAC      | TCTGGATGGA              | ATCACCTCCC                              | CAGCTGAACT    | 1080 |
|                | TTTCCACCTG               | GAGTCCTTGG           | GAATACCGGA      | CGTGATCTTC              | TTTTATAGGT                              | CCAATGATGT    | 1140 |
|                |                          |                      | GGAGATCAAC      |                         |   |               |      |
|                |                          |                      |                 |                         |   |               | 1200 |
|                | AACTGTCCCT               | GGAAGTTTGC           | TGCTGCCAGG      | AACGTGCTCA              | GATGGGACCT                              | GTGATGGCTG    | 1260 |
|                | CAACTTCCAC               | TTCCTGTGGG           | AGAGCGCGGC      | TGCTTGCCCC              | CTCTGCTCAG                              | TGGCTGACTA    | 1320 |
| 55             | CCATGCTATC               | GTCAGCAGCT           | CHCACACACAC     | GATCCAGAAG              | VC-10 Commy Co.                         | TGTGGCGAGA    |      |
| - <del>-</del> | I COOK I CO              | TO CONCUENT          | ~101000100      | OUT CONDUMY             | ACIACITACG                              | TOTOCCAMA     | 1380 |
|                |                          |                      | GCATTTCTCT      |                         |   |               | 1440 |
|                | CATAGATTTC               | TGGCTGAAAG           | TGGGCATCTC      | TGCAGGCACC              | TGTACTGCCA                              | TCCTGCTCAC    | 1500 |
|                |                          |                      |                 |                         |   | ACTCCAAGCT    |      |
|                | COMOTOCIO                |                      |                 | CONTRACTA               | TOMOLINGIA                              | ACICCAAGCI    | 1560 |
| 60             | GGTGATGAAT               | GCTACTCTCA           | AGGACTGTGA      | CCTGCCAGCA              | GCTGACAGCT                              | GCGCCATCAT    | 1620 |
| 60             | GGAAGGCGAG               | GATGTAGAGG           | ACGACCTCAT      | CTTTACCAGC              | AAGAAGTCAC                              | TCTTTGGGAA    | 1680 |
|                | GATCABATCA               | THURSTON             | AGCAGCCACC      | TOTAL CALCAR            | Vallablabana<br>Vallabana               | CAGAGGACTC    | 1740 |
|                |                          |                      |                 |                         |   |               |      |
|                |                          |                      |                 |                         |   | ATGGACCTGT    | 1800 |
|                | GAGAGGCACT               | GCCTGCCTCA           | CCTGCCTCCT      | CACCTTGCAT              | AGCACCTTTG                              | CAAGCCTGCG    | 1860 |
|                | GCGATTTGGG               | TGCCAGCATC           | CTGCAACACC      | CACTRICTRICA            | AATCTCTTCA                              | TTGTGGCCTT    | 1920 |
| 65             | ATCACATOTT               | TOCK A SECOND CO.    | **************  | A DECEMBER OF           | Characterion                            | 7707000017    |      |
| 05             | ATCAGATGIT               | IGAATITCAG           | ATCTTTTTT       | ATAGAGTACC              | CAAACCCCTCC                             | TTTCTGCTTG    | 1980 |
|                | CCTCAAACCT               | GCCAAATATA           | CCCACACTTT      | GTTTGTAAAT              | TATGCCCTTG                              | CTTGTATCTT    | 2040 |
|                | GTTTCCCAAA               | ATGGCCCATC           | CGCCAGAGCC      | ATAGCTTCY2T             | CTCCTCATAA                              | TTCTTATAGC    | 2100 |
|                |                          |                      |                 |                         |   |               |      |
|                |                          |                      |                 |                         |   | GTCCTCTAAC    | 2160 |
| 70             | TTAAGGGCAG               | AAACAGCTGG           | GAGTTTTCCT      | CGCATGCCCT              | CAGCTCATGA                              | TCTCTTCAGG    | 2220 |
| 70             | AGAGAGGGTYZ              | GGTGAGGAGG           | CTCTCTCTTT      | JAN-CAMPINAL CONTRACTOR | ATA ATOMOGR                             | TAGCAGCCTG    |      |
|                | CAMOCA                   | COLUMN TO THE T      | 210100001       |                         | AMARICIICA                              | ANGCAGCUIG    | 2280 |
|                | GATCCATTTC               | CCCTGGATAA           | CCAGCTCAAA      | GGGAGTGAAA              | ATGGTAGTCT                              | GAGGGCAAGG    | 2340 |
|                | GGAGCAAGGC               | CTGGGTAAGA           | AAAGCCTTGA      | AAAGCATAAA              | AAGAGGCCGG                              | GCGCGGTGGC    | 2400 |
|                | TCACCCCCCC               | AATCCCAGCA           | Calabalacian    | COCACCOCC               | CACATCATCA                              | GGTCGGGAGA    |      |
|                | TOCC101                  |                      | 2000000         | COUNTRY COOK            | CHOLICAIGA                              | COLCOGGAGA    | 2460 |
| 75             | LUAGACCAT                | CCIGGCTAAC           | ACGGTGAAGC      | CCCGTCTCTA              | CTGGAAATAC                              | AAAAAATTAG    | 2520 |
| 75             | CCGGGCGTGG               | TGGCGGGTGC           | CTGTGGTCCC      | AGCTACTCGG              | GAGGCTGAGG                              | CGGGAGAATA    | 2580 |
|                | CCCTCCCCC                | GCPFCCCCV            | GC-I-IATON CONC | VCCCC VCVC              | COCCOSTOROS                             | ACTCCATCCA    | 2640 |
|                | COORGOOGGI               | CARACTEC CO          | OTOTA CAULU     | AGCCGMGM1C              | GUGUACIGU                               | ACTULATURA    | 2040 |
|                | GCCTGGGTGA               | CAGAGTGAGA           | CTCTGCCTCA      | ААААААААА               | AAAAAAAGAA                              | AAGCACAAAG    | 2700 |
|                | AGAGGCAACA               | AGGAATGTTT           | TIGITTITYIA     | GACACCCTCT              | CACTCTGTCA                              | CCTAGGCTGG    | 2760 |
|                | YCALC YCACC              | Caty swar an         |                 | G00mc****               |   |               |      |
| 80             | AGIGCAGIGG               | CGIAATCACT           | GITCAGTGCA      | GCCTCAAGCT              | CTIGGGCTCA                              | GGCTATCCTC    | 2820 |
| οU             | CCATCTCAGC               | CTCTCAAGTA           | GCTGGGACTA      | CGAGTGTGCA              | CCACCAGGCT                              | CACTAATTTT    | 2880 |
|                | TGTGTTTTTT               | GTAGACACC            | GGTTTCACC       | TOTTOTOTO               | Chichian                                | AACTCCTGGG    | 2040 |
|                | ביייים א מיייים          |                      |                 | A A CONCOURS            | 20010101                                | -mc1001000    | 2340 |
|                | CICHAGIGAT               | CIGICUGUCT           | CGGCCTCCCA      | AACTGCTGGG              | ATTACAGGCA                              | TAAGCCACTG    |      |
|                | CACROLOGO                | COURT & COUNTY COURT | מאיים ממדידד מ  | COTACCTCAT              | TECHTOTO                                | TARCTARACC    | 3060 |
|                | CACTCAGCCT               | TITMITIGIT           | *********       | COINCIONI               |   | TUUGILAANII   |      |
|                | CACTCAGCCT<br>ATAGATATTC | TCACTGAAGC           | CAAAGGAATA      | AGTTCATCAA              | GAAAATGOO                               | AAAGCCCTGG    | 3120 |

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TGGATACATC CTCCCTATCT TTTTTTTAAA CCTTCCACTA TCACTCTATG ACACTGAAAA
                                                                                     3180
       GAACCAGGTA AGCCCCAAAC CCAGATGTTC CAGCCTTATC CTCTATTGGG TTTACCCACA
       GACATAGCAA ACCCTGTCAG TGAGGAAAAT TCCCCATCCT TGAGTGCCCC CGTCCTAGAA
GTTTGGGCCA TATTATGGAA CAGGGGTCTC TTATTTGAAA AGAGCACAAG GAGGCCAAGA
                                                                                     3300
                                                                                     3360
 5
       TTTTAATGGG GCACTTTAGG GGATACAGCC CACAATGGCA TGGGCCTGAG GTGGCCGTGA
                                                                                     3420
       TGTCTGCTTC TAAGCTTAAC GCATCTGCTC AGGCACAGAA TAAACGTCTA GGCTGGCCAA
       AAAAGGAACT GAATCCCAGG CCCATACGCC AGCACCAGAA TCAAACCAGT CTTCAAGGAA
                                                                                     3540
       GGAAGGCTAG GAGAGTTTAA CAAGATTTC ACTGGGCCCA GCATGGTGGC TCACACCTGT
AATCCCAAGG CAGAATGGTG GCTTGAGCTC AGGAGTTCAA GACCAGCCTG GGCAACACAG
                                                                                     3600
                                                                                     3660
10
       TGAGACCCTG TCTCTAAAAA ATTTAAAAAT AAACAAGGTG TTCACCAAGC TGGGATACTT
                                                                                     3720
       CTCACTATTA AGCCCCTATC TITCTCTTTT TTTCATTCTC AATTGCTTTG TGTGATAAAA
                                                                                     3780
       AACTAAAGAG ACTTCTGGTC CAATTTCTGG CAACATCCCT TCTGAAAGGT GAGTAGAGTG
                                                                                     3840
       GGTGTCTTCT ATGCCCATTT TCCCCAATTT TACACAAACT ATTATCAATG AACTTTTAAG TACCTAGAAT GGGTAAAACC AGAGCAAGAC TTTAAATTAC CTTCTTCTTT CTTCTACTGG
                                                                                     3900
                                                                                     3960
15
       CAGTTCTGCC TCCATCACTA TCAGGCTAGG GTGACCTTCC CTTGGTCAAG CCCCAATTGC
                                                                                      4020
       CCATGATTTG TGCCTGTGCC CTTTCTCCAG TGACCATTTG GTGACCAGAT GGTAGATATA
GAAAGGGGAT GGCATTTGCA AGTGACTAGT CTGCCACAAA ATGCTCATCT GATTAGCCAC
                                                                                     4080
                                                                                     4140
       TGCTGCCCTG GCAATGGCTT TGTAAGAGTC AATGAGAACT AGAGCCAGGC TGTGGTCCCT
                                                                                     4200
       GGCCATCAAC AGTGTTGGTG ACGGCAGGGA GTCCCTTTGG TTTAATAAAT CCAGTTTTTC
                                                                                      4260
20
       TTTGGGTATC CAAATTCTCC CCTCCTTTTG TAGGAGTCAG GCTCTCAGAA CCTGTGTCCA
                                                                                     4320
       TGTTGGAACT TCCCCAGTG TGGATGCAGA TACGCAGCTC CTGAGCTCCA GCCTAAAGTC
TTCTGTAGCC TCAGCAATAC TTGGGCACCT GCTGTCTCAC TGAATAGCTT TCTTTTGTGA
                                                                                     4380
                                                                                      4440
       CAAAGGCCAC AGACAGCCCT TAGACTATTC CGGAAACAGT AGGAAAAATT ACATATGTCT
                                                                                      4500
        TTGACTTCTT TATTCTGACT CCACTGATTT TAGCCATAAT ACTTTAAGGA GCTACTTTTT
                                                                                     4560
25
       ACTACCCCTT ACCGTGCTGA CTTCTGCAGG TCTGCCCTGT GACCTGTCAG GAACTCCTGA
                                                                                     4620
        GTTACGCTAC TGGGGTCACC TGTTGCTCCC CTAGCAAGTT AGGCATGTCA TATATTTTTA
                                                                                      4680
       ACAGCTTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAAC ATACGATTCA ATGGTTTTCA GCAAACTCAC AGAGTTGTCC GCCCACTTGA GAGCAAACAC ATGTTCAATT
                                                                                      4740
                                                                                      4800
        TTCTTTCCT TTTTTTTTT GAGACAGAGT CAGCTTTGTC GCCCAGGCTG GAGTGCAGTG
                                                                                      4860
30
        CCATGATCTT GGCTCACTGC AGCCTCCCCA TCCTGGGTTC AAGTGATCCT TCTGCTTCAG
                                                                                      4920
        CCTCCCCAGT AGCTGGGATT ACAGGCATGC GCCACCACGC CTAGCTAATT TTTGTGTTTT
                                                                                      4980
        TAGTAGAGAT GGGGTTTCAC CGTGTTGGCC AGGCTGGTCT CAAACTCCTG GACTCAAGTG
                                                                                      5040
        ATCCACCCAC CTCGGCCTCC CAAAGTGCTG GGATTGCAGG TGTGAGCCAC CGTGCCTGGC
                                                                                      5100
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                                                                                      5160
35
        TGTCCAAGCT GTTGTTGGTA GAGGGAGTAT GATAAAATGT TTAAATCTCA TTTGGTTACC
                                                                                      5220
        TTGAGTCCTG GAACACGCAG TAACTGTCAT GCTATAGTCA TCATCTGTAT TTGGCTGGGA
                                                                                      5280
        ATACAAATGA AGATTGTGGT GTATTCAAGC AGTAGGGTTT TTGCTTTTGT TTTTGTTTTA
                                                                                      5340
        GTGCCAACAA AACTTTTTTT TGTCTGACTA CATTAAAGAT AAGACTGACT ATATTTATAC
                                                                                      5400
        AACAGAAACT TIGTAATAGA TITTITCAGC TITGTGAAAT CGAATTITTT TICATCAGGG
                                                                                      5460
40
        CTGGTTGGAT TTCCTTTTTA CCCTGTAATC CAAGCGTTAA TAGTTTGTTA GAAGATGGGT
                                                                                      5520
        TATTGCATGT CACTTTTTT TTTTTGTAAA ATAAAAACAT ACCTTAC
                                                                                      5567
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        Nucleic Acid Accession #: NM 004864.1
45
        Coding sequence: 26-952
                                              31
                                                          41
                                                                      51
        CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC
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        TCAGATGCTC CTGGTGTTGC TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT
                                                                                      120
        GGCCGAGGCG AGCCGCGCAA GTTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG
                                                                                      180
        ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG
                                                                                      240
        CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCCTGCA GTCCGGATAC TCACGCCAGA
        AGTGGGGTG GGATCGGGG GCCACCTGCA CCTGGGTATC TCTCGGGCCG CCCTTCCCGA
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                                                                                      360
55
                                                                                      420
        AAGGTCGTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC
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        GCCCGCGCTG CACCTGCGAC TGTCGCCGCC GCCGTCGCAG TCGGACCAAC TGCTGGCAGA
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                                                                                      600
        CCGCAGAGCG CGTGCGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG
                                                                                      660
60
        TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTCGCC
        ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA
                                                                                      780
        CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC
                                                                                      840
        CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT
                                                                                      900
        GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT
                                                                                      960
65
        GGTCCTTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCCTGC CCTGTGGAAT
                                                                                      1020
        GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG
                                                                                      1080
        TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA
        ACTGTGTATT TATTTAAAAC TCTGGTGATA AAAATAAAGC TGTCTGAACT GTTAAAAAAA
                                                                                      1200
                                                                                      1204
70
        Seq ID NO: C432 DNA Sequence
        Nucleic Acid Accession #: NM_052858.1
        Coding sequence: 54..1259
75
                                              31
        GGCACGAGGT GTTGCCCTCA GGTCGCTCCC GGGCGCGGAC ACGGAACCCG GCCATGGAAG
        ATCCGTCGGG GGCTCGCGAG CCCCGGGCCC GGCCGAGAGA GCGGGACCCG GGACGGCGCC
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        CCCACCCAGA CCAAGGCCGC ACCCACGATC GACCGCGGA CCGACCCGGG GACCGCGCA
GGAAGCGAAG CAGCGACGG AACCGGCGAA GGGACGGGGA CCGGGACCCG AAGAGAGACAC
80
                                                                                      240
         AGGAGAGGGA CGGGAACCGC GACCGGAACC GGGACCGGGA GAGGGAGAGA GAGAGGGAAA
                                                                                      300
         GAGACCCGGA CCGAGGCCCC CGCCGGGACA CACACAGGGA CGCGGGCCCT CGCGCAGGTG
                                                                                      360
         AACACGGAGT TTGGGAAAAA CCGCGCCAAA GCCGGACGCG GGACGGAGCC CGGGGACTGA
                                                                                      420
         CCTGGGACGC AGCCGCGCCT CCTGGGCCCG CGCCCTGGGA AGCCCCGGAG CCGCCGCAGC
                                                                                      480
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|     | CGCAGAGGAA                | GGGAGACCCC | GGGCGCCGCA | GACCCGAAAG               | TGAACCCCCT | TCGGAGAGAT               | 540          |
|-----|---------------------------|------------|------------|--------------------------|------------|--------------------------|--------------|
|     | ATCTGCCCTC                | GACCCCCAGG | CCTGGACGAG | AGGAGGTGGA               | ATATTACCAG | TCAGAGGCGG               | 600          |
|     | AAGGACTCCT                |            |            |                          |            |                          | 660          |
| 5   | TGCTGGAGGT                |            |            |                          |            |                          | 720          |
| J   | CAGGGGGCTA                |            |            |                          |            |                          | 780<br>840   |
|     | CTTACAGTGG<br>ACCAGCTAAA  |            |            |                          |            |                          | 900          |
|     | TCTGCTGCCT                |            |            |                          |            |                          | 960          |
|     | TGGTGACCGA                |            |            |                          |            |                          | 1020         |
| 10  | TCTACTTCCA                |            |            |                          |            |                          | 1080         |
|     | TGTACCAAAG                | CAAAGGCTAC | AGCGGTTTCG | GCTGCAGTTT               | CCACGGAGCA | GATATAGGAG               | 1140         |
|     | CTGGAATCTT                |            |            |                          |            |                          | 1200         |
|     | AGGGCTACCG                |            |            |                          |            |                          | 1260         |
| 15  | GGTTTCTAAA                |            |            |                          |            |                          | 1320         |
| 13  | TTCCCAAGAA<br>GTGTGGTGGG  |            |            |                          |            |                          | 1380<br>1440 |
|     | CTTCTGGAGT                |            |            |                          |            |                          | 1500         |
|     | TGGCCGGCCT                |            |            |                          |            |                          | 1560         |
|     | ATCACTTGAG                |            |            |                          |            |                          | 1620         |
| 20  | TAAAATACAA                | AAAAATTAGC | CAGGCGTGGT | GCCGGCCCC                | TGTAATCCCA | GCTACTTGGG               | 1680         |
|     | AGGCTGAGGC                |            |            |                          |            |                          | 1740         |
|     | CGCCACTGCA                | CTCCAGCCCA | GGTGACAGAG | CGAGACTCCA               | TCTCAAAAAA | АААААААА                 | 1800         |
|     | Com ID NO.                | C434 DWB C |            |                          |            |                          |              |
| 25  | Seq ID NO:<br>Nucleic Aci |            |            | пиевсе                   |            |                          |              |
|     |                           | ence: 261. |            | •                        |            |                          |              |
|     |                           |            |            |                          |            |                          |              |
|     | 1                         | 11         | 21         | 31                       | 41         | 51                       |              |
| 30  |                           |            | 00010000   |                          | 1          | 0010000110               | 60           |
| 50  |                           |            |            | TGCTATCGGA<br>GCCAGGGTCT |            |                          | 120          |
|     |                           |            |            |                          |            | CAGCGACCAG               | 180          |
|     |                           |            |            | GAGGCGTGAC               |            |                          | 240          |
| 0.5 |                           |            |            | CTGGGAGGCA               |            |                          | 300          |
| 35  |                           |            |            |                          |            | ACAGTGGCTG               | 360          |
|     |                           |            |            |                          |            | GACCAAGACC               | 420          |
|     |                           |            |            |                          |            | ACCGTCTATT               | 480          |
|     |                           |            |            |                          |            | CCGATTGTTT               | 540<br>600   |
| 40  |                           |            |            |                          |            | GGTATTCAGC               | 660          |
|     |                           |            |            |                          |            | CTTGAGTTGC               | 720          |
|     |                           |            |            |                          |            | GGTGGCATGG               | 780          |
|     |                           |            |            |                          |            | GTTCATGTCA               | 840          |
| 15  |                           |            |            |                          |            | AGATCCAAGA               | 900          |
| 45  |                           |            |            |                          |            | ATCCTTTCTG               | 960          |
|     |                           |            |            |                          |            | GCGATGACCA               | 1020         |
|     |                           |            |            |                          |            | TTTCTAACTG               | 1080<br>1140 |
|     |                           |            |            |                          |            | TTCAATGTTT               | 1200         |
| 50  |                           |            |            |                          |            | CATGATAAAG               | 1260         |
|     |                           |            |            |                          |            | CCAGGAAAAA               | 1320         |
| •   | TATGCAATCG                | TCCCATTGAT | ATACAGGCCA | CTACAATGGA               | TGGAGTTAAC | CTCAGCACCG               | 1380         |
|     |                           |            |            |                          |            | GGCAGAGCCT               | 1440         |
| 55  |                           |            |            |                          |            | CTCACAGTCA               | 1500         |
| JJ  |                           |            |            |                          |            | CAGTCATGGA<br>GCAGAAGAGT | 1560<br>1620 |
|     |                           |            |            |                          |            | GGGAAACCAA               | 1680         |
|     |                           |            |            |                          |            | GTTGGGCTTC               | 1740         |
|     | TGAGCCGGAA                | CATCATAGTG | ATGGGGGAGA | TGGAGGACAA               | ATGCTACCCC | TACAGAAACC               | 1800         |
| 60  |                           |            |            |                          |            | GCTCTGGGAT               | 1860         |
|     |                           |            |            |                          |            | CIGGIGGGIC               | 1920         |
|     |                           |            |            |                          |            | TATGACCCAC               | 1980         |
|     |                           |            |            |                          |            | CACTGCTTCT               | 2040<br>2100 |
| 65  |                           |            |            |                          |            | CTCCTTGTCA               | 2160         |
|     |                           |            |            |                          |            | ATCACAGAGG               | 2220         |
|     |                           |            |            |                          |            | TCCACCTTCT               | 2280         |
|     |                           |            |            |                          |            | GAGGAAACTG               | 2340         |
| 70  |                           |            |            |                          |            | TACTCCCCAG               | 2400         |
| 70  |                           |            |            |                          |            | TCCAACTACC               | 2460         |
|     |                           |            |            |                          |            | AAGGACAAGC               | 2520<br>2580 |
|     |                           |            |            |                          |            | GACCCGCTGA<br>GACCACGGGG | 2640         |
|     |                           |            |            |                          |            | GAGGCTCAGG               | 2700         |
| 75  |                           |            |            |                          |            | GATGAGGCAG               | 2760         |
|     | CCTCTGGAAT                | GCTCAGGG   | TTCAGCCCT  | CCTGCCGCTC               | CCTGCTGAAG | CTGGTGACTA               | 2820         |
|     |                           |            |            |                          |            | GTGGTCAGAG               | 2880         |
|     |                           |            |            |                          |            | GCAGCCCTGC               | 2940         |
| 80  |                           |            |            |                          |            | COTCATTIC                | 3000         |
| 50  |                           |            |            |                          |            | GCTCGTACTC               | 3060<br>3120 |
|     |                           |            |            |                          |            | A AGGGAGGCC              | 3120         |
|     |                           |            |            |                          |            | CGGCCCCAGA               |              |
|     |                           |            |            |                          |            | GAAGGAAAGG               | 3300         |
|     |                           |            |            |                          |            |                          |              |

|   | AAATGACTAG  |  |  |  |   |  | 3360   |
|---|---|--|--|--|---|--|--|
|   | AACCCGCCCT  | CCCCTTGGTG   | TTGGCGGTCC   | CTGTGGCCTT   | CACTTTGTTC  | ACTACCTGTC   | 3420   |
|   | AGCCCAGCCT C  |  |  |  |   |  | 3480<br>3540   |
| 5   | CCAATTTGGC  |  |  |  |   |  | 3600   |
| •   | TGCTGCTTAA  |  |  |  |   |  | 3660   |
|   | TAAGAGGGAG  | AACTCTATCT   | GTGGTTTATA   | ATCTTGCACG   | AGGCACCAGA  | GTCTCCCTGG   | 3720   |
| •   | GTCTTGTGAT  |  |  |  |   |  | 3780   |
| 10  | AGAGGGCCTG  |  |  |  |   |  | 3840   |
| 10  | TTCCCCAGGT  |  |  |  |   |  | 3900   |
|   | GGGAGGTGAC GGAAGGACTT   |  |  |  |   |  | 3960<br>4020   |
|   | TCCTTCTTGT  |  |  |  |   |  | 4080   |
|   | GAACCACTTA  |  |  |  |   |  | 4140   |
| 15  | TTCATTTAAA .  | AAAGATATCT   | ATTTGAAAGT   | TCTCAGAGTT   | GTACATATGT  | TTCACAGTAC   | 4200   |
|   | AGGATCTGTA  |  |  |  |   |  | 4260   |
|   | TTTCTTGGTA  |  |  |  |   |  | 4320   |
|   | TGTAAGACTT .  |  |  |  |   |  | 4380<br>4440   |
| 20  | TGTAAACATT  |  |  |  |   |  | 4500   |
|   | ATGTGCACTT  |  |  |  |   |  | 4560   |
|   | GAGATGTCCT  |  |  |  |   |  | 4620   |
|   | TTGGAAAAAT  |  |  | CATACAAAGG   | ATGTCAAAAA  | АААААААА   | 4680   |
| 25  | АААААААА  | АААААААА   | AA   |  |   |  | 4702   |
| 23  | Seq ID NO:<br>Protein Acc   |  |  |  |   |  |  |
|   |   |  |  |  |   |  |  |
| 30  | 1   | 11   | 21   | 31   | 41<br>1   | 51<br>i  |  |
| 50  | MUGKMWPULW  | TI.CAVRVTVD  | ATSVETPODV   | LRASQGKSVT   | I I I I I I I I I I I I I I I I I I I   | SREGLIOWDK   | 60   |
|   |   |  |  | ISNNAEQSDA   |   |  | 120  |
|   |   |  |  | ETIIGNNIQL   |   |  | 180  |
| 25  |   |  |  | CTSSNEEGTQ   |   |  | 240  |
| 35  |   |  | CRGKDDNTED   | KEDARPNREA   | YEEPPEQLRE  | LSREREEEDD   | 300  |
|   | YRQEEQRSTG  | RESPUREDQ  |  |  |   |  | 319  |
|   | Sea ID NO:  | C218 Prote   | in Sequence  |  |   |  |  |
| 40  |   |  | Sos sequenc  |  |   |  |  |
| 40  |   |  | _  |  |   |  |  |
|   | 1   | 11   | 21   | 31   | 41  | 51   |  |
|   |   |  |  | 7.   | 7-  | 7.   |  |
|   |   |  | 1  | 1  | 1   |  |  |
|   |   | <br>HAVQLRWGPR   | <br>  RRPPLLPLLL   | <br>LLLPPPPPRVG  | <br>GFNLDAEAPA  | <br>VLSGPPGSFF   | 60   |
| 45  | GFSVEFYRPG  | <br>HAVQLRWGPR<br>TDGVSVLVGA   | <br>RRPPLLPLLL<br>PKANTSQPGV   | <br>LLLPPPPPRVG<br>LQGGAVYLCP  | <br>GFNLDAEAPA<br>WGASPTQCTP  | <br>VLSGPPGSFF<br>IEFDSKGSRL   | 120  |
| 45  | GFSVEFYRPG<br>LESSLSSSEG  | <br>HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ   | <br>RRPPLLPLLL<br>PKANTSQPGV<br>WFGATVRAHG   | LLLPPPPRVG<br>LQGGAVYLCP<br>SSILACAPLY   | <br>GFNLDAEAPA<br>WGASPTQCTP<br>SWRTEKEPLS  | VLSGPPGSFF<br>IEFDSKGSRL<br>DPVGTCYLST   |  |
| 45  | GFSVEFYRPG<br>LESSLSSSEG<br>DNFTRILEYA  | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWAA   | <br>RRPPLLPLLL<br>PKANTSQPGV<br>WFGATVRAHG<br>GQGYCQGGFS   | <br>LLLPPPPPRVG<br>LQGGAVYLCP  | GFNLDAEAPA<br>WGASPTQCTP<br>SWRTEKEPLS<br>LGGPGSYFWQ  | VLSGPPGSFF<br>IEFDSKGSRL<br>DPVGTCYLST<br>GQILSATQEQ   | 120<br>180   |
| 45  | GFSVEFYRPG<br>LESSLSSEG<br>DNFTRILEYA<br>IAESYYPEYL<br>GYVTILNGSD   | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWAA<br>INLVQGQLQT<br>IRSLYNFSGE   | RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV  | LLLPPPPRVG<br>LQGGAVYLCP<br>SSILACAPLY<br>AEFTKTGRVV<br>YLGYSVAVGE<br>AATDVNGDGL   | GFNLDAEAPA<br>WGASPTQCTP<br>SWRTEKEPLS<br>LGGPGSYFNQ<br>FSGDDTEDFV<br>DDLLVGAPLL  | <br>VLSGPPGSFF<br>IEFDSKGSRL<br>DPVGTCYLST<br>GQILSATQEQ<br>AGVPKGNLTY<br>MDRTPDGRPQ   | 120<br>180<br>240<br>300<br>360  |
|   | GFSVEPYRPG<br>LESSLSSEG<br>DNFTRILEYA<br>IAESYYPEYL<br>GYVTILNGSD<br>EVGRVYVYLQ   | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDPSWAA<br>INLVQGQLQT<br>IRSLYNPSGE<br>HPAGIEPTPT   | RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG   | LLLPPPPRVG<br>LQGGAVYLCP<br>SSILACAPLY<br>AEFTKTGRVV<br>YLGYSVAVGE<br>AATDVNGDGL<br>RFGSSLTPLG   | GFNLDAEAPA<br>WGASPTQCTP<br>SWRTEKEPLS<br>LGGPGSYFNQ<br>FSGDDTEDFV<br>DDLLVGAPLL<br>DLDQDGYNDV  | ULSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPRGNLTY MDRTPDGRPQ AIGAPPGGET   | 120<br>180<br>240<br>300<br>360<br>420   |
| <b>45</b><br><b>50</b>  | GFSVEFYRPG<br>LESSLSSSEG<br>DNFTRILEYA<br>IAESYYPEYL<br>GYVTILNGSD<br>EVGRVYVYLQ<br>QQGVVFVFPG  | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWA<br>INLVQGQLQT<br>IRSLYNFSGE<br>HPAGIEPTPT<br>GPGGLGSKPS  | RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS  | LLLPPPPRVG<br>LQGGAVYLCP<br>SSILACAPLY<br>ABFTKTGRVV<br>YLGYSVAVGE<br>AATDVNGDGL<br>RFGSSLTPLG<br>HTPDPFGSAL   | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFN PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG  | ULSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATGQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG   | 120<br>180<br>240<br>300<br>360<br>420<br>480  |
|   | GFSVEFYRPG<br>LESSLSSEG<br>DNFTRILEYA<br>IAESYYPEYL<br>GYVTILNGSD<br>EVGRVYVYLQ<br>QQGVVFVPPG<br>VDKAVVYRGR   | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWAA<br>INLVQGQLQT<br>IRSLYNFSGE<br>HPAGIEPTPT<br>GPGGLGSKPS<br>PIVSASASLT   | RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB   | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABFTKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV   | GFNLDAEAPA WGASPTQCTP WGASPTQCTP SWRTEKEPLS LGGPGSYFWQ FSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN   | VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGKHVADSI   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540   |
|   | GFSVEFYRPG<br>LESSLSSEG<br>DNPTRILEYA<br>IAESYYPEYL<br>GYVTILNGSD<br>EVGRVYVYLQ<br>QQGVVFVFPG<br>VDKAVVYRGR<br>GFTVELQLDW   | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWAA<br>INLVQGQLQT<br>IRSLYNFSGE<br>HPAGIEPTPT<br>GPGGLGSKPS<br>PIVSASASLT<br>QKQKGGVRRA   | RRPPLLPLLL PRANTSQPGV WPGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS LPPAMFNPEE LFLASRQATL  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ARETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA  | GFNLDAEAPA GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ FSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY  | VLSGPPGSFF IEFDSKGSRL DFVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGKRVADSI LRNESEFFDK  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540   |
| 50  | GFSVEFYRPG LESSLSSEG DNFTRILES IAESYYPEYL GYVTLNGSD EVGRVYVYLQ QQGVVFVFPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF  | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGSVRRA SLDPQAPVDS   | <br>RRPPLLIPLLL<br>PKANTSQPGV<br>WFGATVRAHG<br>GQGYCQGGFS<br>RQASSIYDDS<br>QMASYFGYAV<br>LTLTGHDEFG<br>QVLQPLWAAS<br>IFPAMFNPEE<br>LFLASRQATL<br>HGLRPALHYQ  | LILIPPPPRVG LQGAVYLCP SSILACAPLY ABFTKTGRVV YLGYSVAVGB AATDVNGDGL RFGSSLTPLG HTPDFFGSAL RSCELEGRPV TQTLLIQNGA SKSRIEDKAQ   | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFWQ FSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLB REDCREMKIY ILLDCGEDNI  | VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDKTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRWADSI LRNESSFRDK CVPDLQLEVF  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600  |
|   | GFSVEFYRPG LESSLSSEG DNFTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVFVFPG VDKAVVYRGR GFTVELQLDG LSFHIALNF GEQNHVYLGD  | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWAA<br>INLVGQLQT<br>IRSLYNPSGE<br>HPAGIEPTPT<br>GPGGLGSKPS<br>PIVSASASLT<br>QKQKGVRRA<br>SLDPQAPVDS<br>KNALNLTFHA   | RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB  | LLLPPPPRVG LQGAVYLCP SSILACAPLY ABFTKTGRVV YLGYSVAVGB AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ AELRVTAPPE   | GFNILDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFWQ FSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY LLLDCGEDNI AEYSGLVRHP  | VLSGPPGSFF UEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKSNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGKHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540   |
| 50  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRYVYLQ QQGVVFVPPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT GKQKGGVRRA SLDPQAPVDS KNALNLTFHA CDLGNPMKAG QVTLNGVSKP  | RRPPLIPLLL   RRPPLIPLL   PKANTSQPGV   WFGATVRAHG   GQGYCQGGFS   RQASSIYDDS   CMASYFGYAV   LTLTGHDEFG   QVLQPLWAAS   IPPAMFNPEE   LFLASRQATL   HGLRPALHYQ   QNVGESGAYE   ASLWGGLRFT   EAVLPPVSDW  | LILIPPPPRVG LIGACAPLY SSILACAPLY AEFTKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ AELRVTAPPE VPHLRDTKKT HPRDPPQKEE   | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFWQ FSGDDTEDFY DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLA REDCREMKIY ILLDCGEDNI AEYSGLVRHP IQPDFQLLSK DLGPAVHHVY   | VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDKTPDGRPQ AIGAPFGGET YPDLIVGSFG ASGKHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY MLNNSQSDVV ELINQSPSI   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660   |
| 50  | GFSVEFYRPG LESSLSSSED DNPYRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVFVFPG VDKAVVYRGR GFTVELQLDW LSPIHLAINF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVGGQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRAS SLIDPQAPVDS KNALNLTFHA CDLGNPMCAG QVTLINGVSG QVALEGQQLLY   | RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYE ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT   | LILIPPPPRVG LQGGAVYLCP SSILACAPLY ABFTKTGRVV YLGYSVAVGB AATDVNGDGL RFGSSLTPLG HTPDFFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL  | GFNILDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFWQ FSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP IQFDFQILSK DLGFAVHHVY ELDPEGSLHH   | VLSGPPGSFF VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGKHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900   |
| 50  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVFVFPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK  | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWAA<br>INLVQQQLQT<br>IRSLYNPSGE<br>HPAGIEPTPT<br>GPGGLGSKPS<br>FIVSASASLT<br>QKQKGGVRRA<br>SLDPQAPUDS<br>KNALMILTFFIA<br>CDLGNPMKAG<br>QVTLNGVSKP<br>QLEGQQLLY<br>QCLEGQCLY   | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS LFPAMFNPEE LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE   | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL SQSLQLHFRV  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI AEYSGLVRHP IQPDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH  | VLSGPPGSFF LEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNPSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960  |
| 50<br>55  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRYVYYLQ QQGVVFVPPG VDKAVVYRGR GFTVELQLDW LSPTHIALNF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQQQLQT IRSLYNFSGE HPAGIEPTPT QFGGLGSKPS PIVSASASLT QKQKGGYRRA SLDPQAPVDS KNALNLTYFIA CULKNPMKAG QVTLNGVSKP QALEGQQLLY CPEABCFFLIR LPRQLPQKER   | RRPPLIPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK   | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL SQSLQLHFRV  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI AEYSGLVRHP IQPDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH  | VLSGPPGSFF VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGKHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020   |
| 50  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRYVYYLQ QQGVVFVPPG VDKAVVYRGR GFTVELQLDW LSPTHIALNF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI   | HAVQLRWGPR<br>TDGVSVLVGA<br>EEPVEYKSLQ<br>PCRSDFSWAA<br>INLVQQQLQT<br>IRSLYNPSGE<br>HPAGIEPTPT<br>GPGGLGSKPS<br>FIVSASASLT<br>QKQKGGVRRA<br>SLDPQAPUDS<br>KNALMILTFFIA<br>CDLGNPMKAG<br>QVTLNGVSKP<br>QLEGQQLLY<br>QCLEGQCLY   | RRPPLIPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK   | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL SQSLQLHFRV  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI AEYSGLVRHP IQPDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH  | VLSGPPGSFF LEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNPSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960  |
| 50<br>55  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHLAINF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFPKRSL  | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSINNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNILTHA CDLGNPMKAG QVTLNGVSKP QALEGQQLLX CPEAECFRLR LPRQLPQKER PYGTAMEKAQ  | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYO QNVGEBGAYB ASLWGGLRFT EAVLPPVSUM VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPKEE TNHPLNFKGL SQSLQLHFRV AEGSYGVPLW  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI AEYSGLVRHP IQPDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH  | VLSGPPGSFF LEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNPSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020   |
| 50<br>55  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRYVYYLG QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFFKRSL SEQ ID NO:   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPVDS KNALNLTFHA CDLGNPMCAG QVTLNGVSKP QALEGQQLLY CPEABCFFLIR LPRQLPQKER PYGTAMEKAQ C219 Prote  | RRPPLIPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK   | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ AELRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGI TNHPINPKGI SQSIQLHFRV AEGSYGVPLW  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI AEYSGLVRHP IQPDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH  | VLSGPPGSFF LEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNPSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020   |
| 50<br>55<br>60  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRYVYYLG QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFFKRSL SEQ ID NO:   | HAVQLRWGPR TDGYSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNILTFRA CDLGNPMKAG QVTLNGVSKP QALESQQLLY CPEAECFRLR LPRQLPQKER PYGTAMEKAQ C219 Prote Cession #:   | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTCHDEFG QVLQPLWAAS LFPAMFNPEE LFLASRQATL HGLRPALHYQ QNYGEBGAYE ASLWGGLRFT EAVLPPVSGM VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL SQSLQLHFRV AEGSYGVPLW   | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP IQFDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH IIILAILFGL  | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DPVGTCYLST  GQILSATQEQ  AGVPKGNLTY  MDKTPDGRPQ  AIGAPFGGET  YPDLIVGSPG  ASGKHVADSI  LRNESSFRDK  CVPDLQLEVF  GNFSSLSCDY  MLNNSQSDVV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020   |
| 50<br>55  | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRYVYYLG QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFFKRSL SEQ ID NO:   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPVDS KNALNLTFHA CDLGNPMCAG QVTLNGVSKP QALEGQQLLY CPEABCFFLIR LPRQLPQKER PYGTAMEKAQ C219 Prote  | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMPNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ AELRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGI TNHPINPKGI SQSIQLHFRV AEGSYGVPLW  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI AEYSGLVRHP IQPDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH  | VLSGPPGSFF LEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNPSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020   |
| 50<br>55<br>60  | GFSVEFYRPG LESSLSSSEG DNFYRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVFVFPG VDKAVVYRGR GFTVELQLDW LSPTHIALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFPKRSL Seq ID NO: Protein Act   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT INSLYNFSGE HPAGIEPTPT QFGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPVDS KNALNLTFHA QVILNGVSKP QALEGQQLLY CPEAECFFLR PYGTAMEKAQ C219 Prote Cession #:  | RRPPLLPLLL RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVLQPLWAAS LFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLPPVSDW VTRYTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  | LILIPPPPRVG LILIPPPPRVG SSILACAPLY ABETKTGRVV YLGYSVAVGB AATDVNGDGL RFGSSLTPLG HTDDFFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ AELRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHB INPKGL SQSLQLHFRV AEGSYGVPLW  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP IQPDPQILSK DLGPAVHHYY ELDPEGSLHH WAKTFLQREH IIILAILFGL  | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DFVGTCYLST  GQILSATQEQ  AGVPKGNLTY  MDRTPPGRPQ  AIGAPFGGET  YPDLIVGSPG  ASGKHVADSI  LRNESEFRDK  CVPDLQLEVF  GNFSSLSCDV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>900<br>91020<br>1049   |
| 50<br>55<br>60  | GFSVEFYRPG LESSLSSSES DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVFPG VDKAVVYRGR GFTVELQLDW LSPIHLAINF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGFQILK YKALKMPYRI YKLGFFKRSL SEQ ID NO: Protein Act   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPVDS KNALNLTFFA CDLGNPMKAG QVTLNGVSKP QALESQQLLY CPEABCFRLR LPRQLPQKER PYGTAMEKAQ C219 Prote cession #:  11  LFWGVVSESF  | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WPGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTCHDEFG QVLQPLWAAS LFPAMPNPEE LFLASRQATL HGLRPALHYQ QNVGEGGAYE ASLWGGLRPT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHEINPKGL SQSLQLHFRV AEGSYGVPLW   | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ABYSGLVRHP IQFDFQILSK DLGPAVHHVY ELDPEGSLHH WAKTFLQREH IIILAILFGL   | VLSGPPGSFF UEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDKTPDGRPQ AIGAPFGGET YPDLIVGSPC ASGKHVADSI LRNESSFRDK CVPDLQLEVF GNFSSLSCDY NLNNSQSDVV ELINGGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51   VEKRRNSGPV  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | GFSVEFYRPG LESSLSSSEG DNFTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFPKRSL  Seq ID NO: Protein Acc  1   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPVDS KNALMLTFFA CDLGNPMKAG QVTLNGVSKP QALEGQQLLY CPEABCFFLR LPRQLPQKER PYGTAMEKAQ C219 Prote cession #:  11  LFWGVVSHSE FGLKVTGKFE   | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS LFPAMFNPEE LFLASRQATL HGLRPALHYQ QNVGEGGAYE ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF   | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLECNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF   | GFNLDAEAPA GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI IQFDFQILSK DLGPAVHHVY ELDPEGSLHH WARTPLQREH IIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE   | VLSGPPGSFF VLSGPPGSFF LEFDSKGSRL DFVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51   VEKRRNSGPV QTHLTYRIEN  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>960<br>900<br>91020<br>1049   |
| 50<br>55<br>60  | GFSVEFYRPG LESSLSSSEG DNFYRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QGGVVFVPPG VDKAVVYRGR GFTVELQLDW LSFHIALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILL YKLGPPKRSL Seq ID NO: Protein Act   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQQQLQTI IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPVDS KNALNLTFHA CDLGNPMKAG QVTLNGVSKP QALESQQLLY CPEARCFRLR LPRQLPQKER PYGTAMEKAQ C219 Prote cession #:  11   | RRPPLLPLLL RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1    PATLETQEQD AETLKVMKQF WSNVTPLTFT  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE ANTOVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLECENPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHEINPKGL SQSLQLHFRV ABGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF KVSECQADIM   | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 1QPDFQILSK DLGPAVHHYY ELDPEGSLHH WAKTPLQREH IIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD   | VLSGPPGSFF UEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDKTPDGRPQ AIGAPFGGET YPDLIVGSPC ASGKHVADSI LRNESSFRDK CVPDLQLEVF GNFSSLSCDY NLNNSQSDVV ELINGGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51   VEKRRNSGPV  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHLAINF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKNPYRI YKLGFPKRSL Seq ID NO: Protein Acc  1  | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSIYNPSGE HPAGIEPTPT GPGGLGSKPS SLDPQAPVDS KNALNITFFA CDLGNPMKAG QVTLNGVSKP QALEQQLLY LPRQLPQKER PYGTAMEKAQ LIP LFRGVVSHSE FGLKVTGKPE DHAIKAPDEL IGGDAHPDEL IGGDAHPDEL IGGDAHPDEL IGGDAHPDEL IGGDAHPDEL IGGDAHPDEL IGDDIGJIQATY  | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS LFPAMFNPEE LFLASRQATL HGLRPALHYQ GNYGESGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1 PATLETQEQD AETLKVMKQF WSNVTPLTFI ERWTNNFREY GRSQNFYQFI ERWTNNFREY  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINFGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQP KVSEQQADIM NLHRVAAHEL GPQTPKACDS   | GFNLDAEAPA GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI ILLDCGEDNI ILLDCGEDNI ILLDCGEDNI ILLDCGEDNI ILLALFGL WARTFLQREH IIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI  | VLSGPPGSFF VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51   VEKRRNSGPV QTHLTYRIEN NSPFDGFGGN NSPFDGFGGN NSPFDGFGGN RGEVMFFKDR  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | GFSVEFYRPG LESSLSSSEG DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNOSRLIV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKNFYRI YKLGPFKRSL  Seq ID NO: Protein Act  MHSPPPLLLL VEKLKQMQEF YTPDLPRADV LAHAFQPGED TFSGDVQLAQ FYMRTNFFYP   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSHPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNLTFHA CDLGNPMCAG QVTLNGVSKP QALEGQLLY LPRQLPQKER PYGTAMEKAQ  C219 Prote Cession #:  LFWGVVSHSE FGLKVTGKPL DHAIEKAPQI IGGDAHPDEI DDIDGIQATY EVELWFISVE  | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF WSNVTPLTFT ERWTNNFRBY GRSQNPVQFI CGRSQNPVQFI CGRSQNPVQFI CGRSQNPVQFI CGRSQNPVQFI  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ AELRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGI SQSIQLHFRV AEGSYGVPLW  31 VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL GPQTPFKACDS AYEFADRDEV  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ FSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI AEYSGLVRHP 10PDFQILSK DLGPAVHHYY ELDPEGSLHR IIILAILFGL  41  YYNLKNDGRQ VLTEENPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RFPKGNKYWA                       | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DFVGTCYLST  GQILSATOEQ  AGVPKGNLTY  MDRTPDGRPQ  AIGAPFGGET  YPDLIVGSFG  ASGKHVADSI  LRNESEFRDK  CVPDLQLEVF  GNFSSLSCDY  MLNNSGDVV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL  51  VEKRRNSGPV  QTHLTYRIEN  NSPPDGPGGN  DIGALMYPSY  RGEVMFPIOR  VQGQNVLHGY                                      | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1049  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | GFSVEFYRPG LESSLSSSES DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QGGVVFVPPG VDKAVVYRGR GFTVELQLDW LSPFHIALNF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFPKRSL  1   MHSFPPLLLL VEKLKQMQET TYPPDLPRADV LAHAFQPGPG TFSGDVQLAQ PYMRTNFPYP PKDIYSSFGF   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGYRRA SLDPQAPVDS KNALNLTYFHA CDLGNPMKAG QVTLNGVSKP QALEGQQLLY CPEASCFPLR LPRQLPQKER PYGTAMEKAQ 1  LFWGVVSHSE FGLKVVGKPD DHAIKKAPQI IGGDAHFDET DDIDGIQATY EVELMPISVE PRTVKHIDAP   | RRPPLIPLL RRPPLIPLL RRPPLIPLL RRPPLIPLL PKANTSQPGV WEGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVIQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1    PATLETQEQDD AETLKVMKQF WSNVTPLTFI ERWTNNFREY GRSQNFVQF WSNVTPLTFI VMPQLPNGLER VMPQLPNGLER VMPQLPNGLER VMPQLPNGLER LSEENTGKTY  | LILIPPPPRVG LILIPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVG ARTOVNGDGL RFGSSLTPLG HTDDFFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHBINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQP KVSEGQADIM NLHRVAAHEL GPQTPKACDS AYEFADRDEV FFVANKYWRY                  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 1QPDFQILSK DLGPAVHHYY ELDPEGSLHH WAKTFLQREH HIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RPFKGNKYWA DEYKRSMDPG           | VLSGPPGSFF VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51   VEKRRNSGPV QTHLTYRIEN NSPFDGFGGN NSPFDGFGGN NSPFDGFGGN RGEVMFFKDR  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GFSVEFYRPG LESSLSSSES DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QGGVVFVPPG VDKAVVYRGR GFTVELQLDW LSPFHIALNF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFPKRSL  1   MHSFPPLLLL VEKLKQMQET TYPPDLPRADV LAHAFQPGPG TFSGDVQLAQ PYMRTNFPYP PKDIYSSFGF   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGYRRA SLDPQAPVDS KNALNLTYFHA CDLGNPMKAG QVTLNGVSKP QALEGQQLLY CPEASCFPLR LPRQLPQKER PYGTAMEKAQ 1  LFWGVVSHSE FGLKVVGKPD DHAIKKAPQI IGGDAHFDET DDIDGIQATY EVELMPISVE PRTVKHIDAP   | RRPPLIPLL RRPPLIPLL RRPPLIPLL RRPPLIPLL PKANTSQPGV WEGATVRAHG GQGYCQGGFS RQASSIYDDS OMASYFGYAV LTLTGHDEFG QVIQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGESGAYB ASLWGGLRFT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1    PATLETQEQDD AETLKVMKQF WSNVTPLTFI ERWTNNFREY GRSQNFVQF WSNVTPLTFI VMPQLPNGLER VMPQLPNGLER VMPQLPNGLER VMPQLPNGLER LSEENTGKTY  | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ AELRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGI SQSIQLHFRV AEGSYGVPLW  31 VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL GPQTPFKACDS AYEFADRDEV  | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 1QPDFQILSK DLGPAVHHYY ELDPEGSLHH WAKTFLQREH HIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RPFKGNKYWA DEYKRSMDPG           | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DFVGTCYLST  GQILSATOEQ  AGVPKGNLTY  MDRTPDGRPQ  AIGAPFGGET  YPDLIVGSFG  ASGKHVADSI  LRNESEFRDK  CVPDLQLEVF  GNFSSLSCDY  MLNNSGDVV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL  51  VEKRRNSGPV  QTHLTYRIEN  NSPPDGPGGN  DIGALMYPSY  RGEVMFPIOR  VQGQNVLHGY                                      | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>960<br>1020<br>1049  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | GFSVEFYRPG LESSLSSSEG DNFTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVPPG VDKAVVYRGR GFTVELQLDW LSPIHLAINF GEQNHVYLGD FAVNOSRLIV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKNPYRI YKLGFPKRSL SEQ ID NO: Protein Acc  1  | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS SLDPQAPVDS KNALMLTFFA CDLGNPMKAG QVTLNGVSKPP QALEGQLLY CPEABCFFLR LPRQLPQKER PYGTAMEKAQ  11 LFWGVVSHSF FGLKVTGKPL DHAISKAFQL LIGGDAHFDEI DDIDGIQATY EVELNFISVE PRTVKHIDAF MKDGFFYFFE   | RRPPLLPLL RRPPLLPLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS LFPAMYNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF WSNVTPLTFI GRSQNFVQFI CRSQNFVQFI WPQLPNGLEF LSEENTGKTY GTRQYKFDPF   | LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLECNPV TQTLLIQNGA SKSRIEDKAQ AELRYTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF KVSEQADIM KVSEQADIM KVSEQADIM GPQTPKACDS AYEFADRDEV FFVANKYWRY                      | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 1QPDFQILSK DLGPAVHHYY ELDPEGSLHH WAKTFLQREH HIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RPFKGNKYWA DEYKRSMDPG           | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DFVGTCYLST  GQILSATOEQ  AGVPKGNLTY  MDRTPDGRPQ  AIGAPFGGET  YPDLIVGSFG  ASGKHVADSI  LRNESEFRDK  CVPDLQLEVF  GNFSSLSCDY  MLNNSGDVV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL  51  VEKRRNSGPV  QTHLTYRIEN  NSPPDGPGGN  DIGALMYPSY  RGEVMFPIOR  VQGQNVLHGY                                      | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GFSVEFYRPG LESSLSSSES DNFTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QOGVVFVFPG VDKAVVYRGR GFTVELQLDW LSPHHALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGPFKRSL  1     HISPPFLLLL VEKLKQMQEF YTPDLERADV LAHAFQPGPG TFSGDVQLAQ FYMRTNFFYP PKDIYSSFGF GIGHKVDAVF SEQ ID NO:   | HAVQLRWGPR HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQQQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSHPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNLTFHA CDLGNPMKAG QVTLNGVSKP QALEGQCLLY CPEARCFRLR LPRQLPQKER PYGTAMEKAQ C219 Prote Cession #:  LFWGVVSHSE FGLKVTGKPC DHAIEKAFQI IGGDAHFDET DDIDGIQAIY PRTVKHIDAF MKDGFFYFFE C220 Prote C220 Prote   | RRPPLLPLLL RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF WSNVTPLTFT CREWTINFRBY GRSQNPVQPI WPQLPNGLER LSEENTGKTY GTRQYKFDFR  | LILIPPPPRVG LILIPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVG ANTOVNGDGL RFGSSLTPLG HTDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHEINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL GPQTPKACDS AYEFADRDEV FFVANKYWRY TKRILTLQKA        | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 1QPDFQILSK DLGPAVHHYY ELDPEGSLHH WAKTFLQREH HIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RPFKGNKYWA DEYKRSMDPG           | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DFVGTCYLST  GQILSATOEQ  AGVPKGNLTY  MDRTPDGRPQ  AIGAPFGGET  YPDLIVGSFG  ASGKHVADSI  LRNESEFRDK  CVPDLQLEVF  GNFSSLSCDY  MLNNSGDVV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL  51  VEKRRNSGPV  QTHLTYRIEN  NSPPDGPGGN  DIGALMYPSY  RGEVMFPIOR  VQGQNVLHGY                                      | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GFSVEFYRPG LESSLSSSES DNFTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QOGVVFVFPG VDKAVVYRGR GFTVELQLDW LSPHHALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGPFKRSL  1     HISPPFLLLL VEKLKQMQEF YTPDLERADV LAHAFQPGPG TFSGDVQLAQ FYMRTNFFYP PKDIYSSFGF GIGHKVDAVF SEQ ID NO:   | HAVQLRWGPR HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQQQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNLTFHA CDLGNPMKAG QVTLNGVSKP QALEGQCLLY CPEARCFRIR LPRQLPQKER PYGTAMEKAQ C219 Prote Cession #:  LFWGVVSHSE FGLKVTGKPC DHAIEKAFQI IGGDAHFDET DDIDGIQAIY PRTVKHIDAF MKDGFFYFFE C220 Prote C220 Prote   | RRPPLLPLL RRPPLLPLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS LFPAMYNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF WSNVTPLTFI GRSQNFVQFI CRSQNFVQFI WPQLPNGLEF LSEENTGKTY GTRQYKFDPF   | LILIPPPPRVG LILIPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVG ANTOVNGDGL RFGSSLTPLG HTDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHEINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL GPQTPKACDS AYEFADRDEV FFVANKYWRY TKRILTLQKA        | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 1QPDFQILSK DLGPAVHHYY ELDPEGSLHH WAKTFLQREH HIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RPFKGNKYWA DEYKRSMDPG           | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DFVGTCYLST  GQILSATOEQ  AGVPKGNLTY  MDRTPDGRPQ  AIGAPFGGET  YPDLIVGSFG  ASGKHVADSI  LRNESEFRDK  CVPDLQLEVF  GNFSSLSCDY  MLNNSGDVV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL  51  VEKRRNSGPV  QTHLTYRIEN  NSPPDGPGGN  DIGALMYPSY  RGEVMFPIOR  VQGQNVLHGY                                      | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | GFSVEFYRPG LESSLSSSES DNFTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QOGVVFVFPG VDKAVVYRGR GFTVELQLDW LSPHHALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGPFKRSL  1     HISPPFLLLL VEKLKQMQEF YTPDLERADV LAHAFQPGPG TFSGDVQLAQ FYMRTNFFYP PKDIYSSFGF GIGHKVDAVF SEQ ID NO:   | HAVQLRWGPR HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQQQLQT IRSLYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNLTFHA CDLGNPMKAG QVTLNGVSKP QALEGQCLLY CPEARCFRIR LPRQLPQKER PYGTAMEKAQ C219 Prote Cession #:  LFWGVVSHSE FGLKVTGKPC DHAIEKAFQI IGGDAHFDET DDIDGIQAIY PRTVKHIDAF MKDGFFYFFE C220 Prote C220 Prote   | RRPPLLPLLL RRPPLLPLLL PKANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF WSNVTPLTFT CREWTINFRBY GRSQNPVQPI WPQLPNGLER LSEENTGKTY GTRQYKFDFR  | LILIPPPPRVG LILIPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVG ANTOVNGDGL RFGSSLTPLG HTDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHEINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL GPQTPKACDS AYEFADRDEV FFVANKYWRY TKRILTLQKA        | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 1QPDFQILSK DLGPAVHHYY ELDPEGSLHH WAKTFLQREH HIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RPFKGNKYWA DEYKRSMDPG           | VLSGPPGSFF  VLSGPPGSFF  IEFDSKGSRL  DFVGTCYLST  GQILSATOEQ  AGVPKGNLTY  MDRTPDGRPQ  AIGAPFGGET  YPDLIVGSFG  ASGKHVADSI  LRNESEFRDK  CVPDLQLEVF  GNFSSLSCDY  MLNNSGDVV  ELINQGPSSI  QQKREAPSRS  QPFSLQCEAV  LLLGLLIYIL  51  VEKRRNSGPV  QTHLTYRIEN  NSPPDGPGGN  DIGALMYPSY  RGEVMFPIOR  VQGQNVLHGY                                      | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>            | GFSVEFYRPG LESSLSSSES DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVFPG VDKAVVYRGR GFTVELQLIM LSPHHALNF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGFQILK YKALKMPYRI YKLGFPKRSL  1   MHSPPPLLLL VEKLKQMQET YTPDLERADV LAHAFQFGFG TFSGDVQLAQ PYMRTNPFYP PKDIYSSFGF GIGHKVDAVF  Seq ID NO: Protein Ac   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSIYNPSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNLIFFRA CDLGNPMKAG QVTLNGVSKP QALESQQLLY CPEABCFRLR LPRQLPQKER PYGTAMEKAQ 11 LFWGVVSHSF FGLKVTGKPE DHAIEKAPQLI DDIDGIQATY EVELNFISVE EVELNFISVE CC20 PROTEC CC20 PROTEC CC210 PROTEC CC210 PROTEC CC220 PROTEC CC220 PROTEC CC220 PROTEC CC230 PROTE | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WPGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMFNPEE LFLASRQATL HGLRPALHYQ QNVGEGGAYE ASLWGGLRFT EAVLFPVSUM CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD WSNVTPLTFI ERWTNNFREY GRSQNFVQPI WPQLPNGLE LSEENTGKTY GTRQYKFDPR  tin Sequence COS SECUENCE COS S | LLLPPPPRVG LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDDPQKEE TNHPINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL GPQTPKACDS AYEFADRDEV TKRILTLQKA                   | GFNLDAEAPA GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP IQFDFQILSK DLGPAVHHVY ELDPEGSLHH WARTFLQREH IIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISPVRGDHRD GHSLGLSHST KLTPDAITTI RFPKGNKYM DEYKRSMDPG NSWFNCRKN  | VLSGPPGSFF VLSGPPGSFF IEFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPC ASGKHVADSI LRNESSFRDK CVPDLQLEVF GNFSSLSCDY NLINNSQSDVV ELINGGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51 VEKRRNSGPV QTHLTYRIEN NSPPDGPGGN NSPPDGPGGN VQGQNVLHGY YPKMIAHDFP   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1020<br>1049   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | GFSVEFYRPG LESSLSSSES DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVFVFPG VDKAVVYRGR GFTVELQLDW LSFIHLAINF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGFQILK YKALKMPYRI YKLGFPKRSL  SEQ ID NO: Protein Acc  1   | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSIYNPSGE HPAGIEPTPT GPGGLGSKPS SLDPQAPVDS KNALNILTFIA CDLGNPMKAG QVTLNGVSKP QALEGQQLLY LPROLPQKER PYGTAMEKAQ LPROLPQKER PYGTAMEKAQ LFWGVVSHSE FGLKVTGKPL DHAIKAPQLL IGGDAHPDEL IGGDAHPDEL IGGDAHPDEL IGGDAHPDEL GGDAHPDEL C220 Prote Ceession #:  11   LFWGVVSHSE PRTVKHIDAP WKDGFFYFFE C220 Prote Ceession #:  | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS LFPAMFNPEB LFLASRQATL HGLRPALHYQ GNYGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF WSNVTPLTFT ERWTNNFREY GRSQNFVQPI CRSQNFVQPI CRSQNFVQP | LLLPPPPRVG LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGL SQSLQLHFRV AEGSYGVPLW  31 VDLVQKYLEK RCGVPDVAQF KVSEQADIM NLHRVAAHEL GPQTPKACDS AYEFADRDEV FFVANKYWKA SE 31   COVDLVQKYLEK | GFNLDAEAPA GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ PSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ILLDCGEDNI IQPDFQILSK DLGPAVHHVY LGPAVHHVY IYNLKNDGRQ VLTEGNPRWE ISFVRGDHRD GHSLGLSHST KLTFDAITTI RFFKGNKYWA DEYKRSMDFG NSWFNCRKN                   | VLSGPPGSFF VLSGPPGSFF UFFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNPSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51 VEKRRNSGPV QTHLTYRIEN NSPFDGPGGN DIGALMYPSY RGEVMFPKDR VQGQNVLHGY YPKMIAHDPP   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1049<br>60<br>120<br>180<br>240<br>300<br>360<br>429 |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | GFSVEFYRPG LESSLSSSEG DNFYRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVFVPPG VDKAVVYRGR GFTVELQLDW LSPHHALNF GEQNHVYLGD FAVNQSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQLLL YKALKYMYRI YKLGPPKRSL  1   HSFPFLLLL VEKLKQMQEF YTFDLFRADV LAHAFQPGPG TFSGDVQLAQ FYMRTMFFYP PKDIYSSFGF GIGHKVDAVF Seq ID NO: Protein Ac 1   CONTROL SEQ ID NO: Protein Ac 1   HSFPFLLLL VEKLKQMQEF ID NO: Protein Ac 1   HSFPPLLLL VEKLKQMQEF LAHAFQRGPG GIGHKVDAVF | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQTI IRSLYNPSGE HPAGIEPTPT GPGGLGSHPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS KNALNLTFHA CDLGNPMCAG QVTLNGVSKP QALEGQLLY LFRQLPQKER PYGTAMEKAQ  11 LFWGVVSHSE FGLKVTGKPE DDLDGLQATY EVELMFISVE PRTVKHIDAA MKDGFFYFFE  C220 Prote cession #:  11  | RRPPLLPLL RRPPLLPLL RRPPLLPLL PRANTSQPGV WFGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTGHDEFG QVLQPLWAAS IFPAMPNPEB LFLASRQATL HGLRPALHYQ QNVGEGGAYB ASLWGGLRFT EAVLFPVSDW VTRVTGLNCT CELGFLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD AETLKVMKQF WSNVTPLTFT CRGSQNPVQFI GRSQNPVQFI GRTQYKFDPR LSEENTGKTY GTRQYKFDPR LSEENTGKTY LTD PATLETQEQD AETLKVMKQF PATLETQEQD AETLKVMKQF   | LLLPPPPRVG LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE ANTOVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEXNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDQPQKEE TNHPINPKGI SQSLQLHFRV AEGSYGVPLW  31 VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL GPQTPFKACDS AYEFADRDEV FFVANKYWRY TKRILTLQKA         | GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ FSGDDTEDFV DDLLVGAPLL DLDQDGYNDV RGGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI AEYSGLVRHP 10PDFQ1LSK DLGPAVHHYY ELDPEGSLHH 11ILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE 1SFVRGDHRD GHSLGLSHST KLTFDAITTI RFPKGNKYWA DEYKRSMDPG NSWFNCRKN            | VLSGPPGSFF VLSGPPGSFF IEFDSKGSRL DFVGTCYLST GQILSATOEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSFG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNFSSLSCDY MLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51 VEKRRNSGPV QTHLTYRIEN NSPPDGPGGN DIGALMYPSY RGEVMPFIDR VQCQNVLHGY YPKMIAHDFP  51 VEKRRNSGPV QTHLTYRIEN VQCQNVLHGY YPKMIAHDFP | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>900<br>910<br>1049<br>60<br>120<br>180<br>240<br>300<br>420<br>469        |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | GFSVEFYRPG LESSLSSSES DNPTRILEYA IAESYYPEYL GYVTILNGSD EVGRVYVYLQ QQGVVPVFPG VDKAVVYRGR GFTVELQLDW LSPIHIALNF GEQNHVYLGD FAVNOSRLLV SFRLSVEAQA SQGVLELSCP SASSGPQILK YKALKMPYRI YKLGFPKRSL  1   MHSFPPLLLL VEKLKQMQEF TFSGDVQLAQ FYMRTNPFYP PKDIYSSFGF GIGHKVDAVF  Seq ID NO: Protein Ac  1   MHSFPPLLLL VEKLKQMGEF YTPDLPRADV  | HAVQLRWGPR TDGVSVLVGA EEPVEYKSLQ PCRSDFSWAA INLVQGQLQT IRSIYNFSGE HPAGIEPTPT GPGGLGSKPS PIVSASASLT QKQKGGVRRA SLDPQAPUDS SLDPQAPUDS KNALNLIFFIA CDLGNPMKAG QVILNGVSKP QALESQQLLY CPEABCFRLR LPRQLPQKER PYGTAMEKAQ 11   LFWGVVSHSF FGLKVTGKPE DHAIEKAPQI DDIDGIQATY EVELNFISVE CC220 Prote Ccession #:  11   CC220 Prote Ccession #:  12   CC220 Prote CC230 Prote CC250 Prote  | RRPPLLPLLL RRPPLLPLLL PRANTSQPGV WPGATVRAHG GQGYCQGGFS RQASSIYDDS QMASYFGYAV LTLTCHDEFG QVIQPLWAAS LIFPAMPNPEE LFLASRQATL HGLRPALHYQ QNVGEGGAYE ASLWGGLRPT EAVLPPVSDW VTRVTGLNCT CELGPLHQQE QVATAVQWTK LKPPATSDA in Sequence NP_002412.1  PATLETQEQD WSNVTPLTFI ERWTNNFREY GRSQNPVQPI WPQLPNGLEM LSEENTGKTY GTRQYKFDPR LSEENTGKTY GTRQYKFDPR LSEENTGKTY GTRQYKFDPR LSEENTGKTY GTRQYKFDPR LSEENTGKTY LSEENTGK | LLLPPPPRVG LLLPPPPRVG LQGGAVYLCP SSILACAPLY ABETKTGRVV YLGYSVAVGE AATDVNGDGL RFGSSLTPLG HTPDPFGSAL RSCSLEGNPV TQTLLIQNGA SKSRIEDKAQ ABLRVTAPPE VPHLRDTKKT HPRDDPQKEE TNHEINPKGL SQSLQLHFRV AEGSYGVPLW  31   VDLVQKYLEK RCGVPDVAQF KVSEGQADIM NLHRVAAHEL FFVANKYWRY TKRILTLQKA                              | GFNLDAEAPA GFNLDAEAPA WGASPTQCTP SWRTEKEPLS LGGPGSYFNQ DDLLVGAPLL DLDQDGYNDV RCGRDLDGNG ACINLSFCLN REDCREMKIY ILLDCGEDNI ASYSGLVRHP IQFDFQILSK DLGPAVHHVY ELDPEGSLHH WAKTFLQREH IIILAILFGL  41   YYNLKNDGRQ VLTEGNPRWE ISPVRGDHRD GNSLGLSHST KLTFDAITTI RPPKGNKYM ADEYKRSMDPG NSWFNCRKN | VLSGPPGSFF VLSGPPGSFF UFFDSKGSRL DPVGTCYLST GQILSATQEQ AGVPKGNLTY MDRTPDGRPQ AIGAPFGGET YPDLIVGSPG ASGRHVADSI LRNESEFRDK CVPDLQLEVF GNPSSLSCDY NLNNSQSDVV ELINQGPSSI QQKREAPSRS QPFSLQCEAV LLLGLLIYIL  51 VEKRRNSGPV QTHLTYRIEN NSPFDGPGGN DIGALMYPSY RGEVMFPKDR VQGQNVLHGY YPKMIAHDPP   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>1049<br>60<br>120<br>180<br>240<br>300<br>360<br>429 |

| 5          | TFSGDVQLAQ<br>FYMRTNPFYP<br>PKDIYSSFGP<br>GIGHKVDAVP | evelnfisvf<br>Prtvkhidaa                             | WPQLPNGLEA<br>LSEENTGKTY                              | AYEFADRDEV<br>FFVANKYWRY                             | RFFKGNKYWA<br>DEYKRSMDPG                             | VQGQNVLHGY   | 300<br>360<br>420<br>469               |
|------------|--|--|---|--|--|--|--|
|            | Seq ID NO:<br>Protein Acc                            |  |   |  |  |  |  |
| 10         | 1  | 11   | 21  | 31   | 41   | 51<br>1  |  |
| 15         | SMSVSWSARI<br>YGMYAYAGWF                             | QNTGSVGMSL<br>LLIIRPAATA<br>QIPLTFCKLT<br>YLNFVTEEVE | TIWTVCGVLS<br>VISLAFGRYI<br>AILIIIVPGV<br>NPEKTIPLAI  | LFGALSYAEL<br>LEPFFIQCEI<br>MQLIKGQTQN<br>CISMAITIGV | GTTIKKSGGH<br>PELAIKLITA<br>FKDAFSGRDS<br>YVLTNVAYPT | YTYILEVFGP<br>VGITVVMVLN<br>SITRLPLAFY<br>TINAEELLLS               | 60<br>120<br>180<br>240<br>300         |
|            | RKHTPLPAVI<br>FKVPLFIPAL                             | VLHPLTMIML   | IFVALSCFGS<br>PSGDLDSLLN<br>LSLYSDPFST<br>L           | FLSFARWLFI   | GLAVAGLIYL   | RYKCPDMHRP   | 360<br>420<br>480<br>501               |
| 20         | Seq ID NO:   | C222 Proteicesion #: 1                               | in Sequence   |  |  |  |  |
|            | 1  | 11   | 21  | 31   | 41   | 51   |  |
| 25         | IEDANLIPPV<br>SNGKAGTLDL                             | PDDKFQDLVD<br>SLTVQGKQHV                             | I PESGGDNSV<br>AVRAEKGFLL<br>VSVEEALLAT<br>KGGVNDNEGG | LASLRQMKKT<br>GQWKSITLFV                             | RGTLLALERK<br>QEDRAQLYID                             | DHSGQVFSVV   | 60<br>120<br>180<br>240                |
| 30         | TLDNNVVNGS<br>VTEENKELAN<br>ATVPDGECCP<br>RTCHIQECDK | SPAIRTNYIG<br>ELRRPPLCYH<br>RCWPSDSADD<br>RFKQDGGWSH | HKTKDLQAIC<br>NGVQYRNNEE<br>GWSPWSEWTS<br>WSPWSSCSVT  | GISCDELSSM<br>WTVDSCTECH<br>CSTSCGNGIQ<br>CGDGVITRIR | VLELRGLRTI<br>CQNSVTICKK<br>QRGRSCDSLN<br>LCNSPSPQMN | VTTLQDSIRK<br>VSCPIMPCSN<br>NRCEGSSVQT<br>GKPCEGEARE<br>CVGDVTENQI | 300<br>360<br>420<br>480<br>540        |
| 35         | CNKQDCPIDG<br>NHNGEHRCEN<br>AKCNYLGHYS<br>LPNSGQEDYD | CLSNPCFAGV<br>TDPGYNCLPC<br>DPMYRCECKP<br>KDGIGDACDD | KCTSYPDGSW<br>PPRFTGSQPF<br>GYAGNGIICG<br>DDDNDKIPDD  | KCGACPPGYS<br>GQGVEHATAN<br>EDTDLDGWPN<br>RDNCPFHYNP | GNGIQCTDVD<br>KQVCKPRNPC<br>ENLVCVANAT<br>AQYDYDRDDV | ECKEVPDACP<br>TDGTHDCNKN<br>YHCKKDNCPN<br>GDRCDNCPYN<br>DQCDNCPLEH | 600<br>660<br>720<br>780<br>840        |
| 40         | NPDQLDSDSD<br>DG1PDDKDNC<br>QM1PLDPKGT<br>DYAGFVFGYQ | RIGDTCDNNQ<br>RLVPNPDQKD<br>SQNDPNWVVR<br>SSSRPYVVMW | DIDEDGHQNN<br>SDGDGRGDAC<br>HQGKELVQTV<br>KQVTQSYWDT  | LDNCPYVPNA<br>KDDFDHDSVP<br>NCDPGLAVGY<br>NPTRAQGYSG | NQADHDKDGK<br>DIDDICPENV<br>DEFNAVDFSG<br>LSVKVVNSTT | GDACDHDDDN<br>DISETDFRRF<br>TFFINTERDD<br>GPGEHLRNAL<br>IMADSGPIYD | 900<br>960<br>1020<br>1080<br>1140     |
| 45         | KTYAGGRLGL<br>Seq ID NO:                             | FVFSQEMVFF<br>C223 Prote                             | SDLKYECRDP  |  |  |  | 1170                                   |
|            | Protein Ac   | cession #:   | NP_002183.1   |  |  |  |  |
| 50         |  |  |   |  |  | 51<br> <br>  QPEMVEAVKK<br>  AEMNELMEQT                            | 60<br>120                              |
| 55         | SEIITFAESG<br>HPQGSLDTGE<br>RIACEQCQES<br>EDHPHRRRR  | TARKTLHFEI EAEEVGLKGE GASLVLLGKE GLECDGKVNI          | SKEGSDLSVV<br>RSELLLSEKV<br>KKKBEBGEGI<br>CCKKQPFVSI  | PRAEVWLFLK VDARKSTWHV KKGGGEGGAG KDIGWNDWII          | VPKANRTRTK<br>PPVSSSIQRI<br>ADEEKEQSHR<br>APSGYHANYO | VTIRLFQQOK<br>LDQGKSSLDV<br>PFLMLQARQS<br>EGECPSHIAG<br>IKKDIQNMIV | 180<br>240<br>300<br>360<br>420<br>426 |
| 60         | BBCGCB   |  |   |  |  |  | 120                                    |
|            | Protein Ac   | cession #:   | in Sequence   | L  |  |  |  |
| 65         | ì  | 11<br>   | 21<br>}   | 31<br>   | 41   | 51<br>   |  |
| <b>5</b> 0 | FLKNTVMBCI<br>NGSHCTDVNI<br>INECETGQHI               | D ACGMQQSVR:<br>E CNAHPCFPR'<br>N CVPNSVCIN:         | r glpsvrplli<br>V rcintspgfi<br>r rgsfqcgpc           | CAPGFCFPGV<br>CEACPPGYSO<br>PGFVGDQASO               | / ACIQTESGGI<br>PTHQGVGLAI<br>CQRGAQRFCI             | WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH                        | 60<br>120<br>180<br>240                |
| 70         | EDVDRDGIGI<br>DTDQDGRGDI<br>VDHDFVGDA                | A CDDDIDGDR:<br>C DSDQDQDGDGD                        | 3 VPNEKDNCP:<br>I RNQADNCPR'<br>3 HQDSRDNCP'          | L VRNPDQRNTI<br>V PNSDQKDSD<br>I VPNSAQEDSI          | D EDKWGDACDI<br>D DGIGDACDI<br>D HDGQGDACDI          | NCVTVPNSGQ<br>CRSQKNDDQK<br>PQKSNPDQAD<br>DDDNDGVPDS               |  |
| 75         | PEGDAQIDPI<br>PGYQDSSSF<br>ESQVRLLWKI                | N WVVLNQGRE<br>Y VVMWKQMEQ<br>D PRNVGWKDK            | I VQTMNSDPG<br>T YWQANPFRA                            | L AVGYTAFNG<br>V AEPGIQLKA<br>P QVGYIRVRF            | V DPEGTFHVN<br>V KSSTGPGEQ                           | FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG                        | 540<br>600<br>660<br>720<br>757        |
| 80         |  | : C225 Prot<br>ccession #:                           | ein Sequenc<br>NP_612464                              | e  |  |  |  |
|            | 1  | 11   | 21<br>  | 31<br>   | 41<br>   | 51<br>   |  |
|            | 1  | •  | •   | •  | ' 1  | 1337   |  |
|            |  |  |   |  | 1  | 1337   |  |

| 5  | GVPGRDGSPG<br>GKIAECTFTK                                      | ANGIPGTPGI<br>MRSNSALRVL   | PGRDGFKGEK<br>FSGSLRLKCR  | SEIPKGKQKA<br>GBCLRESFEE<br>NACCQRWYFT<br>VAIWVGTCSD                       | SWTPNYKQCS<br>FNGAECSGPL   | WSSLNYGIDL<br>PIEAIIYLDQ   | 60<br>120<br>180<br>240<br>243         |
|----|---|--|---|--|--|--|--|
|    | -   | C226 Protei<br>ession #: N   | -   |  |  |  |  |
| 10 |   | 11<br> <br>ALVLVSMLAL<br>PNTIDVPPEE                                      | -   | 31<br> <br>CTVAPRERQN  | 41<br> <br>CGFPGVTFSQ  | 51<br> <br>CANKGCCFDD  | 60<br>84                               |
| 15 |   | C227 Protei  |   |  |  |  |  |
|    | 1   | 11   | 21  | 31   | 41   | 51   |  |
| 20 | nlgfnsiqal<br>Qtlqglsnlm                                      | SETSFAGLTK<br>RLHIDHNKIE   | LELLMIHGNE<br>FIHPQAFNGL  | CACYVPSEVH<br>IPSIPDGALR<br>TSLRLLHLEG<br>NLYLQGNPWT                       | DLSSLQVFKF<br>NLLHQLHPST   | SYNKLRVITG<br>FSTFTFLDYF   | 60<br>120<br>180<br>240                |
| 25 | CKKDKAYEGG<br>DGGSQLILEK<br>VALDFECPMT                        | QLCAMCFSPK<br>FQLPQWSISL<br>RENYEKLWKL                                   | KLYKHEIHKL<br>NMTDEHGNMV<br>IAYYSEVPVK                                  | KDMTCLKPSI<br>NLVCDIKKPM<br>LHRELMLSKD<br>VLLSYYTQYS                       | ESPLRQNRSR<br>DVYKIHLNQT<br>PRVSYQYRQD                                   | SIEEEQEQEE<br>DPPDIDINAT<br>ADEEALYYTG   | 300<br>360<br>420<br>480               |
| 30 | PSGAVQRDQT<br>RIKSMEPSDS<br>ALAIPEAHLS                        | VLEGGPCQLS<br>GLYQCIAQVR<br>WILPNRRIIN                                   | CNVKASESPS<br>DEMDRMVYRV<br>DLANTSHVYM                                  | IFWVLPDGSI<br>LVQSPSTQPA<br>LPNGTLSIPK<br>VREDIVEDEG                       | LKAPMDDPDS<br>EKDTVTIGKN<br>VQVSDSGYYR                                   | KFSILSSGWL<br>PGESVTLPCN<br>CVAVNQQGAD   | 540<br>600<br>660<br>720               |
| 35 | ERWADILAKV<br>SSADVPLLGE                                      | RGKNLPKGTE<br>EEHVLGTISS   | VPPLIKTTSP<br>ASMGLEHNHN  | EKEPETNVAE<br>PSLSLEVTPP<br>GVILVEPEVT<br>YEKPTHEETA                       | FPAVSPPSAS<br>STPLEEVVDD   | PVQTVTSAEE<br>LSEKTEEITS   | 780<br>840<br>900<br>960               |
| 40 | STIGEPGVPG<br>RSSESEGQES                                      | QSHLQGLTDN<br>KSITLPDSTL   | IHLVKSSLST<br>GIMSSMSPVK  | DKMKEDTFAH<br>QDTLLIKKGM<br>KPAETTVGTL<br>PTTFAPSETF                       | KEMSQTLQGG<br>LDKDTTTVTT   | nmlegdpths<br>tprokvapss   | 1020<br>1080<br>1140<br>1200           |
| 40 | VPTAWVDNTV<br>PENKHRNIVT<br>SDGKEIKDDV                        | NTPKQLEMEK<br>PSSETILLPR<br>ATNVDKHKSD                                   | NAEPTSKGTP<br>TVSLKTEGPY<br>ILVTGESITN                                  | RRKHGKRPNK<br>DSLDYMTTTR<br>AIPTSRSLVS                                     | HRYTPSTVSS<br>KIYSSYPKVQ<br>TMGEFKEESS                                   | RASGSKPSPS   | 1260<br>1320<br>1380<br>1440           |
| 45 | TTLSSIKVEV<br>MSLGQTTTTK<br>PSSDRDAFNL                        | ASSQAETTTL<br>PALPSPRISQ<br>STKLELEKQV                                   | DODHLETTVA<br>ASRDSKENVF<br>FGSRSLPRGP                                  | ILLSETRPQN<br>LNYVGNPETE<br>DSQRQDGRVH                                     | HTPTAARMKE<br>ATPVNNEGTQ<br>ASHQLTRVPA                                   | PASSSPSTIL<br>HMSGPNELST<br>KPILPTATVR<br>TIPLPLHMSK   | 1500<br>1560<br>1620<br>1680           |
| 50 | PQLGVTRRPQ<br>TNLQNIPMVS<br>QTVSVTAETD                        | IPTSPAPVMR<br>STQSSISFIT<br>TVFPCEATGE                                   | ERKVIPGSYN<br>SSVQSSGSFH<br>PKPFVTWTKV                                  | RIHSHSTFHL<br>QSSSKFFAGG<br>STGALMTPNT                                     | DFGPPAPPLL<br>PPASKFWSLG<br>RIQRFEVLKN                                   | PFFTNKTLSF HTPQTTGSPS EKPQILTKSP GTLVIRKVQV ECLAKGTPAP                                       | 1740<br>1800<br>1860<br>1920<br>1980   |
| 55 | HVAALPPVIE<br>VFPNGTLYIR<br>GGTLKLDCSA                        | QEKLENISLE<br>NLAPKDSGRY<br>SGDPWPRILW                                   | PGLSIHIHCT<br>ECVAANLVGS<br>RLPSKRMIDA                                  | AKAAPLPSVR<br>ARRTVQLNVQ<br>LPSFDSRIKV                                     | WVLGDGTQIR<br>RAAANARITG<br>FANGTLVVKS                                   | AGADSLAIRL PSQFLHGNLF TSPRRTDVRY VTDKDAGDYL PNPEISWSLP                                       | 2040<br>2100<br>2160<br>2220<br>2280   |
| 60 | DGSLVNSFMO<br>VVTAPATIRN<br>GTLLIQKAQF<br>RKLIDCKAEO          | SDDSGGRTKF<br>KTYLAVQVPY<br>SDSGNYTCLV<br>FIPTPRVLWAL                    | YVVFNNGTLY GDVVTVACEA RNSAGEDRKT PEGVVLPAPY                             | FNEVGMREEG<br>KGEPMPKVTW<br>VWIHVNVQPE<br>YGNRITVHGN                       | DYTCFAENOV<br>LSPTNKVIPI<br>KINGNPNPIT<br>GSLDIRSLRE                     | GKDEMRVRVK SSEKYQIYQD TVREIAAGGS SDSVQLVCMA TPSLVWVLPN                                       | 2340<br>2400<br>2460<br>2520<br>2580   |
| 65 | GTDLQSGQQI<br>KQYHNLVSII<br>ASVFDRGTY\<br>PKADITWELI          | ORFYHKADGN NGETLKLPC CRMETEYGPS  | LHISGLSSVI<br>PPGAGQGRPS<br>VTSIPVIVI                                   | AGAYRCVARN<br>WTLPNGMHLE<br>YPPRITSEP1                                     | AAGHTERLVS<br>GPQTLGRVSI<br>PVIYTRPGNT                                   | LKVGLKPEAN<br>LDNGTLTVRE<br>VKLNCMAMGI<br>MAKNILGSDS   | 2640<br>2700<br>2760<br>2820           |
| 70 |   |  | ein Sequence<br>Eos sequenc   |  |  |  | 2828                                   |
|    | 1<br> <br> <br>  MPGTKI,TRIN                                  | 11<br> <br>  APADYRVII   | 21<br> <br>K TSOEDELDVI   | 31<br>)<br>P DDISVRVMS   | 41<br> <br>  OSVLVSWVD   | 51<br> <br>P VLEKQKKVVA  | 60                                     |
| 75 | SRQYTVRYRI<br>TPESAPTTAI<br>FQNTFFHTPI                        | E KGELARWDY<br>P ENLNVWPVNO<br>R LSNHLEQSP                               | K QIANRRVLII<br>3 KPTVVAASW<br>8 PILETLLLP                              | B NLIPDTVYE<br>D ALPETEGKV<br>W WMVCSLGNA                                  | F AVRISQGERI<br>K VCLLDTGLF:<br>I FSKSGPQTG:                             | D GKWSTSVFQR<br>S VSSFQPSAKS<br>B AWDLTPKPSL<br>P MLDIGGPSFI                                 | 120<br>180<br>240<br>300               |
| 80 | MCYEDP?VS<br>PQGRNAKDL<br>SDTQDQKRT<br>SASPAHHAS<br>PSSVLRDRS | S LTGNSLKSV.<br>L LDLKNKILA<br>L RPPSRHGHS<br>T QGTSHRPSL<br>S VHPGAKPAS | A ASKADVQQN<br>N GGAPRKPQL<br>V VAPGRTAVR<br>P ASLNDNDLV<br>P ARRTPHSGA | T EDNGKPEKPER<br>R AKKAEELDLA<br>A RMPALPRRE<br>D SDEDERAVG<br>A EEDSSASAP | E PSSPSPRAPA<br>Q STEITGEEE<br>G VDKPGPSLA<br>S LHPKGAFAQ<br>P SRLSPPHGG | A SSQHPSVPAS<br>L GSREDSPMSP<br>T QPRPGAPPSA<br>P RPALSPSRQS<br>S SRLLPTQPHL<br>G ESHGDGDRED | 360<br>420<br>480<br>540<br>600<br>660 |
|    |   |  |   |  |  |  |  |

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GGROAEATAO TLRARPASGH FHLLRHKPFA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR
       AHPRVPSHSD SHPKLSSGIH GDEEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPQRG
                                                                                      780
       ASLHRKEPIP ENPKSTGADT HPQGKYSSLA SKAQDVQQST DADTEGHSPK AQPGSTDRHA
                                                                                      840
       SPARPPAARS QQHPSVPRRM TPGRAPDQQP PPPVATSQHH PGPQSRDAGR SPSQPRLSLT
QAGRPRPTSQ GRSHSSSDPY TASSRGMLPT ALQNQDEDAQ GSYDDDSTEV EAQDVRAPAH
                                                                                      900
 5
       AARAKEAAAS LPKHQQVESP TGAGAGGDHR SQRGHAASPA RPSRPGGPQS RARVPSRAAP
                                                                                      1020
        GKSEPPSKRP LSSKSQQSVS AEDEEEEDAG PFKGGKEDLL SSSVPKWPSS STPRGGKDAD
                                                                                      1080
        GSLAKEEREP AIALAPRGGS LAPVKRPLPP PPGSSPRASH VPSRPPPRSA ATVSPVAGTH
                                                                                      1140
       PWPRYTTRAP PGHFSTTPML SLRORMMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVLP
GSNGKPNGQR IINGPQGTKW VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDLE
                                                                                      1200
10
                                                                                      1260
        GTPVVSPDGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKKTTHP PTTTMQPTTT
                                                                                      1320
        TTPLPTTTTP RPTTATTMOP TTTTTPLPTT TPRPTTATTR RTTTRPTTT VRTTTRTTTT
                                                                                      1380
        TTPKPTTPIP TCPPGTLERH DDDGNLIMSS NGIPECYAEE DEFSGLETDT AVPTEEAYVI
                                                                                      1440
        YDEDYEFETS RPPTTTEPST TATTPRVIPE EGAISSFPEE EFDLAGRKRF VAPYVTYLNK
                                                                                      1500
15
        DPSAPCSLTD ALDHFQVDSL DEIIPNDLKK SDLPPQHAPR NITVVAVEGC HSFVIVDWDK
                                                                                      1560
                                                                                      1620
        ATPGDLVTGY LVYSASYEDF IRNKFSTQAS SVTHLPIENL KPNTRYYFKV QAQNPHGYGP
        ISPSVSFVTE SDNPLLVVRP PGGELSGSHS LSNMIPATRT AMDGNM
                                                                                      1666
        Seq ID NO: C229 Protein Sequence
20
        Protein Accession #: NP_003005.1
        MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ
                                                                                      60
25
        YEELVDVNCS AVLRFFFCAM YAPICTLEFL HDPIKPCKSV CQRARDDCEP LMKMYNHSWP
                                                                                      120
        ESLACDELPV YDRGVCISPE AIVTDLPEDV KWIDITPDMM VQERPLDVDC KRLSPDRCKC
                                                                                      180
        KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTQVPLITN
                                                                                      240
        SSCQCPHILP HODVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD
KKKTAGRTSR SNPPKPKGKP PAPKPASPKK NIKTRSAQKR TNPKRV
                                                                                      300
30
        Seq ID NO: C230 Protein Sequence
        Protein Accession #: NP 005931.1
35
        MAPAAWLRSA AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA
         PAPATQEAPR PASSLRPPRC GVPDPSDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ
                                                                                      120
        LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DGPGGILAHA FFPKTHREGD VHFDYDETWT IGDDQGTDLL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR
                                                                                       180
40
                                                                                       240
                                                                                       300
         YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA
         VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA
                                                                                       360
        QYWYYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHISTRRVDS
PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC
                                                                                       420
                                                                                       480
45
         Seq ID NO: C231 Protein Sequence
         Protein Accession #: NP_076927
50
                                             . 31
         MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI
         LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF
                                                                                       120
         TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK
                                                                                       180
 55
         VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH
                                                                                       240
         LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR
                                                                                       300
         LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA
                                                                                       360
         VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF
                                                                                       420
         GIGCAEVNKP GVYTRVTSFL DWIHEOMERD LKT
 60
         Seq ID NO: C232 Protein Sequence
         Protein Accession #: NP_003211
 65
         MLWKLTDNIK YEDCEDRHDG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP
         PYQPIYPQSQ DPYSHVNDPY SLNPLHAQPQ PQHPGWPGQR QSQESGLLHT HRGLPHQLSG
                                                                                       120
          LDPRRDYRRH EDLLHGPHAL SSGLGDLSIH SLPHAIEEVP HVEDPGINIP DQTVIKKGPV
                                                                                       180
         SLEKSNSNAV SAIPINKONI FGGVVNENEV FCSVPGRLSL LSSTSKYKVT VAEVQRRLSP
PECLNASLIG GVLRRAKSKN GGRSLREKLD KIGLNLPAGR RKAANVTLLT SLVEGEAVHL
                                                                                        240
 70
                                                                                        300
         ARDPGYVCET EPPAKAVABY LWRQHSDPNE QVTRKNMLLA TKQICKEFTD LLAQDRSPLG
NSRPNPILEP GIQSCLTHPN LISHGFGSPA VCAAVTALQN YLTEALKAMD KMYLSNNPNS
                                                                                        360
                                                                                        420
                                                                                        437
         HTDNNAKSSD KEEKHRK
 75
          Seq ID NO: C233 Protein Sequence
          Protein Accession #: NP_002979.1
                                               31
  80
          MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCPKPGVI
                                                                                        60
          LLTKRGRQIC ADPNKKWVQK YISDLKLNA
          Seq ID NO: C234 Protein Sequence
          Protein Accession #: NP_004054.1
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| 5<br>10<br>15 | MILQAHLHSL ELTGETDNIF DNRPTFLQSK QINNKTGAIS APKPVENVEN EEKDAYVPYA TLTAHDRDEE TIEVSDKDFK FTGSSKLLYH FGVKYNASSF SLRGDTRGWL NDNPPRLAKD INGTHARLST GIPTVGMAVG | CLLMLYLATG CLLMLYLATG CLLMLYLATG VIEREGLLYY YEGSVRQNSR LTREGSQELN STDPHPIKIT VAKDEYGKPL NTANSFLNYR TLCFVQINVI IIKGDSEGRL KIDHVTGEIF YTGLFFCHPL RHTEFEEREY ILLTTLLVIG | YGQEGKPSGP YGQEGKPSGP NRALDRETRS PGKPFLYVNA PAKNPSYNLV QVRWNDPGAQ SYPLEIHVKV IVEQTPKLPM DINDQIPIFE GVDTDPHTNT NEAPQFSQHV SVAPLDREAG SAPGSLIFEA VVLIRINDGG IILAVVFIRI | LEMPHTFSIYE THNLQVAALD TDLDDPATPN ISVKDMGGQS YSLVDKEKLP KDINDNPPTC DGLPLIQTYA KSDYGNLTLA GYVIIKKPLD FQAKVSEDVA SPYRVQVVAT TDDDQHLFRG RPPLEGIVSL | GGEPSQIIFQ ANGIIVEGPV GGLYYQIVIQ ENSPSOTTSV RFPPSIDQEG GREQLAKQSL EDTNIGSTIL FETRAVSNIV IGTKVGNVTA EVGGSSLSSV PHFTFSLGSG PHFTFSLGSG PYFFCSCVEG | PITIEVKDIN LPMINNVMYF DIIVTENIWK DIYVTQPLDR ENERLGNSIG KKQDTPQYNL TIQATDADEP FKAENPEPLV KDPEGLDISY SEFHLILMDV SLQNDWEVSK SCFRPAGHQT | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>832 |
|---------------|---|--|--|---|--|---|---|
| 20            |   | C235 Protei<br>ession #: N   |  |   | ·  |   |   |
|               | 1   | 11   | 21   | 31  | 41   | 51  |   |
| 25<br>30      | GWEEVSGYDE<br>NIPGSCKETF<br>FGPLSKAGFY<br>CIPNAVEVSV<br>CLPCPPNSRT  | AMNPIRTYQV<br>NLFYYEADSD<br>LAFQDQGACM<br>PLKLYCNGDG<br>TSPAASICTC   | PPLLLLPLLL CNVRESSONN VASASSPFWM SLISVRAFYK EWMVPVGACT HNNFYRADSD HGAGGASACS   | WLRTGFIWRR<br>ENPYVKVDTI<br>KCASTTAGFA<br>CATGHEPAAK<br>SADSACTTVP  | DVQRVYVELK<br>APDESFSRLD<br>LPPETLTGAE<br>ESQCRPCPPG<br>SPPRGVISNV   | FTVRDCNSIP<br>AGRVNTKVRS<br>PTSLVIAPGT<br>SYKAKQGEGP<br>NETSLILEWS  | 60<br>120<br>180<br>240<br>300<br>360<br>420  |
|               | YTFEVQAVNG<br>GVILDYEMKY<br>ETTSERGSGA  | VSGKSPLPPR<br>FEKSEGIAST<br>QQLQEQLPLI   | YAAVNITTNQ<br>VTSQMNSVQL<br>VGSATAGLVF   | AAPSEVPTLR<br>DGLRPDARYV<br>VVAVVVIAIV  | LHSSSGSSLT<br>VQVRARTVAG<br>CLRKQRHGSD   | LSWAPPERPN<br>YGQYSRPAEF<br>SEYTEKLQQY  | 480<br>540<br>600<br>660  |
| 35            | FVAIKTLKVG<br>SFLRLNDGQF<br>RFLEDDPSDP<br>DMSNQDVINA  | YTERQRRDFL<br>TVIQLVGMLR<br>TYTSSLGGKI<br>VEQDYRLPPP   | VREFAKEIDV<br>SEASIMGQFD<br>GIAAGMKYLS<br>PIRWTAPEAI<br>MDCPTALHQL<br>VPDYTTFTTV   | HPNIIRLEGV<br>EMNYVHRDLA<br>AYRKFTSASD<br>MLDCWVRDRN  | VTKSRPVMIL<br>ARNILVNSNL<br>VWSYGIVMWE<br>LRPKFSQIVN   | TEFMENCALD<br>VCKVSDFGLS<br>VMSYGERPYW<br>TLDKLIRNAA  | 720<br>780<br>840<br>900<br>960   |
| 40            | TAEDLLRIGV<br>Seq ID NO:  |  | SSIQDMRLQM<br>in Sequence  |   |  |   | 998   |
| 45            | 1   | 11   | 21   | 31  | 41   | 51  |   |
| 50            | MYVGYVLDKD<br>WGAPFPAPKD<br>TPSSPGAQRP<br>IRRKSELAAN  | SPVYPGPARP<br>DWAAAYGPGP<br>TPYEWMRRSV   | ASLGLGPANY<br>AAPAASPASL<br>AAGGGGGSGK<br>WFQNRRAKER   | <br>GPPAPPPAPP<br>AFGPPPDFSP<br>TRTKDKYRVV  | OYPDPSSYSH<br>VPAPPGPGPG<br>VTDHQRLELE   | VEPAPAPPTA<br>LLAQPLGGPG<br>KEPHYSRYIT<br>ITATPAGPSL  | 60<br>120<br>180<br>240<br>265  |
| 55            |   | cession #:   | in Sequence<br>NP_068813.1   |   |  |   |   |
| 60            | VLIGLLLVLL<br>KDALKLLYSG<br>LPPRARSLKS<br>HARCQWALRG  | GIGFLVWHLQ<br>VPPLGPYHKE<br>FVVTSVVAPP<br>DADSVLSLTF   | YRDVRVQKVF<br>SAVTAFSEGS<br>TDSKTVQRTQ<br>RSFDLASCDE   | NGYMRITNEN<br>VIAYYWSEFS<br>DNSCSFGLHA<br>RGSDLVTVYN  | FVDAYENSNS<br>IPQHLVEBAL<br>RGVELMRFTI<br>ITLSPMEPHAL  | 51<br>  GPGRWVVLAA<br>  TEFVSLASKV<br>  RVMAEERVVM<br>  PGFPDSPYPA<br>  VQLCGTYPPS  | 60<br>120<br>180<br>240<br>300  |
| 65            | PPNIDCTWNI<br>NSNKITVRFH<br>SDELNCSCDA<br>SQQCNGKDDO  | BVPNNQHVKV<br>SDQSYTDTGF<br>GHQFTCKNKF<br>GDGSDEASCE   | RFKFFYLLEF LABYLSYDSS CKPLFWVCDS KVNVVTCTKE  | GVPAGTCPKI DPCPGQFTCE VNDCGDNSDE TYRCLNGLCI   | YVEINGEKYO<br>R TGRCIRKELI<br>B QGCSCPAQTI<br>B SKGNPECDGI   | PNSPYYPGHY GERSQFVVTS CDGWADCTDH RCSNGKCLSK EDCSDGSDEK  | 420<br>480<br>540<br>600  |
| 70            | DRGFRYSDP1<br>AEYSSMVRP1  | CLPDASHVFF<br>CVGFLSGGVDS  | QSQRSAPGVQ<br>AGKAIWVTGW   | ERRLKRIISE<br>GHTQYGGTG/  | A LILQKGEIR  | V LVSAAHCYID V DIALLELEKP V INQTTCENLL C AQRNKPGVYT   | 660<br>720<br>780<br>840<br>855   |
| 75            |   |  | in Sequence<br>Eos sequenc   |   |  | •   |   |
| 80            | SVGKGSFER:<br>MVFKGGRTE<br>FAVGVRFPRI<br>PCEHRTLEM  | S KHFAITVCDX<br>I BLALKYLLHE<br>W EELHALASEI<br>V REFAGNAPCY   | G LDISPERVRY R GLPGGRNASY P RGQHVLLAE N RGSRRTLAV  | V GAFQFSSTP<br>V PQILIIVTD<br>Q VEDATNGLF<br>L AAHCPFYSW  | H LEFPLDSFS<br>G KSQGDVALP<br>S TLSSSAICS<br>K RVFLTHPAT   | 51   V DIMFLLDGSN T QQEVKARIKR S KQLKERGVTV S ATFDCRVEAH C YRTTCPGPCD S SAGTTLDGFL  | 60<br>120<br>180<br>240<br>300<br>360   |

| 5            | RAKVFVKRFV<br>LTGSALRQAA<br>EAVRABLEBI<br>SVGPENFAQM<br>APYLGGVGSA<br>SVLVVGVGPV<br>CMNEGSCVLQ | ERGFGSATRT<br>TGSPKHVMVY<br>QSFVRSCALQ<br>GTALLHIYDK<br>LSEGLRRLAG               | GQDRPRRVVV<br>SDPQDLFNQI<br>FEVNPDVTQV<br>VMTVQRGARP<br>PRDSLIHVAA               | LLTESHSEDE<br>PELQGKLCSK<br>GLVVYGSQVQ<br>GVPKAVVVLT<br>YADLRYHQDV               | VAGPARHARA<br>QRPGCRTQAL<br>TAFGLDTKPT<br>GGRGAEDAAV                             | rellligvgs<br>Dlvfmldtsa<br>Raamlraisq<br>Paqklrnngi   | 420<br>480<br>540<br>600<br>660<br>720<br>755       |
|--------------|--|--|--|--|--|--|---|
| 10           |  | C239 Protei<br>ession #: E   |  | :  |  |  |   |
| 15           | MPPFLLLEAV<br>SVGKGSFERS<br>MVFKGGRTET<br>FAVGVRFPRW<br>PCEHRTLEMV                             | <br>CVFLFSRVPP<br>KHPAITVCDG<br>ELALKYLLHR<br>EELHALASEP<br>REFAGNAPCW           | LDISPERVRV<br>GLPGGRNASV<br>RGQHVLLAEQ<br>RGSRRTLAVL                             | GAFQFSSTPH<br>PQILIIVTDG<br>VEDATNGLFS<br>AAHCPFYSWK                             | LEFPLDSFST<br>KSQGDVALPS<br>TLSSSAICSS<br>RVFLTHPATC                             | QQEVKARIKR<br>KQLKERGVTV<br>ATPDCRVEAH<br>YRTTCPGPCD   | 60<br>120<br>180<br>240<br>300                      |
| 20           | rakvfykrfy<br>Ltgsalrqaa<br>Eavraeleei   | TGSPKHVMVY   | RVGVATYSRE<br>GQDRPRRVVV<br>SDPQDLFNQI   | LLVAVPVGEY<br>LLTESHSEDE<br>PELQGKLCSR   | QDVPDLVWSL<br>VAGPARHARA<br>QRPGCRTQAL   |  | 360<br>420<br>480<br>540<br>600                     |
| 25           | APYLGGVGSA<br>SVLVVGVGPV<br>CMNEGSCVLQ   | GTALLHIYDK<br>LSEGLRRLAG   | VMTVQRGARP<br>PRDSLIHVAA<br>GWEGPHCENR   | GVPKAVVVLT<br>YADLRYHQDV   | GGRGAEDAAV<br>LIEWLCGEAK   | PAQKLRNNGI<br>QPVNLCKPSP<br>HMAPVQEGSS   | 660<br>720<br>780<br>807                            |
| 30           |  | C240 Protei<br>cession #: 2  |  |  |  |  |   |
| 35           | PSGCVCVSGI<br>EKEVAEGSGH   | LRVVSVGDPA   | SRRWVDLDSN<br>RVYGARSWIL   | SEDLSLLLTP<br>GRKPCLQRLL   | MIVGTGGVGG   | 51<br> -<br>GRAGSRAGSS<br>GWARGWVPAQ<br>PCPSPATACR   | 60<br>120<br>180<br>217                             |
| 40           |  | C241 Protes  |  |  |  |  |   |
| <b>45 50</b> | LWWEQKHCWL<br>VSDICKILNI<br>GLYSKTMTPI<br>VDKAKLNAGW<br>LLEEIDCTER<br>SLLEDITDIP               | LKTHWTLDKY<br>RRSEBLSLLK<br>YDPINGTPAS<br>LDSSRSLMEQ<br>EMLIPAALQY<br>KLADNLKLFR | GVQADAKLLF<br>PSGDYFKKKK<br>STMTWFSDSP<br>GIQEDEQLLL<br>HISKLSLSAE<br>PKKLLPKAFK | TPQHKMLRLR<br>KKDKNNKEPI<br>LTEQNCSILA<br>RFKYYSPFDL<br>TQDFAGESEV<br>QYWPIFKDTS | LPNLKMVRLR<br>IEDILNLESS<br>FSQPPQSPEA<br>NPKYDAVRIN<br>DEIEAALSNL<br>IAYFKNKELE | 51<br>  NISQDWSDFA<br>VSFSAVVFKA<br>PTASGSSVSP<br>LADMYQPRSL<br>QLYEQARWAI<br>EVTLEGGKAD<br>QGEPLEKLNL<br>ASKGKTMADS | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480 |
| 55           | SYQPEVLNIL<br>QNVAQMPLVE   | SFLRMKNRNS<br>AKLRFIQAWQ<br>QWNVNWETRQ   | ASQVASSLEN<br>SLPEFGLTYY   | MDMNPECFVS<br>LVRFKGSKKD   | PRCAKKHKSK<br>DILGVSYNRL   | QLAARILEAH<br>IKIDAATGIP<br>IFLSTRSKDQ   | 540<br>600<br>660<br>677                            |
| 60           | Nucleic Ac   | C242 DNA S<br>id Accessio<br>uence: 337.   | n. #: NM_005   | 170  |  |  |   |
| 65           | GCCGCCTGCG<br>CGTCCCACGC<br>AGACGACCTA   | COGCGCCTGC<br>TCCCTGGCGC<br>GGACGCGTGC   | GGAGACCTGC<br>GTACGGCCTC<br>CCTGGGGAGT   | GAGAGTCCGG<br>CCACCACTAG<br>TGCCTGGCGG   | CCCCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC   | 51<br>  TTAAAAACCA<br>  GGGACACGAG<br>  CCCGGGCTCC<br>  GAAGCCCCT<br>  CCTGCGGCGC                                    |   |
| 70           | GCCGGGACCT<br>TCCGCGCCCC<br>CCGGAACTGT   | GGAGCGGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCC   | GGTGGATGCI<br>CGTCCCTGTC<br>CCGGCGGCGCG  | GGCGCGATGC<br>GGCTGCGCTC<br>GCGACCGGCC   | ACGGCGGCAC<br>CCCGGCGGAC<br>CCGCAGAGAC   | ACTGCCCAGG<br>ACCCGCGTCC<br>CGGAGGCGGC<br>GGTGAACTTG   | 360<br>420<br>480                                   |
| 75           | GGCTTCCAGC GTGGAGACGC CACGACGCCCGCC GCGCCCCGGCC TCCCCGGGCC                                     | GCCGCGCACCCCCACCCCCCCCCCCCCCCCCCCCCCCC   | A GCACGTGCCC CGTGGAGTAC GCTGGCGGGG GACCACCCCC GCTCGGAGCCC GCTGAGTCC              | CACGGGGGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCC   | CCAGCAAGA/<br>TGCAGCGCCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCC                            | A GCTGAGCAAG T GCTGGCCGAG T GCGGCCGTCT G CGCTTCTTCG A CTCGTCGGAC A CTTCTCCAGC  | 600<br>660<br>720<br>780<br>840                     |
| 80           |  | : C243 Prote   |  |  |  |  |   |
|              | 1  | 11   | 21   | 31   | 41   | 51   |   |

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MSGGHQLQLA ALWPWLLMAT LQAGFGRTGL VLAAAVESER SAEQKAVIRV IPLKMDPTGK
        LNLTLEGVFA GVAEITPAEG KLMQSHPLYL CNASDDDNLE PGFISIVKLE SPRRAPRPCL
                                                                                      120
       SLASKARMAG ERGASAVLFD ITEDRAAAEQ LQQPLGLTWP VVLIWGNDAE KLMEFVYKNQ
KAHVRIELKE PPAWPDYDVW ILMTVVGTIF VIILASVLRI RCRPRHSRPD PLQQRTAWAI
                                                                                      180
 5
        SQLATRRYQA SCRQARGEWP DSGSSCSSAP VCAICLEEFS EGQELRVISC LHEFHRNCVD
                                                                                      300
        PWLHQHRTCP LCVFNITEGD SFSQSLGPSR SYQEPGRRLH LIRQHPGHAH YHLPAAYLLG
                                                                                      360
        PSRSAVARPP RPGPFLPSQE PGMGPRHHRF PRAAHPRAPG EQQRLAGAQH PYAQGWGMSH
                                                                                      420
        LOSTSOHPAA CPVPLRRARP PDSSGSGESY CTERSGYLAD GPASDSSGP CHGSSSDSVV
                                                                                      480
10
        NCTDISLOGV HGSSSTFCSS LSSDFDPLVY CSPKGDPQRV DMQPSVTSRP RSLDSVVPTG
        ETQVSSHVHY HRHRHHHYKK RFQWHGRKPG PETGVPQSRP PIPRTQPQPE PPSPDQQVTG
                                                                                      600
        SNSAAPSGRL SNPQCPRALP EPAPGPVDAS SICPSTSSLF NLQKSSLSAR HPQRKRRGGP
                                                                                      660
        SEPTPGSRPO DATVHPACQI FPHYTPSVAY PWSPEAHPLI CGPPGLDKRL LPETPGPCYS
                                                                                      720
        NSQPVWLCLT PROPLEPHPP GEGPSEWSSD TAEGRPCPYP HCQVLSAQPG SEEELEELCE
15
        Seg ID NO: C244 DNA Seguence
        Nucleic Acid Accession #: NM_004289
        Coding sequence: 493..1695
20
                                                                        51
                                  21
                                              31
        GCCGCCGCCT CGTCCACCGG AGGAGCCGGC GCCAGCGTGG ACGGCGGCAG CCAGGCTGTG
                                                                                       60
        CAGGGGGGG GCGGGACCC CCGAGCGGCT CGGAGTGGCC CCTTGGACGC CGGGGAAGAG
                                                                                       120
25
        GAGAAGGCAC CCGCGGAACC GACGGCTCAG GTGCCGGACG CTGGCGGATG TGCGAGCGAG
                                                                                       180
        GAGAATGGGG TACTAAGAGA AAAGCACGAA GCTGTGGATC ATAGTTCCCA GCATGAGGAA
                                                                                       240
        AATGAAGAAA GGGTGTCAGC CCAGAAGGAG AACTCACTTC AGCAGAATGA TGATGATGAA
AACAAAATAG CAGAGAAACC TGACTGGGAG GCAGAAAAGA CCACTGAATC TAGAAATGAG
AGACATCTGA ATGGGACAGA TACTTCTTTC TCTCTGGAAG ACTTATTCCA GTTGCTTTCA
                                                                                       300
                                                                                       360
                                                                                       420
30
        TCACAGCCTG AAAATTCACT GGAGGGCATC TCATTGGGAG ATATTCCTCT TCCAGGCAGT
                                                                                       480
        ATCAGTGATG GCATGAATTC TTCAGCACAT TATCATGTAA ACTTCAGCCA GGCTATAAGT CAGGATGTGA ATCTTCATGA GGCCATCTTG CTTTGTCCCA ACAATACATT TAGAAGAGAT
                                                                                       540
                                                                                       600
        CCAACAGCAA GGACTTCACA GTCACAAGAA CCATTTCTGC AGTTAAATTC TCATACCACC
        AATCCTGAGC AAACCCTTCC TGGAACTAAT TTGACAGGAT TTCTTTCACC GGTTGACAAT
                                                                                       720
35
         CATATGAGGA ATCTAACAAG CCAAGACCTA CTGTATGACC TTGACATAAA TATATTTGAT
                                                                                       780
         GAGATAAACT TAATGTCATT GGCCACAGAA GACAACTTTG ATCCAATCGA TGTTTCTCAG
         CTTTTTGATG AACCAGATTC TGATTCTGGC CTTTCTTTAG ATTCAAGTCA CAATAATACC
                                                                                       900
         TCTGTCATCA AGTCTAATTC CTCTCACTCT GTGTGTGATG AAGGTGCTAT AGGTTATTGC
                                                                                       960
         ACTGACCATG AATCTAGTTC CCATCATGAC TTAGAAGGTG CTGTAGGTGG CTACTACCCA
                                                                                       1020
40
         GAACCCAGTA AGCTITGTCA CTTGGATCAA AGTGATTCTG ATTTCCATGG AGATCTTACA
                                                                                       1080
         TTTCAACACG TATTTCATAA CCACACTTAC CACTTACAGC CAACTGCACC AGAATCTACT
                                                                                       1140
         TCTGAACCTT TTCCGTGGCC TGGGAAGTCA CAGAAGATAA GGAGTAGATA CCTTGAAGAC
                                                                                       1200
                                                                                       1260
         ACAGATAGAA ACTTGAGCOG TGATGAACAG CGTGCTAAAG CTTTGCATAT CCCTTTTTCT
         GTAGATGAAA TTGTCGGCAT GCCTGTTGAT TCTTTCAATA GCATGTTAAG TAGATATTAT
                                                                                       1320
45
         CTGACAGACC TACAAGTCTC ACTTATCCGT GACATCAGAC GAAGAGGGAA AAATAAAGTT
                                                                                       1380
         GCTGCGCAGA ACTGTCGTAA ACGCAAATTG GACATAATTT TGAATTTAGA AGATGATGIA
TGTAACTTGC AAGCAAAGAA GGAAACTCTT AAGAGAGAGC AAGCACAATG TAACAAAGCT
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                                                                                       1440
                                                                                       1500
                                                                                       1560
         GATGACCAAG GTAGGCCAGT CAATCCCAAC CACTATGCTC TCCAGTGTAC CCATGATGGA
                                                                                       1620
 50
         AGTATCTTGA TAGTACCCAA AGAACTGGTG GCCTCAGGCC ACAAAAAGGA AACCCAAAAG
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                                                                                       1740
         GAAACTGATT ATTTGGATCA GAAACCATTG AAACTGCTTC AAGAATTGTA TCTTTAAGTA
                                                                                        1800
         CTGCTACTTG AATAACTCAG TTAACGCTGT TTTGAAGCTT ACATGGACAA ATGTTTAGGA
                                                                                       1860
         CTTCAAGATC ACACTTGTGG GCAATCTGGG GGAGCCACAA CTTTTCATGA AGTGCATTGT
                                                                                       1920
 55
         ATACAAAATT CATAGTTATG TCCAAAGAAT AGGTTAACAT GAAAACCCAG TAAGACTTTC
                                                                                       1980
         CATCTTGGCA GCCATCCTTT TTAAGAGTAA GTTGGTTACT TCAAAAAGAG CAAACACTGG
                                                                                       2040
         GGATCARATT ATTITAAGAG GTATTTCAGT TTTAAATGCA ARATAGCCTT ATTITCATTT
AGTITGTIAG CACTATAGTG AGCTTTTCAA ACACTATTTT ARTCTTTATA TTTAACTTAT
                                                                                       2100
                                                                                        2160
         AAATTTTGCT TTCT
 60
         Seg ID NO: C245 Protein Seguence
         Protein Accession #: NP_004433
                                                            41
                                                                         51
 65
         MALRRIGAAL LLLPLLAAVE ETLMDSTTAT AELGWMVHPP SGWEEVSGYD ENMYTIRTYQ
          VCNVFESSON NWLRTKFIRR RGAHRIHVEM KFSVRDCSSI PSVPGSCKET FNLYYYEADF
                                                                                        120
         DSATKTPPNW MENPWVKVDT IAADESFSQV DLGGRVMKIN TEVRSFGPVS RSGFYLAFQD
                                                                                        180
          YGGCMSLIAV RVFYRKCPRI IONGAIFOET LSGAESTSLV AARGSCIANA EEVDVPIKLY
                                                                                        240
 70
         CNGDGEWLVP IGRCMCKAGF EAVENGTVCR GCPSGTFKAN QGDBACTHCP INSRTTSEGA
          TNCVCRNGYY RADLDPLDMP CTTIPSAPQA VISSVNETSL MLEWTPPRDS GGREDLVYNI
                                                                                        360
         ICKSCGSGRG ACTRCGDNVQ YAPRQLGLTE PRIYISDLLA HTQYTFEIQA VNGVTDQSPF
SPQFASVNIT TNQAAPSAVS IMHQVSRTVD SITLSWSQPD QPNGVILDYE LQYYEKELSE
                                                                                        420
                                                                                        480
          YNATAIKSPT NTVTVQGLKA GAIYVFQVRA RTVAGYGRYS GKMYFQTMTE AEYQTSIQEK
 75
          LPLIIGSSAA GLVFLIAVVV IAIVCNRRRG FERADSEYTD KLQHYTSGHM TPGMKIYIDP
                                                                                        600
          PTYEDPNEAV REFAKEIDIS CVKIEQVIGA GEFGEVCSGH LKLPGKREIF VAIKTLKSGY
                                                                                        660
          TEKORROPLS EASIMGOFOH PNVIHLEGVV TKSTPVMIIT EFMENGSLDS PLRONDGOFT
                                                                                        720
          VIQLVGMLRG IAAGMKYLAD MNYVHRDLAA RNILVNSNLV CKVSDFGLSR FLEDDTSDFT
                                                                                        780
          YTSALGGKIP IRWTAPEAIQ YRKFTSASDV WSYGIVMWEV MSYGERPYWD MTNQDVINAI
                                                                                        840
  80
          EODYRLPPPM DCPSALHOLM LDCWOKDRNH RPKFGQIVNT LDKMIRNPNS LKAMAPLSSG
                                                                                        900
          INLPLLDRTI PDYTSFNTVD EWLEAIKMGQ YKESFANAGF TSFDVVSQMM MEDILRVGLT
          LAGHOKKILN SIOVMRAOMN OIOSVEV
                                                                                        987
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Protein Accession #: NP 114148.1 5 MDARRYPOKD LRVKKYLKKF RYVKLISMET SSSSDDSCDS FASDNFANTR LQSVREGCRT RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSENSVT DSNSDSEDES GMNPLEKRAL 120 NIKONKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180 TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR 240 PVEEITEGGV GERLQQFSKR RYITVHWALL VINAVRRLLI PKQTAETQTA GAFEASSVAP AFETVMVKRS GMLCWIRTGI ARLVEBSATA VSAGSEMDGV RLGSLCI 300 10 Seq ID NO: C247 Protein Sequence Protein Accession #: NP\_036577.1 15 MENPSPAAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60 PLFRPPAQWS SLLGAAHSSD YSMWRKNQYV SNGLRDFAER GEAWALMKEI EAAGEALQSV 120 HAVFSAPAVP SGTGQTSAEL EVQRRHSLVS FVVRIVPSPD WFVGVDSLDL CDGDRWREQA 180 20 ALDLYPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT 240 LURLROSPRA PIPPAPULPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTKS 300 RTRYVRVQPA NNGSPCPELE EEAECVPDNC V 331 Seq ID NO: C248 Protein Sequence 25 Protein Accession #: NP\_063947.1 31 MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 30 YFLCGOPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120 GNWFSACTON FTEALAETAC ROMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS GPCLSGSLVS LHCLACGKSL KTPRVVGGEB ASVDSWPWQV SIQYDKQHVC GGSILDPHWV 180 240 LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL 300 TFSGTVRPIC LPFFDEELTP ATPLWIIGWG PTKONGGKMS DILLQASVQV IDSTRCNADD AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 360 35 420 KVSAYLNWIY NVWKAEL Seq ID NO: C249 Protein Sequence Protein Accession #: NP\_003036.1 40 MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLAGAVARE NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNLILS 45 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT 180 LGVKESAMVN KIFTCINVLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKEG 240 KPGVGGFMPF GPSGVLSGAA TCFYAFVGFD CIATTGEEVK NPQKAIPVGI VASLLICPIA YFGVSAALTL MMPYPCLDNN SPLPDAFKHV GWEGAKYAVA VGSLCALSAS LLGSMFFMPR 300 360 VIYAMAEDGL LPKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLVD LMSIGTLLAY 420 50 SLVAACVIVL RYQPEQPNLV YQMASTSDEL DPADQNELAS TNDSQLGFLP EAEMFSLKTI LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGREA LTKGALWAVF LLAGSALLCA 480 540 VVTGVIWRQP ESKTKLSFKV PFLPVLPILS IFVNVYLMMQ LDQGTWVRFA VWMLIGFIIY 600 FGYGLWHSEE ASLDADQART PDGNLDQCK 629 55 Seg ID NO: C250 Protein Seguence Protein Accession #: NP\_002767.1 41 51 60 MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPWQ VSLFNGLSFH CAGVLVDQSW VLTAAHGENK PLWARVGDDH LLLLQGEQLR RTTRSVVHPK YHQGSGPILP RRTDEHDLML LKLARPVVPG PRVRALQLPY RCAQPGDQCQ VAGMGTTAAR 120 180 RVKYNKGLTC SSITILSPKE CEVFYPGVVT NUMICAGLDR GQDPCQSDSG GPLVCDBTLQ 240 GILSWGVYPC GSAQHPAVYT QICKYMSWIN KVIRSN 276 65 Seg ID NO: C251 Protein Seguence Protein Accession #: XP\_095088.3 70 MTRAATAEPG RVSPASPARS TAGLPRAPLQ SLRTLLDILD DWQRGCVHLR EIQSLWVEAR ELPSGVLEGL SQRRGPQPGA AVRSRRGGAV PRGARAVPER CAGTETRRGR RCSGLQRLGG 120 GFRGCPADPC ARGEHRRHTI TSGVDCGLLK OMKELEQEKE VLLQGLEMMA QGRDWYQQQL 180 QOVOEROCRL GOSRASADFG AVGSPRPLGR LLPKVQEVAR WLGELLAEAC AGRALPTSSS 75 GPPCSALTST SSPGWQQQII LMLKEQNRLL TQEVTEKSER ITQLEQKSAL IKQLFEARAL 300 SQQDGGLSPA GPHIEPLTRF RLPVLTWAGA LLSPHSPQLL LPLSADSGGP LHELPDTWFP 360 AVLLWVPSPG KRTAHARLHF HQRPAEGAWQ LGCGAEAAPE TCGTLPHFES HKTTCEPDSL 420 GGPCPQEGDR SWSHLGAAFD VAPAVAKVTP NREDAAGSRH GDICPLCPKG LLTFRDIAIE 480 PSLAEWQCLD HAQQNLYRDV MLENYRNLFS LGMTVSKPDL IACLEQNKEP QNIKRNEMAA 540 80 KHPVTCSHFN QDLQPEQSIK DSLQKVIPRT YGKCGHENLQ LKKCCKRVDE CEVHKGGYND 600 LNOCLSNTON KIFOTHKCVK VFSKFSNSNR HNARYTGKKH LKCKKYGKSF CMFSHLNQHQ 660 IIHTKEKSYK CEECGKSPNH SSSGTTHKRI LTGEKPYRCB ECGKAFRWPS NLTRHKRIHT 720 GEKPYACEEC GQAFRESSTL TNHKRIHTGE RPYKCEECGK AFSVSSALIY HKRIHTGEKP YTCEECGKAF NCSSTLKTHK IIHTGEKPYT CEECGRTPNC SSTVKAHKRI HTGEKPYKCE 780

| 5  | KRIHTGEKPY<br>TGEEPYKCEE   | RTGLFQIRAA 1 TFRDVVIEFS 1 IKRMEMVTKH 1 NQCLSTTQNK 1 NQCLSTTQNK 2 EKPYTCECG 2 TCEECGKAFN 1 CDKAFKWSSS 1 | VRPNRDPSWG<br>LEBWQCLDHA<br>PDLPPELGIK<br>I PQTHKCVKV<br>BECGKPFNCS<br>QAFSRSSTLA<br>CSSTLKKHKI<br>LANHKSMHTG | QQEGSLTDPI<br>QQNLYRDVML<br>DSLQKVIPRR<br>FGKFSNSNRH<br>STLSKHKRIH<br>NHKRIHTGEK<br>IHTGEKPYKC | QRKEEPDLQN ENYRNLVSLG YGKSGHDNLQ KTRHTGKKHF TGEKPYRCEE PYTCEECGKA        | HYDHQNALED IAVSKPDLIT VKTCKSMGBC KCKKYGKSFC CGKAFTWSST FSLSSSLTYH           | 900<br>960<br>1020<br>1080<br>1140<br>1200<br>1260<br>1320 |
|----|--|--|---|--|--|---|--|
|    |  | C252 Protei<br>ession #: N   |   |  |  |   |  |
| 15 | <br>MASRSMRLLL<br>YGNGAHLASI                                     | 11<br> <br> LLSCLAKTGV<br>LSLKEASTIA<br>EMSSNNNFLT   | EYISGYQRSQ  | PIWIGLHDPQ   | 41<br> <br>CYGYFRKLRN<br>KRQQWQWIDG                                      | 51<br> <br>WSDAELECQS<br>AMYLYRSWSG   | 60<br>120<br>158   |
| 20 |  | C253 Protei<br>ession #: X   |   |  |  |   |  |
| 25 | LEDNVQSWKP   | 11<br>VYKKGQDYRF<br>GDTLVIASTD<br>RNIIVMGEME   | YSMYQAEEFQ  | VLPCRSCAPN   | QVKVAGKPMY   | LHIGEEIDGV  | 60<br>120<br>180   |
| 30 | HMGQQLVGQY<br>YNSLGHCFFT<br>DCNAVSTFWM<br>NNRAHSNYRA             | PIHPHLAGDV<br>EDGPEERNTF<br>ANPNINLINC<br>GMIIDNGVKT<br>LRGGDVWLDS                                     | DERGGYDPPT<br>DHCLGLLVKS<br>AAAGSEETGF<br>TEASAKDKRP  | YIRDLSIHHT<br>GTLLPSDRDS<br>WFIFHHVPTG<br>FLSIISARYS   | PSRCVTVHGS<br>KMCKMITGDS<br>PSVGMYSPGY<br>PHQDADPLKP                     | NGLLIKDVVG<br>YPGYIPKPRQ<br>SEHIPLGKFY<br>REPAIIRHFI                        | 240<br>300<br>360<br>420<br>480                            |
| 35 | GTEMMINRIW<br>LAFRLINNAWQ<br>SEYPGSYLTK<br>HPLYLEGALT            | GPGGLDHSGR<br>SCPHNNVTGI<br>NDNWLVRHPD<br>RSTHYQQYQP<br>VHNRLLKQTS                                     | TLPIGQNPPI<br>APEDVPITSR<br>CINVPDWRGA<br>VVTLQKGYTI  | RGIQLYDGPI<br>VFFGEPGPWF<br>ICSGCYAQMY<br>HWDQTAPAEL   | NIQNCTFRKP<br>NQLDMDGDKT<br>IQAYKTSNLR<br>AIWLINFNKG                     | VALEGRHTSA<br>SVFHDVDGSV<br>MKIIKNDFPS<br>DWIRVGLCYP                        | 540<br>600<br>660<br>720<br>780                            |
| 40 | NEREKFAFCS<br>TKDHFLEVKM<br>NSILQGIPWQ                           | MKGCERIKIK<br>ESSKQHFFHL   | ALIPKNAGVS<br>WNDFAYIEVD<br>NSIVLMASKG  | DCTATAYPKF<br>GKKYPSSEDG<br>RYVSRGPWTR   | TERAVVDVPM<br>IQVVVIDGNQ   | PKKLFGSQLK<br>GRVVSHTSFR<br>LKLKEQMAFV                                      | 840<br>900<br>960<br>996                                   |
| 45 |  | C254 Prote<br>cession #: 1   |   |  | 41   | 51  |  |
| 50 | SLAFVDLLLL<br>CLNFSKTTKL<br>QSYWLSFFMV<br>LSKLIVCFLS             | VNISIILYFR<br>SFKCQKLFYF<br>MILFVAFITC   | DFVLLSIRFT<br>FTVILIWISV<br>WEEVTTLVQA<br>IIVLLKVQII  | r Kyhiclftqi<br>/ Layvlgdpai<br>A iritsymnet<br>P ayiemnipwi                                   | ISFTYGFLHY<br>YQSLKAQNAY<br>ILYPPFSSHS                                   | CONFMEYFCI SPHCPFYVSI SYTVRSKKIF VYWFNCHKLN                                 | 60<br>120<br>180<br>240<br>300<br>338                      |
| 55 |  | C255 Protecession #:   |   |  |  |   |  |
| 60 | IFLYVVQPRI<br>FCMCRCCNK  | FPEDTLRKPI<br>GGEMHQRQKI   | QKAYESKID   | Y DKIVYYEAG:<br>A ISLLVICII:   | I ILCCVLGLLI<br>I SIGIFYGFV  | 51<br> <br>  PIGILFELVH<br>  IILMPLVGYF<br>  NHQVRTRIKR<br>  GILDRLRPNI     | 60<br>120<br>180<br>240                                    |
| 65 | IPVLDEIKSI<br>HPSSETCNS:<br>RVQRQTTTV<br>YDSYWWLGG:<br>SFLFCWILM | M ATAIKETKEJ<br>I RLSLSQLNSP<br>V AGIKRVLNSI<br>L VICSLLTLIV<br>I IVVLTFVFGJ                           | LENMISTLK<br>PELRQLPPV<br>GSDIDNVTQ<br>FYYLGLLC<br>NVEKLICEP  | S LHQQSTQLS: D ABLDNVNNV! R LPIQDILSA: G VCGYDRHAT: Y TSKELFRVL                                | S SLTSVKTSLI<br>L RTDLDGLVQ<br>F SVYVNNTES<br>P TTRGCVSNT<br>D TPYLLNEDW | R SSLNDPLCLV Q GYQSLNDIPD Y IHRNLPTLEE G GVFLMVGVGL E YYLSGKLFNK            | 300<br>360<br>420<br>480<br>540                            |
| 70 | LGAAGRKNL<br>LKRDAQTIK<br>NTSSVIIBE<br>PLNLFWFGI                 | Q DFAACGIDRI<br>T IHQQRVLPI<br>T KKYGRTIIG<br>G KATVFLLPA  | M NYDSYLAQT<br>E QSLSTLYQS<br>Y FEHYLQWIE   | G KSPAGVNLL<br>V KILQRTGNG<br>F SISEKVASC  | S FAYDLEAKA<br>L LERVTRILA<br>K PVATALDTA                                | E SLKVNLNIFL N SLPPGNLRNS S LDFAQNFITN V DVFLCSYIID M ENGNNGYHKD            | 600<br>660<br>720<br>780<br>840<br>856                     |
| 75 |  | : C256 Prot<br>ccession #:   |   |  |  |   | 3.00   |
| 80 | 1<br> <br>  MKAIIHLTL<br>  PSFPTATSP<br>  ITASSPNDG              | 11<br> <br>L ALLSVNTAT<br>A PPIISTHSS<br>L ITMVPSETQ   | 21<br> <br>N QGNSADAVI<br>S TIPTPAPPI<br>S NNEMSPTTE  | 31<br> <br>PT TETATSGPT<br>II STHSSSTIF<br>ED NQSSGPPTG  | I PTAADSEST<br>T ALLETSTLN   | 51<br> <br> F PETASTTANT<br>T NVNSLATSDI<br> S TGPSNPCQDD<br>  P EEKHSMAYQD | 120<br>180   |

| 5  | TVTEKINKAI<br>VASSLKCPDA<br>LILTIVGTIA   | DVFGTSVYGQ<br>RSSSSNFLNY<br>CNAQHKQCLI<br>GIVILSMIIA<br>ASRDSQMQNP | DLTLRCDYYG<br>KKSGGAPECA<br>LIVTARSNNK   | CNQTADDCLN<br>CVPGYQEDAN<br>TKHIEEENLI   | GLACDCKSDL<br>GNCQKCAFGY   | QRPNPQSPFC<br>SGLDCKDKFQ   | 300<br>360<br>420<br>480<br>512                      |
|----|--|--|--|--|--|--|--|
|    |  | C257 Protei<br>ession #: N   | -  |  |  |  |  |
| 10 | AQVSITKCSS   | 11<br> <br>CAGRVPALLL<br>DMNGYCLHGQ<br>ITVVGSTYYP                  | CIYLVDMSQN   | YCRCEVGYTG   | VRCEHFFLTV   |  | 60<br>120<br>169                                     |
| 15 |  | C258 Protei  |  |  |  |  |  |
| 20 | AQKLVSSHKP   | 11<br> <br>GPVKATAPVG<br>VQNQKQKQLQ                                | ATSVPHPVSR   | PLNNTQKSKQ   | PLPSAPENNP   | EEELASKQKN   | 60<br>120  |
| 25 | EVEIQSHLRH<br>ANALSYCHSK<br>IEGRMHDEKV   | EDFEIGRPLG<br>PNILRLYGYF<br>RVIHRDIKPE<br>DLWSLGVLCY<br>RPMLREVLEH | HDATRVYLIL<br>NLLLGSAGEL<br>EFLVGKPPFE   | EYAPLGTVYR<br>KIADFGWSVH<br>ANTYQETYKR   | ELQKLSKFDE<br>APSSRRTTLC<br>ISRVEFTFPD   | QRTATYITEL<br>GTLDYLPPEM   | 180<br>240<br>300<br>360<br>403                      |
| 30 |  | C259 Protei<br>cession #: N  |  |  |  |  |  |
| 35 | GQGRGTAMPG   | 11<br> <br>  LLLLGTLLP<br>  EEVLESSQEA<br>  IRKEEGSFQS             | LHVTERKYLK   | RDWCKTQPLK   | QTIHEEGCNS   | RTIINRFCYG   | 60<br>120<br>180<br>184                              |
| 40 |  | C260 Protei<br>cession #: I  |  | 9  |  |  |  |
|    | 1<br> <br>   | 11<br>   | 21<br> <br>  | 31   | 41<br>   | 51<br>}  |  |
| 45 | EKRDLRNFLK<br>NCYLHTAGAL<br>IEIQLKKAYE<br>LFPLEDGSFR                             | FFTFTDGHGG<br>LLKPPLLWSH<br>PSCECHLNNL<br>RIQGFESVQV<br>VFGKAQCNDI | GLIRIIRAKA<br>SQSVNFCERT<br>TQFRNGSIVA<br>VFGFGSKDDE                             | TTDCNSLNGV<br>KIWGTFKINE<br>GYEVVGSSSA<br>YTLPCSSGYR                             | LQCTCEDSYT<br>RPTNDLLNSS<br>SELLSAIEHV<br>GNITAKCESS                             | WFPPSCLDPQ<br>SAIYSKYANG<br>AEKAKTALHK<br>GWQVIRETCV   | 60<br>120<br>180<br>240<br>300                       |
| 50 | ASHFRVSNST<br>PLNFSRKFID<br>SMASLTLGNI   | FSMIVGNATE<br>MEDVISIADN<br>WKGIPVNKSQ<br>LPVSKNGNAQ<br>LVNETQDIVT | ILNSASVTNW<br>LKRGYSYQIK<br>VNGPVISTVI   | TVLLREEKYA<br>MCPQNTSIPI<br>QNYSINEVFL   | SSRLLETLEN<br>RGRVLIGSDQ<br>FFSKIESNLS   | ISTLVPPTAL<br>FQRSLPETII<br>QPHCVFWDFS   | 360<br>420<br>480<br>540<br>600                      |
| 55 | ILCLIIEALF<br>VFFTHFFYLS<br>TQPSNTYKRK<br>DDKATIIRVG                             | WKQIKKSQTS<br>LPFWMLMLGI<br>DVCWLNWSNG<br>KSLLILTPLL<br>NKLSALSSWK | HTRRICMVNI<br>LLAYRIILVF<br>SKPLLAFVVP<br>GLTWGFGIGT                             | ALSLLIADVW<br>HHMAQHLMMA<br>ALAIVAVNFV<br>IVDSQNLAWH                             | FIVGATVDTT<br>VGFCLGYGCP<br>VVLLVLTKLW<br>VIFALLNAFQ                             | VNPSGVCTAA<br>LIISVITIAV<br>RPTVGERLSR<br>GPFILCPGIL   | 660<br>720<br>780<br>840<br>900                      |
| 60 | Seq ID NO:   | C261 Prote   | in Sequence  |  | •  |  | 910  |
|    | 1  | cession #: 1<br>11   | 8 <u>2</u> 000373.1<br>21  | 31   | 41   | 51   |  |
| 65 | <br>  MTSKLAVALL   | 1  | <br>EGAVLPRSAK   | <br>  ELRCQCIKTY   | j  | <br>ELRVIESGPH   | 60<br>99   |
| 70 |  | C262 Prote<br>cession #: 1   |  |  |  |  |  |
| 75 | ECTWQVKAND<br>NLYFLALLIL   | RKYHEQPHFM<br>QAVPQISTLA   | NTKPLCIKES<br>WYTTLVPLLV   | KYANNAIKTY<br>VLGVTAIKDL   | KYNAFTFIPM<br>VDDVARHKMD   | 51<br> <br>AEENREPFRK<br>NLFEOFKRAA<br>KBINNRTCEV  | 60<br>120<br>180                                     |
| 80 | MSLEITDQYL<br>RNTDFCHGLV<br>YWEAQVGNSS<br>WDLQMYYAEK<br>DASQHNHNKI<br>RTDGQLNYQA | QREDTLATFD IFAGADTKIM WYLYDGEDDT DTPAKARTIT EQVDFSWNTY ASPDEGALVN  | GFIBCEEPNN<br>KNSGKTRFKR<br>PSYRGFLIFW<br>LNEQLGQIHY<br>ADGKLAPYDH<br>AARNFGPAFL | RLDKFTGTLF<br>TKIDYLMNYM<br>GYIIVLNTMV<br>IFSDKTGTLT<br>YLIEQIQSGK<br>ARTQNTITIS | WRNTSPPLDA<br>VYTIFVVLIL<br>PISLYVSVEV<br>QNIMTPKKCO<br>EPEVRQFFFL<br>ELGTERTYNV | LDGETNLKFK<br>DKILLRGCVI<br>LSAGLAIGHA<br>IRLGQSHFIN<br>INGQIYGDHR<br>LAVCHTVMVD<br>LAILDFNSDR<br>LRTLCLCYKE | 240<br>300<br>360<br>420<br>480<br>540<br>600<br>660 |
|    |  |  |  | JIAWATAWAT   |  | -VINCRCIVE   | 990  |

|    | LAKADIKIWV KFAPPVQESP RLEAKKEQRQ IKTAHIGVGI FTLVHFWYSP VGQRDLLFNY VITVNFQIGL RQPYIWLTII | KKFMAASVAS<br>LTGDKKETAE<br>FPPGGNRALI<br>KNFVDLACEC<br>SGQEGMQAVM<br>FNGYSAQTAY<br>KRFFVSLLHG<br>DTSYWTFVNA<br>LTVAVCLLPV<br>FSHQRGYADL | NIGFACELLT ITGSWLNEIL SAVICCRVTP SSDYSFAQFR EDWFITLYNV VLTSMILFFI FSIFGSIALY VAIRFLSMTI | EDTTICYGED<br>LEKKTKRNKI<br>KQKAMVVDLV<br>YLQRLLLVHG<br>LYTSLPVLLM<br>PLGAYLQTVG<br>FGIMFDFHSA<br>WPSESDKIQK | INSLLHARME<br>LKLKPPRTEE<br>KRYKKAITLA<br>RWSYIRMCKF<br>GLLDQDVSDK<br>QDGEAPSDYQ<br>GIHVLFPSAF<br>HRKRLKAEEQ | NQRNRGGVYA<br>ERRMRTQSKR<br>IGDGANDVNM<br>LRYFFYKNFA<br>LSLRFPGLYI<br>SFAVTIASAL<br>QFTGTASNAL<br>WQRRQQVFRR | 720<br>780<br>840<br>900<br>960<br>1020<br>1080<br>1140<br>1200 |
|----|---|--|---|--|--|--|---|
|    |   | C263 Protei<br>ession #: X   |   |  |  |  |   |
| 15 | rfeach I sny  | 11<br> <br>WLAAPWGALP<br>TALLLSRDGR  | TLYVGAREAL  | FALSSNLSFL   | PGGEYQELLW   | GADAEKKQQC   | 60<br>120   |
| 20 | GKGRCPFDPN<br>VASAYIPESL<br>TSFLKAQLLC<br>FTMKDVQRVF                                    | CONYIKILLP<br>FKSTALVVDG<br>GSLQGDDDKI<br>SRPDDGFPFN<br>SGLYKEVNRE   | ELYTGTVSSF<br>YFFFSETGQE<br>VLQDVFTLSP<br>TQQWYTVTHP                                    | QGNDPAISRS<br>FEFFENTIVS<br>SPQDWRDTLF<br>VPTPRPGACI   | QSLRPTKTES<br>RIARICKGDE<br>YGVFTSQWHR<br>TNSARERKIN   | SLAWLQDPAF<br>GGERVLQQRW<br>GTTEGSAVCV<br>SSLQLPDRVL   | 180<br>240<br>300<br>360<br>420                                 |
| 25 | PRVHIIEELQ<br>PYCAWSGSSC<br>FQPNTVNTLA<br>EGFQQLVASY                                    | GQVRSRMLLL<br>IFSSGQPVQN<br>KHVSLYQPQL<br>CPLLSNLATR<br>CPEVVEDGVA   | LLLDTHRGLL<br>ATRPWIQDIE<br>LWLRNGAPVN<br>DQTDEGGSVP                                    | YAASHSGVVQ<br>GASAKDLCSA<br>ASASCHVLPT<br>VIISTSRVSA   | VPMANCSLYR<br>SSVVSPSFVP<br>GDLLLVGTQQ<br>PAGGKASWGA   | SCGDCLLARD<br>TGEKPCEQVQ<br>LGEFQCWSLE<br>DRSYWKEFLV   | 480<br>540<br>600<br>660<br>720                                 |
| 30 | PLDHRGYQSL<br>Seq ID NO:  | LPVLFLLYRH<br>SDSPPGSRVF<br>C264 Protes  | TESEKRPLSI<br>in Sequence   |  |  |  | 780<br>837  |
| 25 | Protein Acc   | cession #: 1   | NP_008950.1   |  |  |  |   |
| 35 | KWVGTIHGAA  | 11<br> <br>TSVAAARKGA<br>GTVYEDLRYK<br>ILLSIQSLLG  | LSLEFPSGYP  | YNAPTVKFLT   | PCYHPNVDTQ   | GNICLDILKE   | 60<br>120<br>179  |
| 40 | Seq ID NO:  | C265 Prote   | in Sequence   |  |  |  |   |
| 45 | LFPRLQKLLE  | 11<br> <br>  LLGAVWLLSS<br>SDYFRYYKVN  | LKRPCPFWND  | ISQCGRRDCA   | VKPCQSDEVP   | DGIKSASYKY   | 60<br>120   |
| 50 | LLLNPERYTG<br>CVEKRAFYRL<br>LKNLYFLYLI<br>NSFFAGDKKE                                    | CEQAERLGAV<br>YKGPDAWKIW<br>ISGLHASINV<br>ELRALSKVLP<br>AHKLKEDFRL<br>YEFHLTRQEI   | NVIYEENCFK<br>HLSARYLLQE<br>FFERPDFQLF<br>HFRNISRIMD                                    | PQTIKRPLNP<br>TWLEKKWGHN<br>TGNKIQDEEN<br>CVGCFKCRLW   | LASGQGTSEE<br>ITEFQQRFDG<br>KMLLLEILHE<br>GKLQTQGLGT   | NTFYSWLEGL<br>ILTEGEGPRR<br>IKSPPLHFDB   | 180<br>240<br>300<br>360<br>420<br>468                          |
| 55 | Protein Ac  | C266 Prote<br>cession #:   |   |  |  |  |   |
| 60 | QKARAALHPP<br>GRLGKCSARV  |  | RVLAEVQEGR<br>INVTCTRLIE  | AWINPKEGCK<br>KKKRQQEDYL   | VHVVFSTERY<br>LYKOMKQLKN   | 51<br>  DAGVPRRLLQ<br>  DAGVPRRLLQ<br>  NPESLLQEGE<br>  PLEIVSIPDN   | 60<br>120<br>180<br>228   |
| 65 |   | C267 Protecession #:   |   |  |  |  |   |
| 70 |   | 11<br> <br>  AVILCATVVC<br>  GQRCLNPKSK  |   |  | 41<br> <br>  KVADIEKASI  | 51<br> <br>  MYPSNNCDKI  | 60<br>94  |
| 75 | Protein Ac  | C268 Protectes :cession #:   | FGENESH pre   | dicted   | 4.   |  |   |
| 80 | HSLAKIERSI<br>VLEMKVNHKO  | ASSLFPLDQS   | KSQLYSDLH<br>LRNQDKKCVI   | PGRYGRVILI   | SPTGDNILL  | 51<br> <br>E GDLERLVAPS<br>D AEGILQTHRA<br>T ARVQVRYPNT  | 60<br>120<br>180<br>202   |
|    |   | : C269 Prote<br>ccession #:  |   |  |  |  |   |

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51
      MRLPLLLVFA SVIPGAVLLL DTROFLIYNE DHKRCVDAVS PSAVQTAACN QDAESQKFRW
       VSESQIMSVA FKLCLGVPSK TDWVAITLYA CDSKSEFQKW ECKNDTLLGI KGEDLFFNYG
       NRQEKNIMLY KGSGLWSRWK IYGTTDNLCS RGYEAMYTLL GNANGATCAF PFKFENKWYA
                                                                                180
       DCTSAGRSDG WLWCGTTTDY DTDKLFGYCP LKFEGSESLW NKDPLTSVSY QINSKSALTW
                                                                                240
       HQARKSCQQQ NAELLSITEI HEQTYLTGLT SSLTSGLWIG LNSLSFNSGW QWSDRSPFRY
                                                                                300
       LNWLPGSPSA EPGKSCVSLN PGKNAKWENL ECVQKLGYIC KKGNTTLNSF VIPSESDVPT
                                                                                360
10
       HCPSQWWPYA GHCYKIHRDE KKIQRDALTT CRKEGGDLTS IHTIEELDPI ISQLGYEPND
       ELWIGLNDIK IQMYFEWSDG TPVTFTKWLR GEPSHENNRQ EDCVVMKGKD GYWADRGCEW
                                                                                 480
       PLGYICKMKS RSQGPEIVEV EKGCRKGWKK HHFYCYMIGH TLSTFAEANQ TCNNENAYLT
                                                                                540
       TIEDRYEQAF LTSFVGLRPE KYFWTGLSDI QTKGTFQWTI EEEVRFTHWN SDMPGRKPGC
                                                                                 600
       VAMRTGIAGG LWDVLKCDEK AKFVCKHWAE GVTHPPKPTT TPEPKCPEDW GASSRTSLCF
15
       KLYAKGKHEK KTWFESRDFC RALGGDLASI NNKEEQQTIW RLITASGSYH KLFWLGLTYG
                                                                                720
       SPSEGFTWSD GSPVSYENWA YGEPNNYQNV EYCGELKGDP TMSWNDINCE HLNNWICQIQ
                                                                                780
       KGQTPKPEPT PAPODNPPVT EDGWVIYKDY QYYFSKEKET MDNARAFCKR NFGDLVSIQS
                                                                                840
       ESEKKPLWKY VNRNDAQSAY FIGLLISLDK KFAWMDGSKV DYVSWATGEP NFANEDENCV
       TMYSNSGFWN DINCGYPNAF ICQRHNSSIN ATTVMPTMPS VPSGCKEGWN FYSNKCFKIF
                                                                                 960
20
       GFMEEERKNW QEARKACIGF GGNLVSIQNE KEQAFLTYHM KDSTFSAWTG LNDVNSEHTF
                                                                                 1020
       LWTDGRGVHY TNWGKGYPGG RRSSLSYEDA DCVVIIGGAS NEAGKWMDDT CDSKRGYICQ
                                                                                1080
       TRSDPSLTNP PATIQTDGFV KYGKSSYSLM RQKFQWHEAE TYCKLHNSLI ASILDPYSNA
       FAWLQMETSN ERVWIALNSN LTDNQYTWTD KWRVRYTNWA ADEPKLKSAC VYLDLDGYWK
TAHCNESFYF LCKRSDEIPA TEPPQLPGRC PESDHTAWIP FHGHCYYIES SYTRNWGQAS
                                                                                1200
                                                                                 1260
25
       LECLRMGSSL VSIESAAESS FLSYRVEPLK SKTNFWIGLP RNVEGTWLWI NNSPVSFVNW
                                                                                 1320
       NTGDPSGERN DCVALHASSG FWSNIHCSSY KGYICKRPKI IDAKPTHELL TTKADTRKMD
                                                                                 1380
       PSKPSSNVAG VVIIVILLIL TGAGLAAYFF YKKRRVHLPQ EGAFENTLYF NSQSSPGTSD
                                                                                 1440
                                                                                 1456
       MKDLVGNIEO NEHSVI
30
       Seq ID NO: C270 Protein Sequence
       Protein Accession #: Eos sequence
                                                                   51
35
       MVLLHWCLLW LLFPLSSRTQ KLPTRDEELF QMQIRDKAFF HDSSVIPDGA EISSYLFRDT
                                                                                 60
        PKRYPFVVEE DNTPLSVTVT PCDAPLEWKL SLQELPEDRS GEGSGDLEPL EQQKQQIINE
        EGTELFSYKG NDVEYFISSS SPSGLYQLDL LSTEKDTHFK VYATTTPESD QPYPELPYDP
                                                                                 180
        RVDVTSLGRT TVTLAWKPSP TASLLKQPIQ YCVVINKEHN FKSLCAVEAK LSADDAFMMA
                                                                                 240
       PKPGLDFSPF DFAHFGFPSD NSGKERSFQA KPSPKLGRHV YSRPKVDIQK ICIGNKNIFT VSDLKPDTQY YFDVFVVNIN SNMSTAYVGT FARTKEEAKQ KTVBLKDGKI TDVFVKRKGA
                                                                                 300
40
                                                                                 360
        KFLRFAPVSS HQKVTFFIHS CLDAVQIQVR RDGKLLLSQN VEGIQQFQLR GKPKAKYLVR
                                                                                 420
        LKGNKKGASM LKILATTRPT KQSFPSLPED TRIKAFDKLR TCSSATVAWL GTQERNKFCI
                                                                                 480
        YKKEVDDNYN EDOKKREONO CLGPDIRKKS EKVLCKYFHS ONLOKAVITE TIKGLOPGKS
                                                                                 540
        YLLDVYVIGH GGHSVKYQSK VVKTRKFC
45
        Seg ID NO: C271 Protein Seguence
        Protein Accession #: AAH34229.1
50
        MEKVOLEFEN QEMEKKLOEF RSTRNKEKED RESSEYYWKS GKVGKLVNOS YMMSONKONV
        VKFSAGKVKL KLLKEQIQEP VKPTVNYKMA NSSECEKPKI NGKVCGQCEN KAALLVCLEC
                                                                                 120
        GEDYCSGCFA NVHQKGALKL HRTTLLQARS QILFNVLDVA HQFIKDVNPD EPKEENNSTK
                                                                                 180
        ETSKIQHKPK SVLLQRSSSE VEITTMKRAQ RTKPRKSLLC EGSFDEEASA QSFQEVLSQW
                                                                                 240
55
        RTGNHDDNKK QNLHAAVKDS LBECEVQTNL KIWREPLNIE LKEDILSYMB KLWLKKHRRT
                                                                                 300
        PQEQLFRCYQ IRSHIHMKPL VMHSVLKMKT MKIVMVRRPK YNTQLFYCQ
        Seq ID NO: C272 Protein Sequence
        Protein Accession #: NP_078963.1
60
                                                        41
                                                                    51
        MEKLWLKKHR RTPQEQLFKM LSDTFPHPHE TTGDAQCSQN ENDEDSDGEE TKVQHTALLL
        PVETLNIERP EPSLKIVELD DTYEEFEBA ENIVPYKVKL ADADSORSCA FHDCOKNSFP
YENGIHOHHV FDKGKRDFLN LCLRNSSTYY KONSKGETSN TDFDNIVDPD VYSSDIEKIE
                                                                                 120
65
                                                                                 180
        ESTSFERNLK EKNIGLESNO KSDDSCVSLE SKOTLLGRDL EKAPIEEKLS ODIKESLELS
                                                                                  240
        NLYKRPSFEE SKTTKSSLLL QEIACRSKPI TKQYQGLERF FIFDTNERLN LLPSHRLECN
                                                                                  300
        NSSTRITLAE DREWIPDHSL SEYADNAIVL GVLQGAQSPS SSRKQQKMGQ KSQRPSTANF
PLSNSVKESS SCLSSSHPRS RSAAAQSSSR AASEISEIEY IDITDQNELS LDDTTDQHTL
                                                                                 360
                                                                                  420
 70
        DNLEKELQVL RSLADTSEKL YSLTSEEFPD FSSQSLNISQ ISTDFLKTSH VRGPCGVEEL
        SCSGRDTKIQ SLLSLSESST DEEEEDFINK QHVITLPWSK ST
                                                                                  522
        Seg ID NO: C273 Protein Seguence
        Protein Accession #: NP_005399.1
 75
                                                        41
        MKVSAVLLCL LLMTAAFNPQ GLAQPDALNV PSTCCFTFSS KKISLQRLKS YVITTSRCPQ
        KAVIFRTKLG KEICADPKEK WVQNYMKHLG RKAHTLKT
 80
        Seq ID NO: C274 Protein Sequence
        Protein Accession #: BAC05158.1
                    11
                                21
                                            31
                                                        41
                                                                    51
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| 5        | EPHNAKFPAP<br>LDSNCTIPLI<br>GTWVCLQNCH<br>EPPTGLRIML<br>TDDWDRRLLL<br>IFGLHENVDI<br>IEMALRKYPV<br>SLLVGKVPEI<br>TGAMQNYARK<br>YPKLLFDLMP<br>QPTRHWIKRG | _   | IIILRCLRPD ASLLKFANDK KICEDFTSET DPEFFKGCRG IVENPHYKFS FESLLLTQGG VQEMERFNNL PLGSYITDFL EFEVIPSDTS RIIKSDAYVC | KITPAITNYV<br>SMSGNKFQAI<br>CNSSFRLWLT<br>KELLFINEYD<br>PSGNYFAPPK<br>SKQTGASGST<br>IITIRNTLRD<br>ARLNFLQDWY<br>DTSPEDGVYI | TDKLGKKFVE<br>SLGQGQGPIA<br>SYPSSKFFVT<br>TIPFEAISYL<br>GTYEDYIEFI<br>DQILLEITKD<br>LEKAIKGVVV<br>NSGKPCVFWL<br>HGLYLDGARW | PPPFDLTKSY AKMIKAAIEE ILQNGVKMTN TGECNYGGRV KKLPPTQHPE ILNKLPSDFD MDSALEALSS SGFFFTQAFL DRESGLLAEQ | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>679 |
|----------|--|---|---|--|--|--|---|
| 15       |  | C275 Protei<br>ession #: A  |   |  |  |  |   |
| 20<br>25 | GHVGADDLCQ<br>PLVIDYFQNQ<br>LPGALQARPG<br>VAGGICQCLA<br>LCMSVTTQAG   | 11<br> <br>  LLLLPTLCGP<br>ECEDIVHILN<br>TDSNGICHHL<br>PHTQDLSEQQ<br>ERYSVILLDT<br>NSSEQAIPQA<br>SPLQCIHSPD | KMAKEAIFQD<br>GLCKSRQPEP<br>PPIPLPYCWL<br>LLGRMLPQLV<br>MLQACVGSWL  | TMRKFLEQEC<br>EQEPGMSDPL<br>CRALIKRIQA<br>CRLVLRCSMD   | NVLPLKLLMP<br>PKPLRDPLPD<br>MIPKGALAVA<br>DSAGPRSPTG   | QCNQVLDDYF<br>PLLDKLVLPV<br>VAQVCRVVPL<br>EWLPRDSECH   | 60<br>120<br>180<br>240<br>300<br>360<br>381                                    |
| 30       |  | C276 Protes   |   |  |  |  |   |
| 35       | CYRNGVCYHQ   | 11<br> <br>LLLLLQGSAD<br>RPDENVRRKH<br>KHRGTKKTPS   | MWALVWTCSG  | LLLLSCSICL   | <b>FWWAKRRDVL</b>  | HMPGFLAGPC   | 60<br>120<br>177  |
|          |  | C277 Prote  | -   |  |  |  |   |
| 40       |  | 11<br> <br>  TISLCSYSAT<br>VNELGPEASE   |   |  | 41<br> <br> <br>  NILPFMDPLK   | 51<br> <br> LLLKTLGISV   | 60<br>93  |
| 45       |  | C278 Prote  |   | dicted   |  |  |   |
| 50       | ERCSDVFGVS   | FFWWVRGLAG  | SGAKLQTFTP  | AQEGAPTVQR   | QAEALLKCRQ   | 51<br> <br>TRGIWLGQLE<br>SGRPGRGGAE<br>ISMAESGPSL  | 60<br>120<br>180  |
| 55       | MINQLTGTIQ TVQVTDVNEP FCVVVGMQYP VNIVNLNDEV  | SGSPFLVTHL PQFQGNLAED LISPPKSFRM PRFTSPTRVY VAQRIDRDAG  | YFLGVVTTGM<br>HLRADQPHFN<br>SANGTLFSTT<br>TVLEELSPGT<br>ELRQNPTISL  | EQLDFETGPN AHSHTYVRVV ELDFEAGHRS IVANITAEDP EVLVKDRPYG   | IFDLQIYVKD<br>ATALARHRLR<br>FHLIVEVRDS<br>DDEGFPSHLL<br>GQENRIQITF   | EVGVTDLQVL<br>SSIGSPFLGT<br>GGLKASTELQ<br>YSITTVSKYP<br>IVEDVNDNPA                                 | 240<br>300<br>360<br>420<br>480   |
| 60       | LTIMAEGKEE<br>YQVPPTTCRN<br>NFKLTCTDLD<br>KLLVYVTDDN   | QVTSYMDGSR<br>SRIQATNNED<br>SSPRSFRYSI<br>LMSDRKKAEA  | QRDRACVGKL<br>TSSVTVTVNI<br>GPGNVNNHPT<br>LVETGTVTLS  | LLIKPSDLMR<br>LEENDEKPIC<br>FSPNAGSNVT<br>IKVIPHPTTI   | LSHYHENNSG<br>TPNSYFLALP<br>RLLLTSRFDY<br>ITTTPRPRVT   | GLTVPHGWGS KTCPHDSISS VDLKVGTNIQ AGGFDKIWDY YQVLRKNVYS GETKTAERDV                                  | 540<br>600<br>660<br>720<br>780<br>840  |
| 65       | VVETIQMNTI   |   | EQASLELYAL  | LPSCCDPSPV   | TLRKVQVCGE   | SEETGQCSGH   | 900<br>957  |
|          |  | C279 Prote<br>cession #:  |   |  |  |  |   |
| 70       | 1  | 11<br>  | 21<br>  | 31<br>   | 41   | 51<br>   |   |
| 75       | MINOLTGTIO<br>TCOKFTFSIM<br>SGKIVLIGDI<br>PSYVFDVSER   | VPERTAKGTI<br>DYENPSNLAA  | LLDLNKFCFT<br>GNKYTVIIQV<br>EEKRLLSIC   | DDSEAPNNRE<br>QDVAPPYYK<br>VRAVCHHFGI  | NFTMPSGVGS<br>NVYVYILTSE   | V IVEDVNDNPA<br>GSRFLQDPAG<br>P ENEFPLIFDR<br>P GRPIGQSHPQ   | 60<br>120<br>180<br>240<br>277  |
| 80       |  | : C280 Prote<br>ccession #:   |   |  |  |  |   |
|          |  |   |   |  |  | 51<br> <br>A DFRCDTIQPG<br>E AERAKEVRGS  | 60<br>120   |

| 5  | TLHVCRRSPC<br>PRQHMAKCQL                             | AELSCWEEGN<br>PHPVNCYVSR<br>SGPSVGIVQS<br>GFIQVRYGQK                             | PTEKNVFIVF<br>CTPPPDFNQC                             | MLAVAALSLL<br>LENGPGGKFF                             | LSLAELYHLG<br>NPFSNNMASQ                             | WKKIRQRFVK<br>QNTDNLVTEQ  | 180<br>240<br>300<br>358               |
|----|--|--|--|--|--|---|--|
| J  |  | C281 Protei<br>ession #: N   |  |  |  |   |  |
| 10 | SGSYRVLENS<br>EIQDINDNAP                             | 11<br> <br>  LWAPALTLKN<br>APHLLDVDAD<br>SFSSDQIEMD                              | SGLLYTKQRI<br>ISENAAPGTR                             | DRESLCRHNA<br>FPLTSAHDPD                             | KCQLSLEVFA<br>AGENGLRTYL                             | NDKEICMIKV<br>LTRDDHGLFG  | 60<br>120<br>180                       |
| 15 | PVFEAPSYLV<br>GLIRVKGNLD<br>LSEAAPPGTV<br>FYTVVTDRPL | KFPELVIQKA<br>ELPENAPLGT<br>YEENGMLEID<br>IALVRVTDRD<br>DRETQDEYNV<br>LGSVLAQDPD | VVIDLNATDA<br>VQARDLGPNP<br>SGKNGQLQCR<br>TIVARDGGSP | DEGPNGEVLY<br>IPAHCKVTVK<br>VLGGGGTGGG<br>PLNSTKSFAI | SFSSYVPDRV<br>LIDRNDNAPS<br>GGLGGPGGSV<br>KILDENDNPP | RELFSIDPKT<br>IGFVSVRQGA<br>PFKLEENYDN<br>RFTKGLYVLQ                | 240<br>300<br>360<br>420<br>480<br>540 |
| 20 | NFEQTKAFEF<br>AGLGYLVSTV<br>LVVKVTDHGK<br>AAMITIAVKC | KVLAKDSGAP<br>RALDSDFGES<br>PTLSAVAKLI<br>KRENKEIRTY<br>LATSPMYFDY               | AHLESNATVR<br>GRLTYEIVDG<br>IRSVSGSLPE<br>NCRIAEYSHP | VTVLDVNDNA<br>NDDHLFEIDP<br>GVPRVNGEQH<br>QLGGGKGKKK | PVIVLPTLQN<br>SSGEIRTLHP<br>HWDMSLPLIV<br>KINKNDIMLV | DTAELQVPRN<br>FWEDVTPVVE<br>TLSTISIILL<br>QSEVEERNAM                | 600<br>660<br>720<br>780<br>840        |
| 25 | TNASETPATR Seq ID NO:                                | MSIIQTENFP<br>C282 Protes<br>cession #: 1  | AEPNYMGSRQ<br>Ln Sequence                            |  |  |   | 889                                    |
| 30 | 1  | 11   | 21   | 31   | 41   | 51  |  |
| 35 | <b>PSIMAVLWAL</b>                                    | GGSLGLMFCL<br>VSVSFLVLSC<br>WSFYLGWVSA   | <b>FPSLFPPGHG</b>                                    | PLVSTTAAFA   | AAISMVVAMA   |   | 60<br>120<br>165                       |
| 33 |  | C283 Prote<br>cession #: :   |  |  |  |   |  |
| 40 | ELGRDYRTCL   |  | DKPTQRSVSN   |  |  | 51<br> <br>  PQGDLLTKTQ<br>  MRRYQSRVTQ                             | 60<br>120<br>145                       |
| 45 |  | C284 Prote<br>cession #:   |  |  |  |   |  |
| 50 |  | 11<br> <br>'ILIATALCAF<br>! QVCANPEKKW   |  |  | 41<br> <br>  PLPRAHIKEY                              | 51<br> <br>  FYTSGKCSNP   | 60<br>91                               |
| 55 |  | C285 Protecession #:   |  |  |  |   |  |
| 60 | VGVPEPGQLI<br>TRPSHSEVW<br>LIPEAFGFDI                | FNQCLTAEE: GYGFLSVTIII KVDSYVEKAV  | FSLHGPSNAT<br>LASLLGLILT<br>VAVFGGFYLLI              | C QITSSKFSVI<br>C PLIKKSYFPI<br>C FFERMLKMLI         | CPAVLQQLNI<br>LTPFVGLAI<br>KTYGQNGHTI                | 51<br>  LLEQMGAASR<br>  HPCEDRPKHK<br>  GTLFSNAIFQ<br>  FGNDNFGPQB  | 60<br>120<br>180<br>240                |
| 65 | GTIAWMITL<br>STRQALLFNI                              | DALHNFIDGI   | L AIGASCTLSI<br>L AFGILVGNNI                         | L LQGLSTSIA:<br>F APNIIFALAC                         | CREPPHELA<br>GMFLYISLAI                              | r CLKGPKLSBI<br>G DFVILLNAGM<br>D MFPEMNDMLR                        | 300<br>360<br>420<br>460               |
| 70 |  | : C286 Proteccession #:  |  |  |  |   |  |
| 75 | DCPPGNPAP<br>ERATGQRPH<br>KWLQDVFNV                  | T SNHGPDATE<br>H FLRRGIFFS<br>P LVIQMTDDE  | A EEDFVDPWT<br>H RDMNQVLDA<br>K YLWKDLTLD            | V QTSSAKGID<br>Y ENKKPFYLY<br>Q AYGDAVENA            | Y DKLIVRFGS<br>I GRGPSSEAM<br>K DIIACGFDI            | 51   KAAAGEDYKA S KIDKELINRI H VGHLIPFIPT N KTFIFSDLDY S NSFPQIFRDR |  |
| 80 | TDIQCLIPC<br>LTDTAKQIK                               | A IDQDPYFRM  | T RDVAPRIGY<br>G RDTIEEHRQ                           | P KPALLHSTF<br>F GGNCDVDVS                           | F PALQGAQTK<br>F MYLTFFLED                           | M SASDPNSSIF<br>D DKLEQIRKDY  |  |

Protein Accession #: NP\_004929.1 5 MTVFRQENVD DYYDTGEELG SGQFAVVKKC REKSTGLQYA AKFIKKRRTK SSRRGVSRED 60 IEREVSILKE IQHPNVITLH EVYENKTOVI LILELVAGGE LFDFLAEKES LTEEEATEPL 120 KOILNGVYYL HSLOIAHFDL KPENIMLLDR NVPKPRIKII DFGLAHKIDF GNEFKNIFGT 180 PEFVAPEIVN YEPLGLEADM WSIGVITYIL LSGASPFLGD TKQETLANVS AVNYEFEDEY PSNTSALAKD FIRRLLVKDP KKRMTIQDSL QHPWIKPKDT QQALSRKASA VNMEKFKKFA 300 10 ARKKMKQSVR LISLCQRLSR SFLSRSNMSV ARSDDTLDEE DSFVMKAIIH AINDDNVPGL QHLLGSLSNY DVNQPNKHGT PPLLIAAGCG NIQILQLLIK RGSRIDVQDK GGSNAVYWAA 360 420 RHGHVDTLKF LSENKCPLDV KDKSGEMALH VAARYGHADV AQVTCAASAQ IPISRTKEEE TPLHCAAWHG YYSVAKALCE AGCNVNIKNR EGETPLLTAS ARGYHDIVEC LAEHGADLNA CDKDGHIALH LAVRRCQMEV IKTLLSQGCF VDYQDREGNT PLHVACKDGN MPIVVALCEA 600 15 NCNLDISNKY GRTPLHLAAN NGILDVVRYL CLMGASVEAL TTDGKTAEDL ARSEQHEHVA 660 GLLARLRKOT HRGLFIQQLR PTQNLQPRIK LKLFGHSGSG KTTLVESLKC GLLRSFFRRR RPRLSSTNSS RFPPSPLASK PTVSVSINNL YPGCENVSVR SRSMMFEPGL TKGMLEVFVA 780 PTHHPHCSAD DQSTKAIDIQ NAYLNGVGDF SVWEFSGNPV YFCCYDYFAA NDPTSIHVVV FSLEEPYEIO LNPVIFWLSF LKSLVFVEEP IAFGGKLKNP LQVVLVATHA DIMNVPRPAG 840 900 20 GEFGYDKDTS LLKEIRNRFG NDLHISNKLF VLDAGASGSK DMKVLRNHLQ EIRSQIVSVC PPMTHLCEKI ISTLPSWRKL NGPNQLMSLQ QFVYDVQDQL NPLASEEDLR RIAQQLHSTG 1020 EINIMQSETV QDVLLLDPRW LCTNVLGKLL SVETPRALHH YRGRYTVEDI QRLVPDSDVE 1080 ELLOILDAMD ICARDLSSGT MVDVPALIKT DNLHRSWADE EDEVMVYGGV RIVPVEHLTP 1140 PPCGIFHKVQ VNLCRWIHQQ STEGDADIRL WVNGCKLANR GAELLVLLVN HGQGIEVQVR 1200 25 GLETEKIKCC LLLDSVCSTI ENVMATTLPG LLTVKHYLSP QQLREHHEPV MIYQPRDFPR 1260 AQTLKETSLT NTMGGYKESF SSIMCFGCHD VYSQASLGMD IHASDLNLLT RRKLSRLLDP 1320 PDPLGKDWCL LAMNLGLPDL VAKYNTNNGA PKDFLPSPLH ALLREWTTYP ESTVGTLMSK 1380 LRELGRRDAA DLLLKASSVF KINLDGNGQE AYASSCNSGT SYNSISSVVS R 1431 30 Seg ID NO: C288 Protein Sequence Protein Accession #: NP 002072.1 21 31 41 51 35 MELRARGWWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSDVP QAEISGEHLR ICPOGYTCCT SEMEENLANR SHAELETALR DSSRVLQAML ATQLRSFDDH FQHLLNDSER 120 TLQATFPGAF GELYTQNARA FRDLYSELRL YYRGANLHLE ETLAEFWARL LERLFKQLHP QLLLPDDYLD CLGKQAEALR PFGEAPRELR LRATRAFVAA RSFVQGLGVA SDVVRKVAQV 180 240 PLGPECSRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI 300 40 TDKFWGTSGV ESVIGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 360 RGKLAPRERP PSGTLEKLVS BAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA RGRYLPEVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD 420 480 45 Seg ID NO: C289 Protein Sequence Protein Accession #: AAH30205.1 31 50 MIILIYLFLL LWEDTOGWGF KDGIFHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF 60 EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFGKTGI IDYGIRLNRS 120 ERWDAYCYNP HAKECGGVFT DPKQIFKSPG PPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240 QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHL 55 Seg ID NO: C290 Protein Seguence Protein Accession #: NP\_001973.1 60 MRANDALQVL GLLFSLARGS EVGNSQAVCP GTLNGLSVTG DAENQYQTLY KLYERCEVVM GNLEIVLTGH NADLSFLQWI REVTGYVLVA MNEFSTLPLP NLRVVRGTQV YDGKFAIFVM LNYNTNSSHA LROLRLTOLT EILSGGVYIE KNDKLCHMDT IDWRDIVRDR DAEIVVKDNG 180 RSCPPCHEVC KGRCWGPGSE DCQTLTKTIC APQCNGHCFG PNPNQCCHDE CAGGCSGPQD 240 65 TDCFACRHFN DSGACVPRCP QPLVYNKLTF QLEPNPHTKY QYGGVCVASC PHNFVVDQTS CVRACPPDKM EVDKNGLKMC EPCGGLCPKA CEGTGSGSRF QTVDSSNIDG FVNCTKILGN 360 LDFLITGLING DPWHKIPALD PEKLINVFRTV REITGYLNIO SWPPHMHNFS VFSNLTTIGG 420 RSLYNRGFSL LIMKNLNVTS LGFRSLKEIS AGRIYISANR QLCYHHSLNW TKVLRGPTEB 480 RLDIKHNRPR RDCVAEGKVC DPLCSSGGCW GPGPGQCLSC RNYSRGGVCV THCNFLNGBP 70 REFAHEAECF SCHPECOPMG GTATCNGSGS DTCAQCAHFR DGPHCVSSCP HGVLGAKGPI 600 YKYPDVQNEC RPCHENCTQG CKGPELQDCL GQTLVLIGKT HLTMALTVIA GLVVIFMMLG GTFLYWRGRR IQNKRAMRRY LERGESIEPL DPSEKANKVL ARIFKETELR KLKVLGSGVF 660 720 GTVHKGVWIP EGESIKIPVC IKVIEDKSGR QSFQAVTDHM LAIGSLDHAH IVRLLGLCPG SSLQLVTQYL PLGSLLDHVR QHRGALGPQL LLNWGVQIAK GMYYLEEHGM VHRNLAARNV 840 75 LLKSPSOVOV ADFGVADLLP PDDKOLLYSE AKTPIKWMAL ESIHFGKYTH QSDVWSYGVT 900 VWELMTFGAE PYAGLRLAEV PDLLEKGERL AQPQICTIDV YMVMVKCWMI DENIRPTFKE 960 LANEFTRMAR DPPRYLVIKR ESGPGIAPGP EPHGLTNKKL EEVELEPELD LDLDLEAEED NLATTILGSA LSLPVGTLNR PRGSQSLLSP SSGYMPMNQG NLGGSCQESA VSGSSERCPR 1080 PVSLHPMPRG CLASESSEGH VTGSEAELOE KVSMCRSRSR SRSPRPRGDS AVHSORHSLL 1140 80 TPVTPLSPPG LEEEDVNGYV MPDTHLKGTP SSREGTLSSV GLSSVLGTEE EDEDEEYEYM 1200

NRRRRHSPPH PPRPSSLEEL GYEYMDVGSD LSASLGSTQS CPLHPVPIMP TAGTTPDEDY

EYMNRQRDGG GPGGDYAAMG ACPASEQGYE EMRAFQGPGH QAPHVHYARL KTLRSLEATD

SAFDNPDYWH SRLFPKANAO RT

1260

1320

1342

Protein Accession #: NP\_001207.1 31 51 5 MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120 DPOEPONNAH RDKEGDDOSH WRYGGDPPWP RVSPACAGRF OSPVDIRPOL AAFCPALRPL 180 ELLGFOLPPL PELRLRNNGH SVOLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240 10 VEGHRFPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA 300 EEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS 360 DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420 GLLFAVTSVA FLVOMRROHR RGTKGGVSYR PAEVAETGA 459 15 Seq ID NO: C292 Protein Sequence Protein Accession #: NP\_004198.1 20 MGGAVVDEGP TGVKAPDGGW GWAVLFGCFV ITGFSYAFPK AVSVFFKELI QEFGIGYSDT AWISSILLAM LYGTGPLCSV CVNRFGCRPV MLVGGLFASL GMVAASFCRS IIQVYLTTGV 120 ITGLGLALNF QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGWRGGF LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLLDL SVFRDRGFVL YAVAASVMVL 240 GLFVPPVFVV SYAKDLGVPD TKAAPLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSF 300 25 SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGNVGALQF EVLMAIVGTH KFSSAIGLVL 360 LMEAVAVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLLGNFFCI RKKPKEPQPE VAAAEEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465 Seq ID NO: C293 Protein Sequence 30 Protein Accession #: NP\_000349.1 MALEVRLLAL ALALALGPAA TLAGPAKSPY QLVLQHSRLR GRQHGPNVCA VQKVIGTNRK YFTNCKQWYQ RKICGKSTVI SYECCPGYEK VPGEKGCPAA LPLSNLYETL GVVGSTTTQL 35 120 YTDRTEKLRP EMEGPGSPTI FAPSNEAWAS LPAEVLDSLV SNVNIELLNA LRYHMVGRRV 180 LTDELKHGMT LTSMYQNSNI QIHHYPNGIV TVNCARLLKA DHHATNGVVH LIDKVISTIT 240 NNIQQIISIE DTFFTLRAAV AASGLMTMLE GNGQYTLLAP TNEAFEKIPS ETLNRILGDP EALRDLLNNH ILKSAMCAEA IVAGLSVETL EGTTLEVGCS GDMLTINGKA IISNKDILAT NGVIHYIDEL LIPDSAKTLF ELAAESDVST AIDLFRQAGL GNHLSGSERL TLLAPLNSVF 300 360 40 420 KDGTPPIDAH TRNLLRNHII KDQLASKYLY HGQTLETLGG KKLRVFVYRN SLCIENSCIA 480 AHDKRGRYGT LFTMDRVLTP PMGTVMDVLK GDNRFSMLVA AIQSAGLTET LNREGVYTVF 540 APTNEAFRAL PPRERSRLLG DAKELANILK YHIGDEILVS GGIGALVRLK SLOGDKLEVS 600 LKNNVVSVNK EPVAEPDIMA TNGVVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660 45 SRASQRSVRL APVYQKLLER MKH Seg ID NO: C294 Protein Seguence Protein Accession #: NP\_006527.1 50 MTQRSIAGPI CNLKFVTLLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISN IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH 120 GDDPYTLOYR GCGKEGKYIH FTPNFLLNDN LTAGYGSRGR VFVHEWAHLR WGVFDEYNND 180 55 KPFYINGONO IKVTRCSSDI TGIFVCEKGP CPOENCIISK LFKEGCTFIY NSTONATASI 240 MFMQSLSSVV EFCNASTHNQ EAPNLQNQMC SLRSAWDVIT DSADFHHSFP MNGTELPPPP 300 TFSLVQAGDK VVCLVLDVSS KMAEADRLLQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI 360 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGP EVVEKLNGKA YGSVMILVTS 420 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVPDI SNSNSMIDAF 480 60 SRISSGTGDI FQQHIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540 PDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS AVPPATVEAF VERDSLHPPH PVMIYANVKO GFYPILNATV TATVEPBTGD PVTLRLLDDG 600 660 AGADVIKNDG IYSRYFFSFA ANGRYSLKVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720 IQMNAPRKSV GRNEBERKWG FSRVSSGSF SVLGVPAGPH PDVFPPCKII DLEAVKVEEE LTLSWTAPGE DFDQGQATSY EIRMSKSLQN IQDDFNNAIL VNTSKRNPQQ AGIREIFTFS 780 65 840 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENGT KLL Seg ID NO: C295 Protein Sequence 70 Protein Accession #: Eos sequence MKFLLILLIQ ATASGALPLN SSTSLEKNNV LFGERYLEKF YGLEINKLFV TKMKYSGNLM 75 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHF REMPGGPVWR KHYITYRINN 120 YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHAFDGKGGI 180 LAHAFGPGSG IGGDAHFDED EPWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY 240 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIPF FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIBAAYEIEA RNQVFLFKDD KYWLISNLRP 360 80 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERROMM DPGYPKLITK 420 NFQGIGPKID AVPYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC Seq ID NO: C296 Protein Sequence

Protein Accession #: Eos sequence

Seq ID NO: C291 Protein Sequence

| 5  | REKIQEMQHP<br>YTPDMNREDV<br>LAHAFGPGSG<br>KYVDINTFRL<br>PKDRFFWLKV<br>EPNYPKSIHS | 11<br> <br>ATASGALPLN<br>LGLKVTGQLD<br>DYAIRKAFQV<br>IGGDAHFDED<br>SADDIRGIQS<br>SERPKTSVNL<br>FGFPNFVKKI<br>AVFYSKNKYY | SSTSLEKNNV TSTLEMMHAP WSNVTPLKFS EFWTTHSGGT LYGDPKENOR ISSLWPTLPS DAAVFNPRFY | LFGERYLEKP<br>RCGVPDVHHF<br>KINTGMADIL<br>NLFLTAVHAI<br>LPNPDNSEPA<br>GIEAAYEIEA<br>RTYFFVDNQY | YGLEINKLPV<br>REMPGGPVWR<br>VVFARGAHGD<br>GHSLGLGHSS<br>LCDPNLSFDA<br>RNQVFLFKDD<br>WRYDERRQMM | KHYITYRINN<br>FHAPDGKGGI<br>DPKAVMFPTY<br>VTTVGNKIFF<br>KYWLISNLRP               | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>470 |
|----|--|---|--|--|--|--|---|
|    |  | C297 Protei   |  | IDFIDQRIIR   | 1 BRONSWI GC   |  | 4,0   |
| 15 |  | ession #: N   |  | 31   | 41   | 51   |   |
| 20 | MAKDNSTVRC<br>IGIFVGICLF<br>FLKQMLERYQ<br>DADYPWPRQC                             | FQGLLIFGNV<br>CLSVLGIVGI<br>NNSPPNNDDQ<br>CVMNLKEPL<br>TMFYWSRIEY   | MKSSRKILLA<br>WKNNGVTKTW   | YFILMPIVYA<br>DRLMLQDNCC   | PEVASCITAA<br>GVNGPSDWQK   | TQRDFFTPNL<br>YTSAFRTENN   | 60<br>120<br>180<br>240<br>260                      |
| 25 |  | C298 Protei<br>cession #: N   |  |  |  |  |   |
| 30 | QEPALFSTDN<br>KGPFPQRLNQ   | 11<br> <br>  LLLLQVCWLQ<br>DDFTVRNGET<br>LKSNKDRDTK<br>NGASVEDPMN   | VQERRSLKER<br>IFYSITGPGA   | NPLKIFPSKR<br>DSPPEGVFAV   | I LRRHKRDWV<br>EKETGWLLLN  | VAPISVPENG<br>KPLDREEIAK   | 60<br>120<br>180<br>240                             |
| 35 | DEDDAIYTYN<br>TDMDGDGSTT<br>AWRATYLIMG   | GVAYSIHSQ<br>TAVAVVEILD<br>GDDGDHFTIT<br>VEDVNEAPVF   | EPKDPHDLMF<br>ANDNAPMFDP<br>THPESNQGIL                                       | TIHRSTGTIS<br>QKYEAHVPEN<br>TTRKGLDFEA   | VISSGLDREK<br>AVGHEVQRLT<br>KNQHTLYVEV   | VPEYTLTIQA<br>VTDLDAPNSP<br>TNEAPFVLKL   | 300<br>360<br>420<br>480                            |
| 40 | DPAGWLAMDP<br>VNDHGPVPEP<br>TVVLSLKKPL<br>GAVLALLFLL<br>GLEARPEVVL               | DSGQVTAVGT<br>RQITICNQSP<br>KQDTYDVHLS  | LDREDEQFVR<br>VRQVLNITDK<br>LSDHGNKEQL<br>RKIKEPLLLP<br>TPMYRPRPAN           | NNIYEVMVLA<br>DLSPHTSPFQ<br>TVIRATVCDC<br>EDDTRDNVFY<br>PDEIGNFIIE                             | MDNGSPPTTG<br>AQLTDDSDIY<br>HGHVETCPGP<br>YGEEGGGEED<br>NLKAANTDPT                             | TGTLLLTLID<br>WTAEVNEEGD<br>WKGGFILPVL<br>QDYDITQLHR                             | 540<br>600<br>660<br>720<br>780                     |
| 45 |  | C299 Prote<br>cession #:  |  |  |  |  |   |
| 50 | FIMSCVGFAV<br>INVWNICPLF   | KGLGYASMVI  | LCYKNGGGVP<br>VPYCNTYYIM   | LIPYVLIALV<br>VLAWGFYYLV   | GGIPIPFLEI<br>KSFTTTLPWA   | 51<br>   | 60<br>120<br>180<br>240                             |
| 55 | GSPQVWIDAG<br>SILGFMAAEQ<br>GVEGFITGLI<br>TTLLWQAFWE<br>YYEPLVYNNT               | TQIFPSYAIG OVHISKVAES DLLPASYYFR CVVVAWVYGA YVYPWWGEAM  | GPGLAFIAYP<br>FORBISVALO<br>DRFMDDIACM<br>GWAFALSSML                         | NRFNNNCYKD<br>RAVTLMPVAP<br>CALCFVIDLS<br>IGYRPCPWMK<br>CVPLHLLGCL                             | AIILALINSG<br>LWAALFFFML<br>MVTDGGMYVF<br>WCWSFFTPLV   | YYLKPDWSKL<br>TSFPAGFVVP<br>LLLGLDSQFV<br>QLFDYYSASG<br>CMGIFIFNVV<br>WQHLTQPIWG | 300<br>360<br>420<br>480<br>540<br>600              |
| 60 | Seq ID NO:   | ADVRGLTTLI<br>C300 Protectesion #:  | in Sequence  |  |  |  | 635   |
| 65 | LTTLWSLSV  | A IFSVGGMIGS  | FSVGLFVNRE   | GRRNSMLMMN   | LLAPVSAVL  | 51<br> <br>  RYGESILPTT<br>  GFSKLGKSPB  | 60<br>120   |
| 70 | GNKDLWPLLI<br>LQEMKEESR(<br>AGVQQPVYA:<br>LPWMSYLSIV                             | L SIIFIPALL(<br>) MMREKKVTII<br>F IGSGIVNTAI<br>V AIFGFVAFFI  | CIVLPFCPES LELFRSPAYRO TVVSLFVVEF VGPGPIPWF1                                 | PRFLLINRNE PILIAVVLQI R AGRRTLHLIC VAELFSQGPF  | ENRAKSVLKI<br>SQQLSGINAV<br>LAGMAGCAII<br>PAAIAVAGPS   | AQVFGLDSIM C LRGTADVTHD FYYSTSIFEK MTIALALLEQ NWTSNFIVGM GASQSDKTPE              | 180<br>240<br>300<br>360<br>420<br>480              |
| 75 | ELFHPLGAD:<br>Seq ID NO  | S QV<br>: C301 Prote  | ein Sequence   |  |  |  | 492   |
|    |  | ccession #:   | XP_035292.2  | 2  | 41   | E1   |   |
| 80 | GTIIGSGIF<br>LEVYGSLPA   | V TPTGVLKEA<br>F LKLWIELLI  | S SPGLALVVW<br>I RPSSQYIVAI  | A ACGVFSIVG/<br>L VPATYLLKPI   | LCYAELGTT<br>PPTCPVPEE   | 51<br> <br>  TLLNGVAIIV<br>  SKSGGDYAYM<br>  AKLVACLCVL<br>  FSFEGTKLDV          | 60<br>120<br>180<br>240                             |

| 5   | GNIVLALYSG<br>STEQMLSSEA<br>SILSMIHPQL<br>RKPELERPIK<br>KPKWLLQGIF   | VAVDFGNYHL<br>LTPVPSLVFT<br>VNLALPVFFI  | GVMSWIIPVF<br>CVMTLLYAFS<br>LACLFLIAVS  | VGLSCFGSVN<br>KDIFSVINFF  | GSLFTSSRLF<br>SFFNWLCVAL   | FVGSREGHLP<br>AIIGMIWLRH   | 300<br>360<br>420<br>480<br>507  |
|---|--|---|---|---|--|--|--|
|   | Seq ID NO:<br>Protein Acc  |   |   |   |  |  |  |
| 10  |  |   | _   | 31<br>  | 41   | 51<br>   |  |
| 15  | MNWSIFEGLL<br>SNVCFDEFFP<br>GKKRGGLWWT<br>SEKNIFTLFM<br>DDLLSGDLIF   | VSHVRLWALQ<br>YVCSLVFKAS<br>VATAAICILL  | LILVTCPSLL<br>VDIAFLYVFH<br>NLVELIYLVS  | VVMHVAYREV<br>SFYPKYILPP<br>KRCHECLAAR  | QEKRHREAHG<br>VVKCHADPCP   | ENSGRLYLNP<br>NIVDCFISKP   | 60<br>120<br>180<br>240<br>273   |
| 20  | Seq ID NO:<br>Protein Acc  |   |   |   |  |  |  |
|   | 1  | 11  | 21  | 31  | 41   | 51   |  |
| 25  | VTKDQANCRW<br>RSQKDICRYS   | AATEQEEGIS<br>KTAVKTRVCR  | VEGKKKVKNG<br>LKVECTQLDH<br>KDFPESSLKL<br>PDMANQRKTA  | EFSCVFAGNP<br>VSSTLFGNTK  | TSCLKLKDER<br>PRKEKTEMSP   | VYWKQVARNL<br>REHIKGKETT   | 60<br>120<br>180<br>234  |
| 30  |  | C304 Protei<br>cession #: F   |   |   |  |  |  |
|   | 1  | 11  | 21  | 31  | 41   | 51   |  |
| 35  | RNITEAVMVS<br>ASIVVNNPDL   | ENFOIEAPNY<br>LMFCDQAGSR  | LIKVKFGESI<br>LSKESEVLIY<br>RMIRFRFDSF<br>LTVHTSLVCS  | ARRDSQCIDC<br>DKTIEFPILK  | FQAFLPVHCR<br>CWAHSEVAAP   |  | 60<br>120<br>180<br>225  |
| 40  | -  | C305 Proteicession #: 1   | _   | 31  | 41   | 51   |  |
|   | 1  | Ī   | ĩ   | Ĩ   | i"   | ĩ.   |  |
|   |  |   |   |   |  |  |  |
| 45  | RGESKSLGPA<br>ITYWIQNYSE   | LLLLQKQLSL<br>DLPRAVIDDA  | PETGELDSAT<br>FARAFALWSA  | LKAMRTPROG<br>VTPLTFTRVY  | VPDLGRFQTF<br>SRDADIVIQF   | GVAEHGDGYP   | 60<br>120<br>180   |
|   | RGESKSLGPA<br>ITYWIQNYSE<br>FDGKDGLLAH<br>YSACTTDGRS<br>ACTTDGRSDG   | LLLLQKQLSL<br>DLPRAVIDDA<br>AFPPGPGIQG<br>DGLPWCSTTA<br>YRWCATTANY  | PETGELDSAT<br>FARAFALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCP  | LKAMRTPRCG<br>VTPLTPTRVY<br>SLGKGVVVPT<br>CPSERLYTRD<br>TRADSTVMGG  | VPDLGRFQTF<br>SRDADIVIQF<br>RFGNADGAAC<br>GNADGKPCQF<br>NSAGELCVFP   | EGDLKWHHHN<br>GVAEHGDGYP<br>HPPFIFEGRS<br>PFIFQGQSYS<br>FTFLGKEYST   | 120<br>180<br>240<br>300<br>360  |
| 50  | RGESKSLGPA<br>ITYWIQNYSE<br>FDGKDGLLAH<br>YSACTTDGRSDG<br>ACTTDGRSDG<br>CTSEGRGDGR<br>PMYRFTEGPP<br>PTAGPTGPPS   | LLLLQKQLSL<br>DLPRAVIDDA<br>AFPPGPGIQG<br>DGLPWCSTTA<br>YRWCATTANY<br>LWCATTSNFD<br>LHKDDVNGIR<br>AGPTGPPTAG  | PETGELDSAT<br>FARAFALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCP<br>SDKKWGFCPD<br>HLYGPRPEPE<br>PSTATTVPLS  | LKAMRTPRCG<br>VTPLTFTRVY<br>SLGKGVVVPT<br>CPSERLYTRD<br>TRADSTVMGG<br>QGYSLFLVAA<br>PRPPTTTTPQ<br>PVDDACNVNI  | VPDLGRFQTF<br>SRDADIVIQF<br>RFGNADGAAC<br>GNADGKPCQF<br>NSAGELCVFP<br>HEFGHALGLD<br>PTAPPTVCPT<br>FDAIAEIGNQ   | EGDLKWHHHN<br>GVAEHGDGYP<br>HPPFIFEGRS<br>PFIFQGQSYS   | 120<br>180<br>240<br>300   |
| 50  | RGESKSLGPA<br>ITYWIQNYSE<br>FDGKDGLLAH<br>YSACTTDGRSDG<br>CTSEGRGDGR<br>PMYRFTEGPP<br>PTAGPTGPPS<br>RFSEGRGSRP<br>LDKLGLGADV   | LILLQKQLSL<br>DLPRAVIDDA<br>APPPGPGIQG<br>DCLPWCSTTA<br>YRNCATTANY<br>LWCATTSNFD<br>LHKDDVNGIR<br>AGPTGPPTAG<br>QGPFLIADKW<br>AQVTGALRSG  | PETGELDSAT<br>FARAFALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCPD<br>SDKKWGFCPD<br>HLYGPRPEPE<br>PSTATTVPLS<br>PALPRKLDSV   | LKAMRTPRCG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI PEEPLSKKLP RLWRFDVKAQ   | VPDLGRFQTF<br>SRDADIVIQE<br>RFGNADGAC<br>GNADGKPCQF<br>NSAGELCVFP<br>HEFGHALGLD<br>PTAPPTVCPT<br>FDAIAEIGNQ<br>FPSGRQVWYY<br>MVDPRSASEV  | EGDLKWHHEN<br>GVAEHGDGYP<br>HPPFIFEGRS<br>PFIFEGREYST<br>HSSVPEALMY<br>GPPTVHPSER<br>LYLFKDGKYW  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540   |
|   | RGESKSLGPA ITYWIQNYSE FDGKDGLLAH YSACTTDGRSDG CTSEGRGDGR PMYRPTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVPQYREK Seq ID NO:   | LILLQKQLSL<br>DLPRAVIDDA<br>AFPPGPGIQG<br>DGLPWCSTTA<br>YRWCATTANY<br>LWCATTSNF<br>LHKDDVNGIR<br>AGPTGPPTAG<br>QGPFLIADKW<br>AQVTGALRSG<br>AYFCQDRFYW   | PETGELDSAT<br>FARAPALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCP<br>SDKKWGFCPD<br>HLYGPRPEPE<br>PSTATTVPLS<br>PALPRKLDSV<br>RGKMLLFSGR<br>RVSSRSELNQ<br>in Sequence   | LKAMRTPRCG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI FEEPLSKKLF RLWRFDVKAQ VDQVGYVTYD  | VPDLGRFQTF<br>SRDADIVIQE<br>RFGNADGAC<br>GNADGKPCQF<br>NSAGELCVFP<br>HEFGHALGLD<br>PTAPPTVCPT<br>FDAIAEIGNQ<br>FPSGRQVWYY<br>MVDPRSASEV  | EGDLKWHHEN GVAEHGDGYP HPPFIFEGRS PFIFQGQSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660   |
| 50  | RGESKSLGPA ITYWIQNYSE FDGKDGLLAH YSACTTDGRSDG CTSEGRGDGR PMYRPTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVPQYREK Seq ID NO:   | LILLQKQLSL<br>DLPRAVIDDA<br>AFPPGPGIQG<br>DGLPWCSTTA<br>YRNCATTANY<br>LWCATTSNFD<br>LHKDDVNGIR<br>AGFTGPPTAG<br>QGPFLIADKW<br>AQVTGALRSG<br>AYFCQDRPYW<br>C306 Prote  | PETGELDSAT<br>FARAPALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCP<br>SDKKWGFCPD<br>HLYGPRPEPE<br>PSTATTVPLS<br>PALPRKLDSV<br>RGKMLLFSGR<br>RVSSRSELNQ<br>in Sequence   | LKAMRTPRCG VTPLTFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI FEEPLSKKLF RLWRFDVKAQ VDQVGYVTYD  | VPDLGRFQTF<br>SRDADIVIQE<br>RFGNADGAC<br>GNADGKPCQF<br>NSAGELCVFP<br>HEFGHALGLD<br>PTAPPTVCPT<br>FDAIAEIGNQ<br>FPSGRQVWYY<br>MVDPRSASEV  | EGDLKWHHEN GVAEHGDGYP HPPFIFEGRS PFIFQGQSYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660   |
| 50  | RGESKSLGPA ITYWIONYSE FDGKOGLLAH YSACTIDGRS ACTIDGRSDG CTSEGRGDGR PMYRFTGSPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK Seq ID NO: Protein Act  | LLLLQKQLSL DLPRAVIDDA APPPGPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW C306 Prote cession #: 1    RLLLAALISV GCQRESIVVM   | PETGELDSAT<br>FARAPALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCP<br>SDKKWGFCPD<br>HLYGPRPEPE<br>PSTATTVPLS<br>PALPRKLDSV<br>RGKMLLFSGR<br>RVSSRSELNQ<br>in Sequence<br>NP_000204<br>21<br> <br>SLSGTLANRC<br>ESSFQITEST   | LKAMRTPRCG VTPLIFTRYY SLGKGVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAB PRPPTTTTPQ PVDDACNVNI PEEPLSKKLP RLWRPDVKAQ VDQVGYVTYD  31   KKAPVKSCTE QIDTTLRRSQ   | VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF NSAGELCVFP HEFGHALGL PTAPPTVCPT FDAIAEIGNQ FPSGRQVWYY MVDPRSASEV ILQCPED  41   CVRVDKDCAY MSPQGLRVRL   | EGDLKWHHHN GVAEHGDGYP HPPFIFEGRS PFIFQGGYS FTFLGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMPPGVPLD  51   CTDEMFRDRR RPGEERHFEL   | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>707   |
| 50  | RGESKSLGPA ITYWIONYSE FDGKDGLIAH YSACTIDGRS ACTIDGRSDG CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THUVFQYREK Seq ID NO: Protein Act  | LLLLQKQLSL DLPRAVIDDA APPPGPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW  C306 Prote cession #: 1   | PETGELDSAT<br>FARAPALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCPD<br>HLYGPRPEPE<br>PSTATTVPLS<br>PALPRKLDSV<br>RGKMLLFSGR<br>RVSSRSBLNQ<br>in Sequence<br>NP_000204<br>21<br> <br>SLSGTLANRC<br>ESSFQITEST<br>SMSDDLDNLK<br>FSFKNVISLT<br>FSTESAPHYE  | LKAMRTPRCG VTPLIFTRVY SLGKGVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI PEEPLSKRLP RLWRPDVKAQ VDQVGYVTYD  31   KKAPVKSCTE QIDTTLRRSQ KMGQNLAVVLAG ADGANVLAGI   | VPDLGRFQTF SRDADIVIQF RFGNADGAAC GNADGKPCQF NSAGELCVFP HEFGHALGLIO PTAPPTVCPT FDAIAEIGNQ FFSGRQVWYY MVDPRSASEV ILQCPED  41   CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL  | EGDLKWHHHN GVAEHEDGYP HPPFIFEGRS PFIFQGQSYS FTFIGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMPPGVPLD  | 120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>707  |
| 50<br>55<br>60  | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTTDGRSDG CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSR RFSEGRGSR Seq ID NO: Protein Act  1   MAGPRPSPWA CNTQAELLAA EVFEPLESPV PQTDMRPEKL QTAVCTRDIG TQDYPSVPTL EAFNRIRSNL  | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGFTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW  11   RLLLAALISV GCQRESIVM KEPWPNSDPP MRPDSTHLLV VRLLAKHNII DIRALDSPRG  | PETGELDSAT<br>FARAFALWSA<br>DAHFDDDELW<br>NYDTDDRFGF<br>DRDKLFGFCPD<br>HLYGPRPEPE<br>PSTATTVPLS<br>PALPRKLDSV<br>RGKMLLFSGR<br>RVSSRSELNQ<br>in Sequence<br>NP_000204<br>21<br> <br>SLSGTLANRC<br>ESSFQITEST<br>SMSDDLDNLK<br>FSFKNVISLT<br>FSTESAFHYE<br>PIFAVTNYSY<br>LRTEVTSKMF  | LKAMRTPRCG VTPLIFTRVY SLGKGVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PVDDACNVNI FEEPLSKKIF RLWRPPVKAQ VDQVGYVTYD  31   KKAPVKSCTE QIDTTLRRQQ KMGQNLAVL EDVDEFRNKL ADGANVLAGI QKTRTGSFHI  | VPDLGRFQTF SRDADIVIQF RFGNADGAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FPSGRQVWY MVDPRSASEV ILQCPED  41   CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RRGEVGIYQV   | EGDLKMHHN GVAEHEDGYP HPFFIFEGRS PFIFGGSYS FTFLGKSYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMPPGVPLD  51   CTDEMFRDRR RPGEERHFEL PGKYVDKVSV APEGGFDAIL DTTGTYTQYR   | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>660<br>707   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTDGRSG CTSEGRGDGR PMYRPTEGPP PTAGPTOPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK Seq ID NO: Protein Act    MAGPRPSFWA CNTQAELLAA EVFEPLESPV PQTDMRPKLL CYTAVCTRDIG TQDYPSVPTL EAFNRIRSNLL THVCQLPEDQ CSEGWSGGTC   | LLLLQKQLSL DLPRAVIDDA APPPEPGIQG DGLPWCSTTA YRNCATTANY LHKDDVNGIR AGFTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRFYW  C306 Prote cession #: 1                RLLLAALISV GCQRESIVVM DLYILMDFSN KEFWPNSDPP WRPDSTHLLV VRLLAKHNII DIRALDSPRG KGNIHLKPSF NCSTGSLSDI  | PETGELDSAT PARAPALWSA DAHFDDDELW NYDTDDRFGF DRDKLFGFCP SDKKWGFCPD HLYGPRPEPB FSTATTVPLS PALPRKLDSV RCEMILFSGR RVSSRSBLNQ in Sequence NP_000204  21   SLSGTLANNC ESSFQITEST SMSDDLDNLK FSFRNVISLT FSTESAFHYE PIPAVTNYSY LRTEVTSKMF FSDGLKMDAGI QPCLREGEDK  | LKAMRTPRCG VTPLIFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PUDDACNVNI FEEPLSKKLP RLWRFDVKAQ VDQVGYVTYD  31   KKAPVKSCTE QUDTTLRRSQ KMGQNLARVL EDVDEPRNKL ADGANVLAGI SYYEKLHTYF QKTRTGSFHI ICDVCTCELQ PCSGRGECQC   | VPDLGRFQTF SRDADIVIQE RFGNADGAAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDATAEIGNQ FPSGRQVWY MVDPRSASEV ILQCPED  41   CVRVDEDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RRGEVGTYQV KEVRSARCSF   | EGDLKWHHHM GVAEHGDGYP HPPFIFGRS PFIFQGSYS FTFIGKSYST HSSVPEALMY GPPTVHPSER LYLIKUGKYW TGASVLGPR DRMFPGVPLD  51   CTDEMFRDRR RPGGERHFEL FFGKFVDKVSV ABEGGFDAIL DTTGTTYGYR DSSNIVELLE QURALEHVDG VMGDFVCGQCV YBGQFCEVDN  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>600<br>660<br>707   |
| 50<br>55<br>60  | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTTGRSDG CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVPQYREK  Seq ID NO: Protein Ac  1   MAGPRPSPWA CNTQAELLAA EVFEPLESPV PQTDMRPEKL QTAVCTRDIG TQDYPSVPTL EAFNRIRSNL THVCQLPEDQ CSEGWSGGTC FQCPRTSGFL CHCHQQSLYT  | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGPTGPPTAG AQPTGPLIADK AQVTGALRSG AYFCQDRFYW  C306 Prote cession #: '  """  """  """  """  """  """  """  | PETGELDSAT FARAFALWSA DAHFDDDELW NYDTDDRFGF DRDKLFGFCPD HLYGPRPEPE PSTATTVPLS FALPKLDSV IN SEQUENCE PD00204  21   SLSGTLANEC ESSFQITEST SMSDDLDNLK FSFRNVISLT FSTESAFHYE PIFAVTNYSE LRTEVTSKMF SDGLKMDAGI QPCLREGEDK QCVCEPGMTG IHPGLCEDLR  | LKAMRTPRCG VTPLIFTRVY SLGKGVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAG PRPPTTTTPQ PVDDACNVNI FEEPLSKKLP RLWRPPVKAQ VDQVGYVTYD  31   KKAPVKSCTE QIDTTLRSQQ KMGQNLAVL EDVDEFRNKL ADGANVLAGI SYYEKLHTYF QKTRTGSFHI ICDVCTCELQ PCSGRGEQQC PSCDCPLSNA SCVQCQAWGT   | VPDLGRFQTF SRDADIVIQF SRDADIVIQF RFGNADGAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FFSGRQVWVY MVDPRSASEV ILQCPED  41   CVRVDKDCAY MSPQGLRVRL SQLTSDYIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RRGEVGTYQV KEVRSARCSF GHCVCYGEAR TCIDSNGGIC GEKKGRTCEE  | EGDLKWHHHN GVAEHEDGYP HPPFIFEGRS PFIFQGQSYS FTFIGKEYST HSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMPPGVPLD  51   CTDEMFRDRR REGERHFEL PGKPVDKVSV APEGGFDAIL DTTGTYTQYR DSSNIVELLE QURALEHVDG VRGPFVCGQCV YEGQFCEVDN LNGRGHCEGGR CKPKVKMVDE   | 120<br>180<br>240<br>300<br>360<br>420<br>660<br>707<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>660   |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTDGRSGDG CTSEGRGDG PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK  Seq ID NO: Protein Act      AGGPRPSFWA CNTQAELLAA EVFEPLESPV PQTDMRPHKL QTAVCTRDIG TQDYPSVPTL EAFNRIRSNL THVCQLPEDQ CSEGWSGGTC FQCPRTSGFL CHCHQQSLYVT LLYPLLALLLL  | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGFTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW  C306 Prote cession #: '  "ILLLAALISV GCQRESIVVM DLYILMDFSN KEPWPNSDPP WRPDSTHLLV VRLLAKHNII DIRALDSPRG KGNIHLKPSF INCSTGSLSDI CNDRGRCSMG DTICEINYSA CSFRDEDDDC LCWEXCACCK  | PETGELDSAT FARAFALWSA DAHFDDDELW NYDTDDRFGF DRDKKLFGFCP PSDKKWGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGEMILFSGR RVSSRSELNQ IN SEQUENCE NP_000204  21   SLSGTLANRC ESSFQITEST SMSDDLDNLK FSFRWVISLT FSTESAFHYE PIFAVTNYSY LRTEVTSKMF SDGLKMDAGI QPCLREGEDK QCVCEPGWTG IHPGLCEDLR TYSYTMEGOL  | LKAMRTPRCG VTPLIFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PUDDACNVNI PEEPLSKKLP RLWRPPVKAQ VDQVGYVTYD  31   KKAPVKSCTE QUDTTLRRSQ KMGQNLARVL EDVDEPRNKLL ADGANVLAGI SYYEKLHTYF QKTRTGSPHI ICDVCTCELQ PCSGRGEQQ PSCDCPLSNA SCVQCQAWGT APGPNSTVLV RGHMVGFKED   | VPDLGRFQTF SRDADIVIQE RFGNADGAAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ PPSGRQVWVY MVDPRSASEV ILQCPED  41    CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RRGEVGIYQV KEVRSACSE GHCVCYGEGR TCIDSNGGIC GEKKGRTCEE HKKKDCPPGS HYMLRENLMA   | EGDLKWHHHIN GVAEHEDGYP HPPFIFGRS PFIFQGSYS FTFIGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMFPGVPLD  51   CTDEMFRDRR RPGEERHFEL FGKYVDKVSV APEGGFDAIL DTTGTYTQYR DSSNIVELLE QLRALEHVDG NGDFVCGQCV YEGGFCEVDN NGRGHCECGR CYFEVKMVDE  | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>707  |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>                       | RGESKSLGPA ITYWIONYSE FOGKOGLIAH YSACTTDGRS ACTTTGRSDG CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK  Seq ID NO: Protein Act   | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRFYW  C306 Prote cession #: 1    RLLLAALISV GCQRESIVVM MDLYILMDFSN KEPWPNSDPP WRPDSTHLLV VRLLAKHNIG DIRALDSPRG KGNIHLKPSF NCSTGSLSDI CNDRGRCSMG DTICEINYSA CSFRDEDDDC LCWEYCACCK RWKVTNNMQR LNEYYRQISG   | PETGELDSAT FARAPALWSA DAHFDDDELW NYDTDDRFGF DRDKLFGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGENLLPSGR RVSSRSELNQ in Sequence NP_000204  21    SLSGTLANRC ESSFQITEST SMSDDLDHLK FSFRNVISLT FSTESAFHYE PIFAVTNYSY LRTEVISKMP SDGLKMDAGI QPCLREGEDK QCVCEPGWTG CVCEPGWTG TYSYTMEGDG ACLALLPCCN PGFATHAASI VHKLQQTKFR   | LKAMRTPRCG VTPLIFTRVY SLGKGVVPT CPSERLYTRD TRADSTVMGA PRPPTTTPQ PVDDACNVNI PEEPLSKKLF RLWRPDVKAQ VDQVGYVTYD  31    KKAPVKSCTE QIDTTLRRSQ KMGQNLARVL EDVDEPRNKL ADGANVLAGI SYYEKLHTYF ICDVCTCELQ PCSGRGEQQC PSCDCPLSNA SCVQQAWGT APGPNSTVLV RGHMVGFKED UPTELVPYGL QQPNAGKKQD   | VPDLGRFQTF SRDADIVIQF SRDADIVIQF RFGNADGAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FFSGRQVWVY MVDPRSASEV ILQCPED  41    CVRVDEDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE ERGEVCYGEAR TCIDSNGGIC GEKKGRTCEE HKKKDCPPGS HYMLRENLMA SLRLARLCTE HTIVDTVLMF   | EGDLKMHHHN GVAEHGDGY HPPFIFGRS PFIFGGSYS FFIFGKSYST HSVPEALMY GPPTVHESER LYLFKDGKYW TGASVLGPRR DRMPPGVPLD  51   CTDEMFRDRR REGERHFEL PGKFVDKVSV APEGGFDAIL DTTGTYTQYR CQLRALEHUDG VRGDFVCGQCV YEGGFCEVDN NGRGHCECGR CWFEVKMVDE FWWLIPLLLL SDBLDTPMLR NLLKPDTREC NLLKPDTREC NLLKPDTREC NESKPALLK  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>707  |
| 50<br>55<br>60<br>65<br>70  | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTDGRSG CTSEGRGDGR CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK  Seq ID NO: Protein Acc  1   MAGGPRPSFWA CNTQAELLAA EVFEPLESPV PQTDMRPHKL QTAVCTRDIG TQDYPSVPTL EAFNRIRSNL THVCQLPEDG CSEGWSGGTC FQCPRTSGFL CHCHQQSLYL LLPLLALLLL SGNLKGRDVV AQLRQEVEEN LTEKQVEQRA  | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRWCATTANY LWCATTSNFD LHKDDVNGIR AGFTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW  C306 Prote cession #: 1      RLLLAALISV GCQRESIVVM DLYILMDFSN KEPWPNSDPP WRPDSTHLLV VRLLAKHNII DIRALDSPRG KGNIHLKPSF NCSTGSLSDI CNDRGRCSMG DTICEINYSA CSFROEDDDC LCWKYCACCK RWKVTNNMQR KWKVTNNMQR LYVRQISG LYMEVYRQISG FHDLKVAPGY  | PETGELDSAT PARAPALWSA DAHFDDELW NYDTDDRFGF DRDKLFGFCP PROKKLFGFCP PSTATTVPLS PALPRKLDSV RGEMILFSGR RVSSRSBLNQ IN SEQUENCE NP_000204  21   SLSGTLANNC ESSFCITEST SMSDDLDNLK FSFRNVISLT FSTESAFHYE PIFAVTNYSY LRTEVTSKMF SDGLKMDAGI QPCLREGEDK QCVCEPGWTG LHPGLCEDLR TYSYTMEGOG ACLALLPCCN PGFATHAASI VHKLQQTKFF VYLTADQDAF   | LKAMRTPRCG VTPLIFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PUDDACNVNI PEEPLSKKLP RLWRPPUKAQ VDQVGYVTYD  31   KKAPVKSCTE QUDTTLRRSQ KMGQNLARVL EDVDEPRNKLL ADGANVLAGI SYYEKLHTYF QKTRTGSFHI ICDVCTCELQ PCSGRGECQC PSCDCPLSNA SCVQCQAWGT APGPNSTVLV RGHMVGFKED NPTELVPYGL QQPNAGKKQD GMVEFQEGVE   | VPDLGRFOTF SRDADIVIÇE SRDADIVIÇE RFGNADGAAC GNADGKPCQF NSAGELCVFP NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ PPSGRQVWVY MVDPRSASEV ILQCPED  41    CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RGGVGIYQL KEVRSARCSE GHCVCYGEGR TCIDSNGGIC GEKKGRTCEE HKKKDCPPGS HYMLRENLMA SLRLARLCTE HTIVDTVLMM LVDVRVPLFI  | EGDLKWHHHIN GVAEHGDGYP HPPFIFGRS PPIFQQSYS FTFIGKSYST HSSVPEALMY GPPTVHPSER LYLIFKDGKYW TGASVLGPR DRMFPGVPLD  51   CTDEMFRDRR RPGEERHFEL FFGKPVDKVSV APEGGFNAIL DTTGTYTQYR DSSNIVELLE QLRALEHVDG NGDFVCQCV YEGQFCEVDN NGRGHCECGR CWFKVKMYDE STHULLL SDHLDTPMLR NLLKPDTREC PFSARPALLK RPEDDDEKQL  | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>707<br>60<br>120<br>180<br>240<br>360<br>420<br>480<br>660<br>720<br>780<br>840<br>900<br>960  |
| 50<br>55<br>60<br>65<br>70  | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTTGRSDG CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP PLOKLGLGADV THDVPQYREK  Seq ID NO: Protein Ac  I   MAGPRPSPWA CNTQAELLAAA EVFEPLESPV PQTDMRPEKL QTAVCTRDIG TQDYPSVPIT LEAFNRIRSNL THVCQLPEDQ CSEGWSGGTC PQCPRTSGFL CHCHQQSLYT LKRAEEVVVR LLPLLALLLL SGNLKGRDVV AQLRQEVEEN LTEKQVEQRA LVEAIDVPAG KSQVSYRTQD  | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGPTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRFYW  C306 Prote cession #: '  """ """ """ """ """ """ """ """ """   | PETGELDSAT FARAPALWSA DAHFDDDELW NYDTDDRFGF DRDKLFGFCPD HLYGPRPEPE PSTATTVPLS FALPKLDSV IN SEQUENCE NP_000204  21   SLSGTLANRC ESSFQITEST SMSDDLDNLK FSFRAVISLT FSTESAFHYE PIPAVTNYSK SDGLKMDAGI QPCLREGEDK QCVCEPGWTG IHPGLCEDLR TYSYTMEGGS ACLALLPCCN PGFATHAASI VHKLQQTKFR YTLTADQDAR ITIIKEQARL PVEGELLFQE  | LKAMRTPRCG VTPLIFTRVY SLGKGVVPT CPSERLYTRD TRADSTVMGA RPPTTTTPQ PUDDACNVNI FEEPLSKKIP RLWRPPVKAQ VDQVGYVTYD  31    KKAPVKSCTE QIDTTLRRQQ KMGQNLARVL EDVDEFRNKL ADGANVLAGI SYYEKLHTYF QKTRTGSFHI ICDVCTCELQ PCSGRGEQQC PSCDCPLSNA SCVQQAWGT APGPNSTVLV RGHMVGFKED NPTELVPYGL QQPNAGKKQD CMVEPCGSVE VVSPEQPEFS GEAWKELQVK   | VPDLGRFQTF SRDADIVIQF RFGNADGAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FFSGRQVWVY MVDPRSASEV ILQCPED  41   CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RRGEVGTQQV KEVRSARCSF GHCVCYGEAR TCIDSNGGIC GEKKGRTCEF HKKKDCPPGS HYMLRENLMS SLRLARLCTF HTIVDTVLMF LIVDVRVELFI VSRGDQVARI LLELQEVDSI  | EGDLKWHHHN GVAEHGDGYP HPPFIFGRS PFIFQGQSYS FTFIGKEYST HSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMPPGVPLD  51   CTDEMFRDRR REGERHFEL PGKFVDKVSV APEGGFDAIL DTTGTYTQYR CDSNIVELLE QURALEHVDG VEGQCV YEQOFCEVDN NGGFHCECGR CNFKVMVDE FWHLIPLLLL SDHLDTPMLR NLKPDTREC PRSAKPALLK REEDDDEKQL PVIRRVLDGG LEGRQVRPH  | 120<br>180<br>240<br>300<br>360<br>420<br>540<br>660<br>707<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>780<br>900<br>960<br>1020<br>1080          |
| 50<br>55<br>60<br>65<br>70  | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTTDGRSDG CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSR LOKLGLGADV THDVPQYREK  Seq ID NO: Protein Ac  I MAGPRPSPWA CNTQAELLAA EVFEPLESPV PQTDMRPEKL QTAVCTRDIE TQYPSVPTL EAFNRIRSNL THVCQLPEDQ CSEGWSGQTC CHCHQQSLYT LKRAEEVVY AQLRQEVEEN LUPLLALLLL SGNLKGRDVV AQLRQEVEEN LUPKAGRUVENPKGA KSQVSYRTQD VQLSNPKFGA KKIHFNWLPF   | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNPD LHKDDVNGIR AGFTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW  C306 Prote Cession #: '  11   RLLLAALISV GCQRESIVVM DLYILMDFSN KEPWENSDPP WRPDSTHLLV VRLLAKHNII DIRALDSPRG KGNIHLKPSF INCSTGSLSDI CADRGRCSMG DTICEINYSA CSFRDEDDDC LCMEXCACCK RWKVTNNMQR LNEYYRQISG FHDLKVAPGY TATLGRRLVN GTAQCNRCYI HLGQPHSTTI SGKPRGYRVX                             | PETGELDSAT FARAPALWSAT PARAPALWSAT DAHFDDDELW NYDTDDRFGF DRDKKWGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGRMLLFSGR RVSSRSBLNQ in Sequence NP_000204  21   SLSGTLANRC ESSFQITEST SMSDDLDNLK FSFRNVISLT FSTESAFHYE LRTEVTSKMF SDGLKMDAGI QPCLREGEDK QCVCEPGWTG LIPPGLCEDLR TYSYTMEGD ACLALLPCCN PGFATHAASI VHKLQQTKFR TYTLTADQDAR ITIIKEQARL PVEGELLFQE LIROPDELDR TYNQGDSSSE   | LKAMRTPRCG VTPLIFTRUY SLGKGVVVPT SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PUDDACNVNI PEEPLSKKLP RLWRPPVKAQ VDQVGYVTYD  31    KKAPVKSCTE QUDTTLRRSQ KMGQNLARVL EDVDEPRNKL ADGANVLAGI SYYEKLHTYF QKTRTGSPHI ICDVCTCELQ PCSGRGEQQC PSCDCPLSNA SCVQCQAWGT APGPNSTVLV RGHMVGFKED NPTELVPYGL QQPNAGKKQD GMVEFQEGVE VVSPEQPEFS GEAWKELQVK SPTSQMLSSC AHLLDSKVPS                      | VPDLGRFQTF SRDADIVIÇE SRDADIVIÇE RFGNADGAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ PPSGRQVWY WVDPRSASEV ILQCPED  41    CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RGEVCYGEGR GHCVCYGEGR TCIDSNGGIC GEKKGRTCEE HKKDCPPE HKKDCPPE HKKDCPES HYMLRENLMA SLRLARLCTE HTIVDTVLMA LLVDVRVPLFI VSRGDQVARI LLVDVRVPLFI VSRGDQVARI LLLLQVDSI LLLLQVDSI LLLLQVDSI LLLLQVDSI LLLLLQVDSI LLLLLLQVDSI LLLLLLQVDSI LLLLLLQVDSI LLLLLLQVDSI LLLLLQVDSI LLLLLQVDSI LLLLLLQVDSI LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL | EGDLKWHHHN GVAEHEDGYP HPPFIFEGRS PFIFGGSYS FTFIGKEYST HSSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR DRMFPGVPLD  51   CTDEMFRDRR RPGEERHFEL FPGKYVDKVSV APEGFDAIL DSSNIVELLE QURALEHVDG NGBFVCGQCV YBGQFCEYDN NGRGHCECGR CNFKVKMVDE FWHLIPLLLL SDELDTPMLR SDELDTPMLR CHERQVRFH RPEDDBEKQL FVIRRVLDGG LEGRQVRFH CONPNKAAGG DYEKKVCAYG                          | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>707<br>60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>1020<br>1080<br>1080                |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTTGGRSDG CTSEGRGGR RPMYRFTEGPP PTAGPTGPPS RFSEGRGSR RFSEGRGSR SEQ ID NO: Protein Ac  1   MAGPRPSFWA CNTQAELLAA EVFEPLSPV PQTDMRPEKL QTAVCTRDIG TQDYPSVPTL EAFNRIRSNL THVCQLPEDQ CSEGWSGQTC FQCPRTSGFL CHCHQQSLYT LKPLALLLL SGNLKGRDVV AQLRQEVEEN LTEKQVEQRA LVEAIDVPAG KSQVSYRTQB VQLSNPRFGA RKIHFNWLPF AQGEGPYSSL  | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRNCATTANY LWCATTSNFD LHKDDVNGIR AGFTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW  C306 Protecession #: 1    RLLLAALISV GCQRESIVIM DLYILMDFSN KEPWPNSDPP MRPDSTHLLV VRLLAKHNII DIRALDSPRG KGNHLKPSF NCSTGSLSDI CNDRGRCSMG DTICEINYSA CSFRDEDDDC LCWKYCACCK RWKVTNNMQR LNEVYRQISG FHDLKVAPG TATLGRRLVN GTAQGNRDYI HLGQPHSTTII SGKPMGYRVK VSCRTHQEVF                        | PETGELDSAT FARAPALWSA DAHFDDDELW NYDTDDRFGF DRDKLFGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSY RCSKWGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSY RVSSRSBLNQ  1 SEQUENCE NP_000204  21   SLSGTLANRC ESSFQITEST SMSDDLDNLK FSFKNVISLT FSTESAFHYE PIFAVTNYSY LRTEVTSKMF SDGLKMDAGI QPCLREGEDLE TYSYTMEGDG ACLALLPCCN PGFATHASI VHKLQQTKFE YTLTADQDAE ITIIKEQARL PVEGELLPQE LIRDPDELDGE TYBUQGDSSE SEPGRLAFNW                     | LKAMRTPRCG VTPLIFTTCY SLGKSYVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PUDDACNVNI FEEPLSKKIP RLWRPPVKAQ VDQVGYVTYD  31   KKAPVKSCTE QIDTTLRRQQ KMGQNLAVL EDVDEFRNKL ADGANVLAGI SYYEKLTYF QKTRTGSFHI ICDVCTCELQ PCSGRGEOCQ PSCDCPLSNA SCVQCAWGT APGPNSTVLU RGHMVGFKED NPTELVPYGL QVNAGKQD GMVEFQESCE VVSPEQPEFS GEAWKELQVK SFTSQMLSGQ AHLLDSKVPS VSSTVIQLSW                            | VPDLGRFQTF SEDADIVIQF SEDADIVIQF REGNADGAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ FPSGRQVWVY MVDPRSASEV ILQCPED  41   CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE GGEVCYGEGR TCIDSNGGIC GEKKGRTCEE HKKKDCPPGS HYMLRENLMA SLRLARLCTE HTIVDTVLME LVDVRVPLFI VSRGDQVARI LLELQEVDSI PPFHGDLGAE VELTNLYPYG AEPAETNGEI KAFGAGAGE VELTNLYPYG AEPAETNGEI   | EGDLKWHHHIN GVAEHGDGYP HPPFIFGRS PPIFQQSYS FTFIGKSYST RSVPEALMY GPPTVHPSER LYLIFKDGKYW TGASVLGPR DRMPPGVPLD  51   CTDEMFRDRR RPGGERHFEL PGKFVDKVSV APEGGFNAIL DTTGTYTQYR DRSNIVELLE QLRALEHVDG NGDFVCGQCV YBGQFCEVDN NGRGHCECGR CWFKVKMVDE STHULLL SDHLDTPMLR NLLKPDTREC PRSRAPALLK RPEDDDEKQL PYLRVLDGG LRGRQVRPH QNENAKAAGS                              | 120<br>180<br>300<br>360<br>420<br>480<br>540<br>660<br>707<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>660<br>660<br>720<br>780<br>840<br>960<br>1020<br>1020<br>1020         |
| <ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul> | RGESKSLGPA ITYWIONYSE FDGKDGLLAH YSACTTDGRS ACTTDGRSG CTSEGRGDGR PMYRFTEGPP PTAGPTGPPS RFSEGRGSRP LDKLGLGADV THDVFQYREK  Seq ID NO: Protein Act      AGGPRPSFWA CNTQAELLAA EVFEPLESPV PQTDMRPHKL QTAVCTRDIG TQDYPSVPTL EAFNRIRSNL THVCQLPEDQ CSEGWSGGTC FQCPRTSGFL CHCHQQSLYT LKRAEEVVVR AQLRQEVEEN LYELIALLLLL SGNLKGRDVVV AQLRQEVEEN LVEAIDVPAG KSQVSYTTQL VQLSNPKFGA RKIHFNWLPF AQGGPYSSL NDDNRPIGPM KRPMSIPIIF | LLLLQKQLSL DLPRAVIDDA APPEPGIQG DGLPWCSTTA YRWCATTANY LWCATTSNFD LHKDDVNGIR AGFTGPPTAG QGPFLIADKW AQVTGALRSG AYFCQDRPYW  C306 Prote Cession #: '  "ILLLAALISV GCQRESIVVM DLYILMDFSN KEPWPNSDPP WRPDSTHLLV VRLLAKHNII DIRALDSPRG KGHHLKPSF NCSTGSLSDI CNDRGRCSMG DTICEINYSA CSFRDEDDDC LCMXCACCK RWKVINNMQRG LNEVYRQISG FHDLKVAPGY TATLGRRLVN GTAQCNRDYII HLGQPHSTTI SGKPMGYRVK VSCRTRQEVE KKVLVDNPKN DIPIUDAQSG | PETGELDSAT PARAPALWSA DAHFDDDELW NYDTDDRFGF DRDKKLFGFCP PSDKKWGFCPD HLYGPRPEPE PSTATTVPLS PALPRKLDSV RGEMILFSGR RVSSRSBLNQ in Sequence NP_000204  21   SLSGTLANRC ESSFQITEST SMSDDLDNLK FSFRWVISLT FSTESAFHYE PIFAVTNYSY LRTEVTSKMF SDGLKNDAGI QPCLREGEDK QCVCEPGWTG IHPGLCEDLR TYSYTMEGD ACLALLPCCN PGFATHAASI VHKLQQTKFF YTLTADQDAR ITIIKEQARL PVEGELLFQE IIRDPELDR YWIQGDSESE SEPGRLAFNY RMLLIENTRE EDYDSFLMYS | LKAMRTPRCG VTPLIFTRVY SLGKGVVVPT CPSERLYTRD TRADSTVMGG QGYSLFLVAA PRPPTTTTPQ PUDDACNVNI PEEPLSKKLP RLWRPPVKAQ VDQVGYVTYD  31   KKAPVKSCTE QUDTTLRRSQ KMGQNLARVL EDVDEPRNKLL ADGANVLAGI SYYEKLHTYF QKTRTGSPHI ICDVCTCELQ PCSGREQQC PSCDCPLSNA SCVQCQAWGT APGPNSTVLV RGHMVGFKED NPTELWPYGL QQPNAGKKQD GMVEFQEGVE VVSPEQPEFS GEAWKELQVK SPTSQNLSSC AHLLDSKVPS VSSTVTQLSW SQPYRTYTKG DDVLRSPSGS | VPDLGRFQTF SRDADIVIÇE SRDADIVIÇE RFGNADGAAC GNADGKPCQF NSAGELCVFP HEFGHALGLD PTAPPTVCPT FDAIAEIGNQ PPSGRQVWVY MVDPRSASEV ILQCPED  41    CVRVDKDCAY MSPQGLRVRL SQLTSDYTIG QGERISGNLD MSRNDERCHL FVSSLGVLQE RGEVGIYQV KEVRSARCSF GHCVCYGEGR CGCKKGRTCEE HKKGDCPPGS HYMLRENLMA SLRLARLCTE HTIVDTVLMF LVDVRVPLFI VSRGDQVARI LLELQEVDS VELTNLYPYC AEPAETNGEI RNGAGWGPES RNGAGWGPES RNGAGWGPES RNGAGWGPES RNGAGWGPES RNGAGWGPES RNGAGWGPES RNGAGWGPES RNGAGWGPES   | EGDLKWHHHN GVAEHEDGYP HPPFIFGRS PFIFQQSYS FTFIGKEYST HSVPEALMY GPPTVHPSER LYLFKDGKYW TGASVLGPRR LYLFKDGKYW TGASVLGPRR LYLFKDGKYW TGASVLGPRR CTDEMFRDRR REGERHFEL FGKFVDKVSV APEGGFDAIL DTTGTYTQYR LYBGQFCEYDN SMGRGHCECGR CNFKVKMVDE FWHLIPLLLL SDHLDTPMLR NLLKPDTREC PSSAKPALLK RPEDDDEKGL PVIRRVLDGG LRGRQVRRPH QNPNAKAAGS LYEKVCAYG TAYBVCAYG TAYBVCAYG | 120<br>180<br>240<br>300<br>360<br>420<br>660<br>707<br>60<br>120<br>180<br>240<br>300<br>420<br>480<br>540<br>660<br>720<br>780<br>840<br>900<br>960<br>960<br>1020<br>1080<br>1140<br>1260 |

| 5  | SHSTTLPRDY<br>SVEYQLLNGG<br>QVHPQSPLCP<br>AQGGGPATAF<br>PFPQLGSRAG | FPGSTNSLHR<br>STLTSVSSHD<br>ELHRLNI PNP<br>LPGSAFTLST<br>RVDGDSPESR<br>LFQHPLQSEY<br>LSTHMDQQFF | SRLTAGVPDT<br>AQTSVVVEDL<br>PSAPGPLVFT<br>LTVPGLSENV<br>SSITTTHTSA | PTRLVFSALG<br>LPNHSYVFRV<br>ALSPDSLQLS<br>PYKFKVQART               | PTSLRVSWQE<br>RAQSQEGWGR<br>WERPRRPNGD<br>TEGFGPEREG               | PRCERPLQGY<br>EREGVITIES<br>IVGYLVTCEM<br>IITIESQDGG               | 1500<br>1560<br>1620<br>1680<br>1740<br>1800<br>1822 |
|----|--|---|--|--|--|--|--|
| 10 |  | C307 Protei<br>ession #: N  |  |  |  |  |  |
| 15 | GLAVWIFFHI<br>FYANMYTSIV<br>NGQPTEDNIH<br>ISQSSRKRKH               | 11<br> <br>PNNELHGQES<br>RNKTSFIFYL<br>FLGLISIDRY<br>DCSKLKSPLG<br>NQSIRVVVAV<br>PIIYFFMCRS     | KNIVVADLIM<br>LKVVKPFGDS<br>VKWHTAVTYV<br>FFTCFLPYHL               | TLTFPFRIVH<br>RMYSITFTKV<br>NSCLFVAVLV<br>CRIPFTFSHL               | DAGFGPWYFK<br>LSVCVWVIMA<br>ILIGCYIAIS<br>DRLLDESAQK               | PILCRYTSVL<br>VLSLPNIILT<br>RYIHKSSRQF<br>ILYYCKEITL               | 60<br>120<br>180<br>240<br>300<br>358                |
| 20 | Seq ID NO:   | C308 Protei   | in Sequence  |  |  |  |  |
| 25 | GPLLPIFIQF   | 11<br> <br>SLVISQGADG<br>GLYSPRIDPD<br>TVNSPPQFQE   | YVGRVRLQKG   | ASLQIEGLRV   | EDQGWYECRV   | PFLDQHIPED   | 60<br>120<br>180                                     |
| 30 | QGQVQVQNGT<br>SQDVSLACHA<br>CVPSNGLLHP<br>EGSLIIALGN<br>LIPCSAQGDP | LRIRRVERGS<br>EAYPANLTYS<br>PSASAYLTVL<br>EDALGEYSCT<br>PPVVSWTKVG                              | SGVYTCQASS<br>WFQDNINVFH<br>CMPGVIRCPV<br>PYNSLGTAGP<br>RGLQGQAQVD | TEGSATHATQ<br>ISRLQPRVQI<br>RANPPLLFVS<br>SPVTRVLLKA<br>SNSSLILRPL | LLVLGPPVIV<br>LVDGSLRLLA<br>WTKDGKALQL<br>PPAFIERPKE<br>TKEAHGHWEC | VPPKNSTVNA<br>TQPDDAGCYT<br>DKFPGWSQGT<br>EYFQEVGREL<br>SASNAVARVA | 240<br>300<br>360<br>420<br>480                      |
| 35 | WVSLAVPVGA<br>PTEIPPPLSP<br>TETELLVPGL<br>AGVVGGVCFL               | SPHVVTNVSV<br>AHLLVPGLQP<br>PRGLVAVRTP<br>IKDVLYEFRL<br>GVAVLVSILA                              | HTQYQFSVLA<br>RGVLLHWDPP<br>VAFAGSFVSD<br>GCLLNRRRAA               | QNKLGSGPFS<br>ELVPKRLDGY<br>PSNTANVSTS<br>RRRRKRLRQD               | EIVLSAPEGL<br>VLEGRQGSQG<br>GLEVYPSRTQ<br>PPLIFSPTGK               | PTTPAAPGLP<br>WEVLDPAVAG<br>LPGLLPQPVL<br>SAAPSALGSG               | 540<br>600<br>660<br>720<br>780                      |
| 40 | PTVAAPQERS<br>LPGPGPLLQY<br>PRESLPGAVV<br>PSTAPSAGGS               | QGSPVPSLRQ<br>GREQAEPRTP<br>LSLPPPREMN<br>GAGATAEPPY<br>YLSPAPGDTS<br>ASSRLRPEAE                | AQRLARSFDC<br>VDGDWPPLEE<br>TALADWTLRE<br>SWASGPERWP               | SSSSPSGAPQ<br>PSPAAPPDYM<br>RLLPGLLPAA<br>RREHVVTVSK               | PLCIEDISPV<br>DTRRCPTSSF<br>PRGSLTSQSS<br>RRNTSVDENY               | APPPAAPPSP<br>LRSPETPPVS<br>GRGSASFLRP<br>EWDSEFPGDM               | 900<br>960<br>1020<br>1080                           |
| 45 | DATRARLPAY   | RQPVPHPEQA  | TLL .  | GCDLATARVI   | GPBARCAALK   | EEFLAFRRR  | 1140<br>1163   |
| 50 | į  | 11  | 21   | 31   | 41   | 51   |  |
| 55 | KVIPRNRVLG<br>PAQDLFDYIT<br>IDFGSGALLH<br>DQEILEABLH               | APPGTPTPPP<br>WSPLSDSVTC<br>EKGPLGEGPS<br>DEPYTDFDGT<br>FPAHVSPDCC<br>TLSLAWPGLA                | PLEVALLWKV<br>RCFPGQVVAA<br>RVYSPPEWIS<br>ALIRRCLAPK               | GAGGGHPGVI<br>IQHCHSRGVV<br>RHQYHALPAT<br>PSSRPSLEEI               | RLLDWFETQE<br>HRDIKDENIL<br>VWSLGILLYD                             | GFMLVLERPL<br>IDLRRGCAKL<br>MVCGDIPFER                             | 60<br>120<br>180<br>240<br>300<br>334                |
| 60 |  | C310 Prote  |  |  |  |  |  |
| 65 | VWKRGDMRWK<br>RNEAGLSADP<br>GQYFQKLGRC                             | YVYNWTAWSE<br>SVRVSVNTAN  | VLTSDSPALV<br>DSDGENGTGQ<br>VTLGPQLMEV                             | GSNITFAVNL<br>SHHNVPPDGK<br>TVYRRHGRAY                             | IFPROQKEDA<br>PFPHHPGWRR<br>VPIAQVKDVY                             | NGNIVYERNC   | 60<br>120<br>180<br>240<br>300                       |
| 70 | HTYVLNGTFS<br>RYGHFQATIT<br>CEITQNTVCS<br>PLRMANSALI               | INLTVKAAAP<br>IVEGILEVNI  | GPCPPPPPPP<br>IQMTDVLMPV<br>TVRRTFNGSG<br>VISLLVYKKH               | RPSKPTPSLG<br>PWPESSLIDF<br>TYCVNLTLGD                             | PAGDNPLELS<br>VVTCQGSIPT<br>DTSLALTSTL                             | RIPDENCQIN<br>EVCTIISDPT<br>ISVPDRDPAS                             | 360<br>420<br>480<br>540<br>560                      |
| 75 |  | C311 Prote  |  |  |  |  |  |
| 80 | QSPINIDEDL<br>FKASKITFHW<br>ILPEVGTEEN                             | TQVNVNLKKL<br>GKCNMSSDGS<br>LDFKAIIDGV  | KFQGWDKTSL<br>EHSLEGQKFP<br>ESVSRFGKQA                             | ENTFIHNTGK<br>LEMQIYCFDA<br>ALDPFILLNL                             | TVEINLTNDY<br>DRFSSFEEAV<br>LPNSTDKYYI                             |  | 60<br>120<br>180<br>240<br>300                       |

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TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK
       HEFLIDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE
                                                                                     480
       LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN
       RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND
                                                                                     540
       GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS
                                                                                     600
       ENISOGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP
                                                                                     720
       TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP
                                                                                     780
       LVIVSALTFI CLVVLVGILI YWRKCFQTAH PYLEDSTSPR VISTPPTPIF PISDDVGAIP
                                                                                     840
        IKHFPKHVAD LHASSGFTEE FEEVQSCTVD LGITADSSNH PDNKHKNRYI NIVAYDHSRV
10
        KLAQLAEKDG KLTDYINANY VDGYNRPKAY IAAQGPLKST AEDFWRMIWB HNVEVIVMIT
       NLVEKGRRKC DOYWPADGSE EYGNFLVTQK SVQVLAYYTV RNFTLRNTKI KKGSQKGRPS
                                                                                     1020
        GRVVTQYHYT QWPDMGVPEY SLPVLTFVRK AAYAKRHAVG PVVVHCSAGV GRTGTYIVLD
                                                                                     1080
                                                                                      1140
        SMLQQIQHEG TVNIFGFLKH IRSQRNYLVQ TEEQYVPIHD TLVEAILSKE TEVLDSHIHA
        YVNALLIPGP AGKTKLEKQF QLLSQSNIQQ SDYSAALKQC NREKNRTSSI IPVERSRVGI
15
                                                                                      1200
        SSLSGEGTDY INASYIMGYY QSNEFIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDGQNM
                                                                                      1260
        AEDEFVYWPN KDEPINCESF KVTLMAEEHK CLSNEEKLII QDFILEATQD DYVLEVRHFQ
                                                                                      1320
        CPKWPNPDSP ISKTFELISV IKEEAANRDG PMIVHDEHGG VTAGTFCALT TLMHQLEKEN
                                                                                      1380
        SVDVYQVAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI
                                                                                      1440
20
                                                                                      1448
        Seq ID NO: C312 Protein Sequence
        Protein Accession #: XP_031379
25
                                                           41
        MRILKRFLAC IOLLCVCRLD WANGYYROOR KLVEEIGWSY TGALNOKNWG KKYPTCNSPK
                                                                                      120
        OSPINIDEDL TOVNVNLKKL KFOGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV
        FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS
                                                                                      180
        ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC
30
        TOTVOWIVEK DIVSISESQL AVECEVLIMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY
                                                                                      300
         TGKEBIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK
                                                                                      360
        HEFLITOGYOD LGAILMNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DMPELDLFPE
LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTITHYNRI GTKYNEAKTN
                                                                                      420
                                                                                      480
         RSPTRGSEPS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND
35
                                                                                      540
        GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSGSS PATSAIPFIS
ENISQGYIFS SENPETITTD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSPSAGPVMS QGPSVTDLEM PHYSTFAYFP
                                                                                      600
                                                                                      660
                                                                                       720
         TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNQI
                                                                                       780
 40
         LNTTPAASSS DSALHATPVF PSVDVSPESI LSSYDGAPLL PFSSASFSSE LFRHLHTVSQ
                                                                                       840
         ILPQVTSATE SDKVPLHASL PVAGGDLLLE PSLAQYSDVL STTHAASETL EFGSESGVLY
         KTLMFSOVEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG
                                                                                       960
         SLFSGPSHIP IPKSSLITPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS
                                                                                       1020
                                                                                       1080
         PVSVAEFTYT TSVFGDDNKA LSKSEIIYGN ETELQIPSFN EMVYPSESTV MPNMYDNVNK
         LNASLQETSV SISSTKGMFP GSLAHTTTKV FDHEISQVPE NNFSVQPTHT VSQASGDTSL
 45
                                                                                       1140
         KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP
                                                                                       1200
         AVPSDPILVE TPKVDKISST MLHLIVSNSA SSENMLHSTS VPVFDVSPTS HMHSASLQGL
                                                                                       1260
                                                                                       1320
         TISYASEKYE PVLLKSESSH QWVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID
         EPLNTLINKL IHSDBILTST KSSVTGKVFA GIPTVASDTF VSTDHSVPIG NCHVAITAVS
PHRDGSVTST KLLFPSKATS ELSHSAKSDA GLVGGGEDGD TDDDGDDDDD DRGSDGLSIH
                                                                                       1380
 50
                                                                                       1440
         KCMSCSSYRE SQEKVMNDSD THENSLMDQN NPISYSLSEN SEEDNRVTSV SSDSQTGMDR
                                                                                       1500
         SPEKSPSANG LSOKINDEKE ENDIGTESAL LPLEFESKAW AVLTSDEESG SEGGTSDSLN
ENETSTDFSF ADTNEKDADG ILAAGDSEIT PGFPQSPTSS VTSENSEVFH VSEAEASNSS
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         HESRIGLAEG LESEKKAVIP LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR
                                                                                       1680
         VISTPPTPIF PISDDVGAIP IKEPPKHYAD LHASSGPTEB FETLKEFYQE VQSCTVDLGI
TADSSNHPDN KHKNRYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA
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                                                                                       1740
         OGPLKSTAED FWRMIWEHNV EVIVMITNLV EKGRRKCDQY WPADGSEEYG NFLVTQKSVQ
                                                                                       1860
         VLAYYTVRNF TLRNTKIKKG SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFVRKAAY
                                                                                       1920
         AKRHAVGPVV VHCSAGVGRT GTYIVLDSML QQIQHEGTVN IFGFLKHIRS QRNYLVQTEE
QYVPIHDTLV EAILSKETEV LDSHIHAYVN ALLIPGPAGK TKLEKQFQLL SQSNIQQSDY
                                                                                       1980
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                                                                                       2040
          SAALKOCNRE KURTSSIIPV ERSRUGISSL SGEGTDYINA SYIMGYYQSN EPIITQHPLL
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                                                                                       2160
         HTIKDFWRMI WDHNAQLVVM IPDGQNMAED EFVYWPNKDE PINCESFKVT LMAEEHKCLS
          NEEKLIIQDF ILEATQDDYV LEVRHFQCPK WPNPDSPISK TFELISVIKE EAANRDGPMI
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                                                                                        240
          TOTVOWIVEK DIVSISESQL AVECEVLIMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY
                                                                                        300
          TGKEBIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE
                                                                                        360
          LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN
                                                                                        480
          RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLAD
  80
                                                                                        540
          GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSPKLD TGAEDSSGSS PATSAIPFIS
          ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI
                                                                                        660
          TAOPDVGSGR ESFLOTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYPP
                                                                                        720
           TEVTPHAPTP SSRQQDLVST VNVVYSQTTQ PVYNAEASNS SHESRIGLAE GLESEKKAVI
                                                                                        780
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| 5  | PLVIVSALTF PIKHFPKHVA I VAYDHSRVKL VEVIVMITHL GSQKGRPSGR TGTYIVLDSM VLDSHIHAYV VERSRVGISS MIPDGQNMAE VLEVRHFQCP MHQLEKENSV AALPDGNIAE SEG ID NO: | DLHASSGFTE AQLAEMOGKL  VEKGRRKCDQ  VVTQYHYTQW  LQQIQHESTV  NALLI PGPAG  LSGEGTDY IN  DEFVYWPNKD  KWPNPDSFIS  DVYQVAKMIN  SLESLV | EFETLKEFYQ TDYINANYVD YWPADGSEEY PDMGVPEYSL NIFGFLKHIR KTKLEKGFQL ASYIMGYYQS EPINCESFKV KTFELISVIK LMRPGVFADI | EVQSCTVDLG GYNRPKAYIA GNFLVTQKSV PVLTFVRKAA SQRNYLVQTE LSQSNIQQSD NEFIITQHPL TLMAEEHKCL EEAANRDGPM | ITADSSNHPD   AQGPLESTAE   QVLAYYTVRN YAKRHAVGPV EQYVFIHDTL YSAALKQCNR LHTIKDFWRM SNEEKLIQD IVHDEHGGVT | NKHKNRYINI DFWRMIWEHN FTLRNTKIKK VVHCSAGVGR VEAILSKETE EKNRTSSIIP IWDHNAQLVV FILEATQDDY AGTFCALTTL | 840<br>900<br>960<br>1020<br>1080<br>1140<br>1200<br>1360<br>1380<br>1440 |
|----|--|---|---|--|---|--|---|
| 15 | Protein Acc  | ession #:   | Eos sequend   |  | 41  | 51   |   |
| •• | 1<br> <br>  MRILKRFLAC   | 11<br> <br> QLLCVCRLD   | 21<br>WANGYYRQQR  |  | 1   | 1  | 60  |
| 20 | QSPINIDEDL<br>MVFKASKITF<br>LSILPEVGTE<br>PCTDTDWIVF   | HWGKCNMSSD<br>ENLDFKAIID<br>KDTVSISESO  | GSEHSLEGOK<br>GVESVSRFGK<br>LAVFCEVLTM  | FPLEMQIYCF<br>QAALDPFILL<br>QQSGYVMLMD   | DADRFSSFEE<br>NLLPNSTDKY<br>YLQNNFREQQ  | AVKGKGKLRA<br>YIYNGSLTSP<br>YKPSRQVFSS   | 120<br>180<br>240<br>300  |
| 25 | YTGKEEIHEA<br>KHEFLTDGYQ<br>ELIGTEEIIK<br>NRSPTRGSEF<br>DGSKTVLRSP   | DLGAILNNLL<br>EEEEGKDIEE<br>SGKGDVPNTS<br>HMNLSGTAES  | PNMSYVLQIV<br>GAIVNPGRDS<br>LNSTSQPVTK<br>LNTVSITEYE  | AICTNGLYGK<br>ATNQIRKKEP<br>LATEXDISLT<br>EESLLTSFKL   | YSDQLIVDMP<br>QISTTTHYNR<br>SQTVTELPPH<br>DTGAEDSSGS  | TDNPELDLPP<br>IGTKYNEAKT<br>TVEGTSASLN<br>SPATSAIPPI   | 360<br>420<br>480<br>540<br>600   |
| 30 | ITAOPDVGSG<br>PTEVTPHAFT<br>PLVIVSALTF   | RESFLQTNYT<br>PSSRQQDLVS<br>ICLVVLVGIL  | EIRVDESEKT<br>TVNVVYSQTT<br>IYWRKCFQTA  | TKSFSAGPVM<br>QPVYNEASNS<br>HFYLEDSTSP   | EESLKDPSME<br>SQGPSVTDLE<br>SHESRIGLAE<br>RVISTPPTPI<br>ITADSSNHPD                                    | MPHYSTFAYF<br>GLESEKKAVI<br>FPISDDVGAI   | 660<br>720<br>780<br>840<br>900   |
| 35 | VEVIVMITNL<br>GSQKGRPSGR<br>TGTYIVLDSM   | VEKGRRKCDQ<br>VVTQYHYTQW<br>LQQIQHEGTV  | YWPADGSEEY<br>PDMGVPEYSL<br>NIFGFLKHIR  | GNFLVTQKSV<br>PVLTFVRKAA<br>SQRNYLVQTE   | AQGPLKSTAE<br>QVLAYYTVRN<br>YAKRHAVGPV<br>EQYVPIHDTL<br>YSAALKQCNR                                    | FTLRNTKIKK<br>VVHCSAGVGR<br>VEAILSKETE   | 960<br>1020<br>1080<br>1140<br>1200                                       |
| 40 | VERSRVGISS<br>MIPDGQNMAE<br>VLEVRHFQCP   | LSGEGTDYIN<br>DEFVYWPNKD<br>KWPNPDSPIS<br>DVYQVAKMIN  | ASYIMGYYQS<br>EPINCESFKV<br>KTFELISVIK  | nefiitohpl<br>Tlmaeehkcl<br>Eeaanrogpm   | LHTIKDFWRM<br>SNEEKLIIQD<br>IVHDEHGGVT  |  | 1260<br>1320<br>1380<br>1440<br>1456                                      |
| 45 | Seq ID NO:   | C315 Prote  | in Sequence<br>Eos sequenc  |  |   |  |   |
|    | 1  | 11<br>1   | 21<br>i   | 31   | 41<br>  | 51<br>1  |   |
| 50 | QSPINIDEDL<br>FKASKITFHW<br>ILPEVGTEEN   | TOVNVNLKKI<br>GKCNMSSDGS<br>LDPKAIIDGV  | KFQGWDKTSL<br>EHSLEGQKFF<br>BSVSRFGKQA  | ENTFIHNTGE<br>LEMQIYCFDA<br>ALDPFILLNI   | TVEINLTNDY DRFSSFEEAV LPNSTDKYYI  | KKYPTCNSPK<br>RVSGGVSEMV<br>KGKGKLRALS<br>YNGSLTSPPC   | 60<br>120<br>180<br>240   |
| 55 | TGKEEIHEAV<br>HEFLTDGYQD<br>LIGTEEIIKE   | CSSEPENVQA<br>LGAILNNLLE<br>EEEGKDIEEG  | DPENYTSLLV<br>NMSYVLQIVA<br>AIVNPGRDSA  | TWERPRVVYI ICTNGLYGKY TNQIRKKEP(   | TMIEKFAVLY<br>SDQLIVDMPT<br>ISTTTHYNRI  | KFSRQVFSSY QQLDGEDQTK DNPBLDLFPE GTKYNEAKTN VEGTSASLND   | 300<br>360<br>420<br>480<br>540   |
| 60 | ENISQGYIFS<br>TAQPDVGSGR<br>TEVTPHAFTP<br>LVIVSALTFI   | SENPETITYI<br>ESPLQTNYTE<br>SSRQQDLVST<br>CLVVLVGILI  | VLIPESARNA<br>IRVDESEKTI<br>VNVVYSQTT<br>YWRKCFQTAL   | SEDSTSSGSI<br>KSPSAGPVMS<br>PVYNEASNSS<br>FYLEDSTSPI   | E ESLKDPSMEG<br>G QGPSVTDLEM<br>G HESRIGLAEG<br>R VISTPPTPIF  | PATSAIPFIS NVWFPSSTDI PHYSTFAYFP LESEKKAVIP PISDDVGAIP   | 600<br>660<br>720<br>780<br>840   |
| 65 | aydhsrvkla<br>Evivmitnlv<br>SQKGRPSGRV   | QLAEKDGKLT<br>EKGRRKCDQT<br>VTQYHYTQWI  | DYINANYVDO<br>WPADGSEEYO<br>DMGVPEYSLI  | ynrpkayia<br>Hivtoksvo<br>Vltfvrkaa  | a ogplkstaet<br>O vlayytvrne<br>Y akrhavgpvv  | KHKNRYINIV FWRMIWEHNV TLRNTKIKKG VHCSAGVGRT KAILSKETEV   | 900<br>960<br>1020<br>1080<br>1140  |
| 70 | LDSHIHAYVN<br>SRVAGTILLS<br>YIMGYYQSNE<br>INCESFKVTI   | ALLIPGPAGI<br>GSNIQQSDY:<br>FIITQHPLLI<br>MAEEHKCLSI  | C TKLEKQFQGI<br>E AALKQCNREI<br>H TIKDFWRMI<br>N EEKLIIQDF:   | L TLSPRLECRO  C NRTSSIIPV  O DHNAQLVVM  L LEATQDDYV  | G TISAHCNLPI<br>E RSRVGISSLS<br>I PDGQNMAEDI<br>L EVRHFQCPK   | PGLTDPPTSA GEGTDYINAS FVYWPNKDEP PNPDSPISKT YQVAKMINLM   | 1200<br>1260<br>1320<br>1380<br>1440                                      |
| 75 | Seq ID NO:   | C316 Prot   | S LVGTRQEEN<br>ein Sequenc<br>Eos sequen  | е  | A LPDGNIAESI  | E ESLV   | 1494  |
| 80 | QSPINIDED!<br>FKASKITFHY   | TQVNVNLKK<br>GKCNMSSDG  | L KFQGWDKTS<br>S EHSLEGQKF  | L ENTFIHNTG<br>P LEMQIYCFD   | K TVEINLTND'<br>A DRFSSFEEA'  | 51<br> <br>G KKYPTCNSPK<br>Y RVSGGVSEMV<br>V KGKGKLRALS<br>I YNGSLTSPPC                            | 60<br>120<br>180<br>240   |

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TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK
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                                                                                         360
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        ESRIGLAEGL ESEKKAVIPL VIVSALTFIC LVVLVGILIY WRKCFQTAHF YLEDSTSPRV
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        ISTPPTPIFP ISDDVGAIPI KHFPKHVADL HASSGFTEEP ETLKEFYQEV QSCTVDLGIT
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        ADSSNHPDNK HKNRYINIVA YDHSRVKLAQ LAEKGGKLTD YINANYYDGY NRFKAYIAAQ
GPLKSTAEDF WRMIWEHNVE VIVMITNLVE KGRRKCDQYW PADGSEEYGN FLVTQKSVQV
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                                                                                          660
        LAYYTVRNFT LRNTKIKKGS QKGRPSGRVV TQYHYTQWPD MGVPEYSLPV LTFVRKAAYA
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        KRHAVGPVVV HCSAGVGRTG TYIVLDSMLQ QIQHEGTVNI FGFLKHIRSQ RNYLVQTEEQ
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        YVFIHDTLVE ALLSKETEVL DSHIHAYVNA LLIPGPAGKT KLEKOFOLLS OSNIOOSDYS
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        TIKDFWRMIW DHNAQLVVMI PDGQNMAEDE FVYWPNKDEP INCESFKVTL MAEEHKCLSN
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                                                                                          300
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                                                                                          960
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LDSHIHAYVN ALLIPGPAGK TKLEKQFQGL TLSPRLBCRG TISAHCNLPL PGLTDPPTSA
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                                                                                          1200
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                                                                                           1260
         YIMGYYQSNE PIITQHPLLH TIKDFWRMIW DHNAQLVVMI PDGQNMAEDE FVYWPNKDEP
                                                                                          1320
         INCESPKYTL MAEEHKCLSN EEKLIIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT
FELISVIKEE AANRDGPMIV HDEHGGVTAG TFCALTILMH QLEKENSVDV YQVAKMINLM
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                                                                                          1440
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                                                                                           120
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         FKASKITFHW GKCNMSSDGS EHSLEGOKFP LEMQIYCFDA DRFSSFEBAV KGKGKLRALS
ILFEVGTEEN LOFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC
                                                                                           180
                                                                                           240
          TDIVDWIVFK DIVSISESQL AVFCEVLIMQ QSGYVMLMDY LQNNFREQQY KPSRQVFSSY
                                                                                           300
          TGKEBIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK
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         HEPLITOGYQD LGAILMNLLP MMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE
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          TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP
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                                                                                           840
                                                                                           900
          AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV
          EVIVMITNLV EKGRRKCDQY WPADGSEEYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG
SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFVRKAAY AKRHAVGPVV VHCSAGVGRT
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                                                                                           1080
          GTYIVLDSML QQIQHEGTVN IFGFLKHIRS QRNYLVQTEE QYVFIHDTLV BAILSKETEV
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          ERSRVGISSL SGEGTDYINA SYIMGYYQSN EFIITQHPLL HTIKDFWRMI WDHNAQLVVM
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          IPDGONMARD EPVYWPNKDE PINCESFKVT LMAEEHKCLS NEEKLIIODF ILEATOAWRS
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          LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR
          VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI
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LSIVCLMITQ LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW
       ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMPEA AAVGSLLAGG
                                                                                  300
                                                                                  360
       PVVAILGMIY NVIILGPTGF LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE
       VLITIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQS ITVGVAPIVV VIASVVTFSV
HMTLGFDLTA AQAFTVVTVP NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK
                                                                                  480
       NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA
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        VLAEQKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG
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       KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS
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        CCLRPDLAIL PSSDLTEIGE RGANLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG
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       NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI
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        FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS
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        VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS
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        VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM
        KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP
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15
        LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL
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        LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT
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        GLFOPTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM
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        RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD
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20
        SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT
                                                                                   1380
        MLTIAHRLHT VLGSDRIMVL AOGOVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG
        Seg ID NO: C320 Protein Seguence
        Protein Accession #: NP_005679.1
25
        MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECODAL ETAARAEGLS
        LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TPSWLSSLAR
                                                                                   120
30
        VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI
                                                                                   180
        LSIVCIMITO LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW
ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG
                                                                                   240
        PVVAILGMIY NVIILGPTGF LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE
                                                                                   360
        VLTYIKFIKM YAWVKAPSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV
                                                                                   420
35
        HMTLGFDLTA AQAFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK
         NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA
        VLAEOKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG
                                                                                   600
         KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS
                                                                                   660
        CCLRPDLAIL PSSDLTEIGE RGANLSGGOR QRISLARALY SDRSIYILDD PLSALDAHVG
NHIFNSAIRK HLKSKTVLPV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI
                                                                                   720
40
                                                                                   780
         FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS
                                                                                   840
         VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS
                                                                                   900
         VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM
                                                                                   960
         KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP
                                                                                   1020
 45
         LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQBL
                                                                                   1080
         LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HCQIPPAYAG LAISYAVQLT
                                                                                   1140
         GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM
                                                                                    1200
         RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD
                                                                                    1260
         IGLADLRSKL SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKE CIAQLPLKLE
                                                                                   1320
 50
         SEVMENGONF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIGE TIREAFADCT
                                                                                    1380
         MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG
         Seq ID NO: C321 Protein Sequence
         Protein Accession #: NP_005553.1
 55
         MPALWLGCCL CFSLLLPAAR ATSRREVCDC NGKSRQCIFD RELHROTGNG FRCLNCNDNT
         DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCKPGVTG ARCDRCLPGF
                                                                                    120
 60
         HMLTDAGCTQ DQRLLDSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGGN
                                                                                    180
         PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVDGWKA VQRNGSPAKL QWSQRHQDVF
SSAQRLDPVY PVAPAKFLGN QQVSYGQSLS FDYRVDRGGR HPSAHDVILE GAGLRITAPL
                                                                                    240
         MPLGKTLPCG LTKTYTPRLN EHPSNNWSPQ LSYFEYRRLL RNLTALRIRA TYGEYSTGYI
                                                                                    360
         DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPCNCQG
                                                                                    420
         GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCHNGFSC SVMPETEEVV
 65
          CNNCPPGVTG ARCELCADGY FGDPPGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK
                                                                                    540
         CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS EPVGCRSDGT CVCKPGFGGP
                                                                                    600
                                                                                    660
         NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL
         QDILRDAQIS EGASRSIGLQ LAKVRSQENS YQSKLDDLKM TVERVRALGS QYQNRVRDTH
RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR
                                                                                    720
  70
                                                                                    780
          ETEDYSKQAL SLVRKALHEG VGSGSGSPDG AVVQGLVEKL EKTKSLAQQL TREATQAEIE
                                                                                    840
          ADRSYQHSLR LLDSVSRLQG VSDQSFQVEB AKRIKQKADS LSTLVTRHMD EPKRTQKNLG
                                                                                    900
          NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL
                                                                                     960
          OVDNRKAEAR EAMKRLSYIS OKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE
                                                                                    1020
  75
          IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE
                                                                                    1080
          AÇKVDTRAKN AGVTIQDTLN TLDGLLHLMD QPLSVDEEGL VLLEQKLSRA KTQINSQLRP
MMSELEERAR QQRGHLHLLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ
                                                                                     1140
                                                                                     1193
          Seq ID NO: C322 Protein Sequence
  80
          Protein Accession #: NP_066924.1
          MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG
```

|                      | QIQCKVFDSL L<br>IGGAIFLLAG L<br>LLCCSCPRKT T  | AILVATAWY (  | NRIVQEFYD E   | MTPVNARYE I  | MKCMKCLED D<br>GQALFTGWA A   | DEVQKMRMAV<br>LASLCLLGGA  | 120<br>180<br>211   |
|----------------------|---|--|---|--|--|---|---|
| 5                    | Seq ID NO: C<br>Protein Acce  |  |   |  |  |   |   |
| 10<br>15             | 1 I<br>MSSWIRWHGP P<br>MSVDPENITE I<br>NFTRNKLTSL S<br>SKNIPLANLQ I<br>METSHTQGSL F<br>WCIPFTVKGN I   | MARLWGFCW IFIANQKRLE SRKHFRHLDL IPNCGLPSAN RITNISSDDS  | LVVGFWRAAF /<br>IINEDDVEAY V<br>SELILVGNPP (<br>LAAPNLTVEB (<br>GKQISCVAEN )  | ACPTSCKCSA S<br>JGLRNLTIVD S<br>TCSCDIMWIK S<br>SKSITLSCSV S<br>LVGEDQDSVN S   | SRIWCSDPSP ( SGLKFVAHKA I TLQEAKSSPD T AGDPVPNMYW I LTVHFAPTIT I   | FLKNSNLQHI<br>TQDLYCLNES<br>DVGNLVSKHM<br>FLESPTSDHH  | 60<br>120<br>180<br>240<br>300<br>360   |
|                      | LIAKNEYGKD E<br>DVTDKTGREH I  | EKQISAHFMG !<br>LSVYAVVVIA   | WPGIDDGANP 1<br>SVVGFCLLVM 1  | MYPDVIYEDY (   | GTAANDIGDT '   | enrsnei PST   | 420<br>477  |
| 20                   | Seq ID NO: 0  |  |   |  |  |   |   |
| 25                   | <br>  MSSWIRWHGP  <br>  MSVDPENITE  <br>  NFTRNKLTSL  <br>  SKNIPLANLQ  <br>  NETSHTOGSL  | AMARLWGFCW IFIANQKRLE SRKHFRHLDL IPNCGLPSAN RITNISSDDS   | LVVGFWRAAF<br>I INEDDVEAY<br>SELILVGNPF<br>LAAPNLTVEE<br>GKQISCVAEN   | ACPTSCKCSA VGLRNLTIVD TCSCDIMWIK GKSITLSCSV LVGEDQDSVN   | SRIWCSDPSP<br>SGLKPVAHKA<br>TLQEAKSSPD<br>AGDPVPNMYW<br>LTVHFAPTIT   | FLKNSNLQHI<br>TQDLYCLNES<br>DVGNLVSKHM<br>FLESPTSDHH  | 60<br>120<br>180<br>240<br>300  |
| 30                   | WCIPFTVKGN<br>LIAKNEYGKD<br>DVTDKTGREH<br>LHHISNGSNT<br>KRELGEGAFG  | PKPALQWFYN<br>EKQISAHFMG<br>LSVYAVVVIA<br>PSSSEGGPDA<br>KVFLAECYNL   | GAILNESKYI<br>WPGIDDGANP<br>SVVGPCLLVM<br>VIIGMTKIPV<br>CPEQDKILVA  | CTKIHVTNHT<br>NYPDVIYEDY<br>LFLLKLARHS<br>IENPQYFGIT<br>VKTLKDASDN   | EYHGCLQLDN<br>GTAANDIGDT<br>KFGMKGPASV<br>NSQLKPDTFV<br>ARKDFHREAE   | PTHMNNGDYT<br>TNRSNEIPST<br>ISNDDDSASP<br>QHIKRHNIVL<br>LLTNLQHEHI  | 360<br>420<br>480<br>540<br>600   |
| 35                   | VKFYGVCVEG<br>AAGMVYLASQ<br>PPESIMYRKF  | DPLIMVFEYM<br>HFVHRDLATR<br>TTESDVWSLG   | KHCDLNKFLR<br>NCLVGENLLV<br>VVLWEIFTYG<br>KGIHTLLQNL  | AHGPDAVLMA<br>KIGDFGMSRD<br>KQPWYQLSNN   | EGNPPTELTQ<br>VYSTDYYRVG<br>EVIECITQGR   | SQMLHIAQQI<br>GHTMLPIRWM  | 660<br>720<br>780<br>822  |
| 40                   | Seq ID NO:<br>Protein Acc   |  | in Sequence<br>Sos sequence   |  |  |   |   |
|                      |   |  |   |  |  |   |   |
| 45<br>50             | nsvdpenite<br>nftrnkltsl<br>skniplanlq<br>netshtqgsl<br>wcipftvkgn<br>liakneygkd  | IFIANQKRLE<br>SRKHFRHLDL<br>IPNCGLPSAN<br>RITNISSDDS<br>PKPALQWFYN<br>EKQISAHFMG   | 21<br> <br>LVVGFWRAAF<br>  IINEDDVEAY<br>SELILIVENPF<br>LAAPNLTVEE<br>GKQISCVAEN<br>GAILNESKYI<br>WPGIDDGANP<br>SVVGFCLLVM  | VGLRNLTIVD<br>TCSCDIMWIK<br>GKSITLSCSV<br>LVGEDQDSVN<br>CTKIHVTNHT<br>NYPDVIYEDY   | SGLKFVAHKA<br>TLQEAKSSPD<br>AGDPVPNMYW<br>LTVHFAPTIT<br>EYHGCLQLDN<br>GTAANDIGDT   | FLKNSNLQHI<br>TQDLYCLNES<br>DVGNLVSKHM<br>PLESPTSDHH<br>PTHMNNGDYT<br>TNRSNEIPST  | 60<br>120<br>180<br>240<br>300<br>360<br>420  |
| 50                   | MSWIRWHGP<br>NSVDPENITE:<br>NFTRKLITSL<br>SKNIPLANLQ<br>NETSHTQGSL<br>WCIPPTVKGN<br>LIAKNEYGKD<br>DVTDKTGREH<br>Seq ID NO:  | AMARLWGFCW IFIANQKRLE SRKHFRHLDL IPNCGLPSAN RITNISSDDS PKPALQWFYN EKQISAHFMG LSVYAVVVIA C326 Prote   | LVVGFWRAAP IINEDDVEAY SELILVGNPF LAAPNLTVEE GKQISCVAEN GAILNESKYI   | ACPTSCKCSA VGLRNLTIVD TCSCDIMWIK GKSITLSCSV LVGEDQDSVN CTKIHVTNHT NYPDVIYEDY   | SRIWCSDPSP<br>SGLKFVAHKA<br>TLQEAKSSPD<br>AGDPVPNMYW<br>LTVHFAPTIT<br>EYHGCLQLDN<br>GTAANDIGDT   | GIVAPPRLEP<br>FLKNSNLQHI<br>TQDLYCLINES<br>DVGNLVSKHM<br>PLESPTSDHH<br>PTHMNNGDYT<br>TNRSNEIPST   | 120<br>180<br>240<br>300<br>360<br>420  |
|                      | MSWIRWHGP NSVDPENITE NFTRNKLTSL SKNIPLANLQ NETSHTQGSL WCIPFTVKGN LIAKNEYGKD DVTDKTGREH Seq ID NO: Protein Acc   | AMARLMGFCW AMARLMGFCW IFIANQKRLE SRKHFRHLDL IPNCGLPSAN RITHISDDIS PKPALQWFYN EKQISAHFMG LSVYAVVVIA C326 Prote cession #;   | LVVGFWRAAF<br>LINEDDVEAY<br>SELILVGNPF<br>LAAPNLTVEE<br>GKQISCVAEN<br>GAILNESKYI<br>WPGIDDGANP<br>SVVGFCLLVM<br>in Sequence<br>NP_570843.1  | ACPTSCKCSA WGLRNLTIVD TCSCDIMMIK GKSITLSCSV LVGEDQDSVM CTKIHVTNHT MYPDVIYEDY LFILKLARHS  | SRIWCSDPSP<br>SGLKFVAHKA<br>TIQEAKSSPD<br>AGDFVPNMYW<br>LTVHFAPTIT<br>EYHGCLQLDN<br>GTAANDIGDT<br>KFGMKGFVLF   | GIVAPPRLEP<br>FLKNSNLQHI<br>TQDLYCLMES<br>DVGNLVSKHM<br>PLESPTSDHH<br>PTHMNNGDYT<br>TNRSNEIPST<br>HKIPLDG   | 120<br>180<br>240<br>300<br>360<br>420<br>477   |
| 50                   | MSSWIRWHGP MSVDPENITE NFTRNKLTSL SKNIPLANLQ NETSHTQGSL WCIPFTVKGN LIAKNEYGKD DVTDKTGREH Seq ID NO: Protein Acc  1   MPLKHYLLLL LNTHITELME FQGLDSLESL GKNSLTHISP FHNNHNLQRL  | AMARLMGFCW AMARLMGFCW IFILANQKRLE SRKHFRHLDL IPNCGLPSAN RITNISSDDS PKPALQWFYN EKQISARPMG LSVYAVVVIA C326 Prote cession #: ' 11   VGCQAWGAGL SPFLMISALI LLSSNQLLQI RVFQHLGNLQ YLSNNHISQL  | LVVGFWRAAF IINEDDVEAY SELILVGNPF LAAPNLTVEE GKQISCVAEN GAILNESKYI WPGIDDGANP SVVGFCLLVM in Sequence NP_570843.1 21 AYHGCPSECT ALRIERNELS OPAHPSQCSN VLRLYENRLT PPSIFMOLPQ   | ACPTSCKCSA VGLENLITVD TCSCDIMWIK GKSITLSCSV LVGEDQDSVN CTKIHVINHT NYPDVIYEDY LFLLKLARHS  31   CSRASQVECT RITPGAFRNL LKELQLEGNH DIPMGTFDGL LNRLILFGMS   | SRIWCSDPSP SGLKPVAHKA TLQEAKSSPD AGDPVPNMYW LTVHFAPTIT EYHGCLQLDN GTAANDIGDT KFGMKGFVLF  41   GARIVAVPTP GSLRYLSLAN LEYIPDGAFD VNLQELALQQ  | GIVAPPRLEP FLKNSNLQHI TODLYCLNES DVGNLVEKHM PLESPTSDHH PTHMNNGDYT TNRSNEIPST HKIPLDG  51   LEWNAMSLQI NKLQVLPIGL HLVGLTKLNL HLVGLTKLNL EMPNLRELWIL                                  | 120<br>180<br>240<br>300<br>360<br>420<br>477<br>60<br>120<br>180<br>240<br>300                             |
| 50<br>55             | MSWIRWHGP MSVDPENITE NFTRIKLITSL SKNIPLANLQ METSHTQGSL WCIPPTVKGN LIAKNEYGKD DVTDKTGREH  Seq ID NO: Protein Acc  MPLKHYLLLL LIMTHITELME FQGLDSLESL GKNSLTHISP FHNHNLQRL YDNHISSLPD FRMLANLQNI YDNFWRCDSD VPSYPETFWY   | AMARLMGFCW AMARLMGFCW IFILANQKRLE SRKHFRHLDL IPNCGLPSAN RITNISSDDS PKPALQWFYN EKQISAHPMG LSVYAVVVIA  C326 Prote cession #:  VGCQAWGAGL SPFIMISALI LLSSNQLLQI RVFQHLGNILQ VISNNHLSQL SLQNNHLRQL ILDLRNWLLI INTESTPOTT  | LVVGFWRAAF IINEDDVEAY SELILVGNPF LAAPNLTVEE GRQISCVAEN GAILNESKYI WPGIDDGANP SVVGFCLLVM in Sequence NP_570843.1 21   AYHGCPSECT ALRIEKNELS QPAHFSQCSN VLRLYERRLT PENFINQLPQ VLILSRNQIS PGNIPANVNG   | ACPTSCKCSA WGLRNLTVD TCSCDIMMIK GKSITLSCSV LVGEDQDSVIN CTKIHVINHT NYPDVIYEDY LFLLKLARHS  31   CSRASQVECT RITPGAFRNL LKELQLHGNH DIPMGTFFGAL LMRLITLFGNS FISPGAFNGL LMALGLQNNGC PVEDYTDLTI   | SRIWCSDPSP SGLKFVAHKA TIQEAKSSPD AGDPVPNMYW LTVHFAPTIT EYHGCLQLDN GTAANDIGDT KFGMKGFVLF  41 GARIVAVPTP GSLRYLSLAN LEYIPDGAFD VNLQELALQQ LKELSIGIFG TELRELSLHT LEMLPLGIFD GQSLIIINVN IQVIDDRSVW   | GIVAPPRLEP FLKNSNLQHI TQDLYCLMES DVGNLVSKHM PLESPTSDHH PTHMNNGDYT TMRSNEIPST HKIPLDG  51 LPWNAMSLQI NKLQVLPIGL HLVGLTKLNL NQIGLLSPGL  | 120<br>180<br>240<br>300<br>360<br>420<br>477   |
| 50<br>55<br>60       | MSSWIRWHGP MSVDPENITE NFTRIKLITSL SKNIPLANLQ NETSHTQGSL WCIPFTVKGN LIAKNEYGKD DVTDKTGREH Seq ID NO: Protein Acc  1   MPLKHYLLLL LINTHITELME FQGLDSLESL GKNSLTHISP FHNNHNLQRL YDMHISSLPD FRMLANLQNI YDMYRCDSD VPSYPETPWY IAAIVIGIVA Seq ID NO:   | AMARLMGFCW AMARLMGFCW IFIANQKRLE SRKHFRHLDL IPNCGLPSAN RITNISSDDS PKPALQWFYN EKQISARFMG LSVYAVVVIA  C326 Prote cession #:  11   VGCQAWGAGL SPFLMISALI LLSSNQLLQI RVFQHLGNLQI YLSNNHLSQI SLQNNRLRQI SLQNNRLRQI DTPSYPDTT LACSLAACVC C327 Prote  | LVVGFWRAAF IIMEDDVEAY SELILVGNPF LAAPNLTVEE GKQISCVAEN GAILNESKYI WPGIDDGANP SVVGFCLLVM in Sequence NP_570843.1  21   AYHGCPSECT ALRIERNELS QPAHPSQCSN VLRLYERRLT PPSIFMOLPQ VLILSRNQIS PGIFANVNG NQPRLGTDTV SVSSTTELTS   | ACPTSCKCSA ACPTSCKCSA VGLENLITVD TCSCDIMWIK GKSITLSCSV LVGEDQDSVIN CTKIHVINHT NYPDVIYEDY LFLLKLARHS  31   CSRASQVECT RITPGAFRNL LKELQLHGNH DIPMGTFDGL LMALQLHCGNH PVCFSPANVE PVCFSPANVE PVESPANVE PVEDYTDLTI VLMQNKAPNE  | SRIWCSDPSP SGLKFVAHKA TIQEAKSSPD AGDPVPNMYW LTVHFAPTIT EYHGCLQLDN GTAANDIGDT KFGMKGFVLF  41 GARIVAVPTP GSLRYLSLAN LEYIPDGAFD VNLQELALQQ LKELSIGIFG TELRELSLHT LEMLPLGIFD GQSLIIINVN IQVIDDRSVW   | GIVAPPRLEP FLKNSNLQHI TQDLYCLNES DVGNLVEKHM PLESPTSDHH PTHMNNGDYT TNRSNEIPST HKIPLDG  51   LEWNAMSLQI NKLQVLPIGL HLVGLTKLINL NQIGLLSPGL PMPNLRELWL NALQDLDGNV HLGKLCELRL VAVPSVHVPE | 120<br>180<br>240<br>300<br>360<br>420<br>477<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540 |
| 50<br>55<br>60<br>65 | MSSWIRWHGP MSVDPENITE NFTRKLITSL SKNIPLANLQ METSHTQGSL WCIPPTVKGN LIAKNEYGKD DVTDKTGREH Seq ID NO: Protein Acc  1   MPLKHYLLLL LINTHITELME FQGLDSLESL GKNSLTHISP FRHNANLQNI YDNPWRCDSD VBSYPETFWY IAAIVIGIVA  Seq ID NO: Protein Acc  1   MRALLARLLL HCEIDKSKTC YCRNPDNRRR GGEFTTIENC RSRLNSNTQC PSMYNDPQPC | AMARLMGFCW AMARLMGFCW IFILANQKRLE SRKHFRHLDL IFNCGLPSAN RITNISSDDS PKPALQWFYN EKQISAHPMG LSVYAVVVIA  C326 Prote Cession #:  VGCQAWGAGL SPFIMISALI LLSSNQLLQI RVFPGLIGNIQ VLISNNHISQL VLISNNHISQL SLQNRILRQI CULVVSDSKK CYENGHSYRC PMCYVCVGLI PMCYVCVGLI PMCYVCVGLI SEMKFEVENL | LVVGFWRAAF IINEDDVEAY SELILVGNPF LAAPNLTVEE GKQISCVAEN GAILNESKYI WPGIDDGANP SVVGFCLLVM in Sequence NP_570843.1  21   AYHGCPSECT ALRIENNELS OPAHPSOCSN VLRLYENRLT PPSIFMOLPO VLILSRNQIS CCCCKKRSOA SIN Sequence NP_002649.1    SSNELHQVPSE SKASTDTMGRI K PLVQECMVHH R RGGSVTYVC K ENSTDYLYP | ACPTSCKCSA ACPTSCKCSA VGLRNLITVD TCSCDIMMIK GKSTILSCSV LVGEDQDSVIN CTKIHVINHT NYPDVIYEDY LFLLKLARHS  31   CSRASQVECT RITPGAFRNL LKELQLHGNH DIPMGTFGGL LMALIQLNING PVCFSPANVE PVEFSPANVE PVEFSPANGE LMALIQLNING PVCFSPANVE PVEDYTDLTI VLMQMKAPNE  31   CCDCLMGGTCC CCDCMGGTCC CCDGMSSATVI CCDCLMGGTCV CADGKKPSSI G GSLISPCWV: AHHNDIALLI E QLKMTVVKL CALLINTTVKL CA | SRIWCSDPSP SGLKPVAHKA TIQEAKSSPD AGDPVPNMYW LTVHFAPTIT EYHGCLQLDN GTAANDIGDT KFGMKGFVLF  41 GARIVAVPTP GSLRYLSLAN LEYIPDGAFD VNLQELALQQ LKELSLGIFG TELRELSLHT LEMLPLGIFD GQSLIINVN TQVTDDRSVW C 41 SNKYFSNIHW QQTYHAHRSI PEELKFQCQC SATHCFIDYI SIRKEGRCAG SHRECQQPHY | GIVAPPRLEP FLKNSNLQHI TQDLYCLNES DVGNLVEKHM PLESPTSDHH PTHMNNGDYT TNRSNEIPST HKIPLDG  51   LEWNAMSLQI NKLQVLPIGL HLVGLTKLINL NQIGLLSPGL PMPNLRELWL NALQDLDGNV HLGKLCELRL VAVPSVHVPE | 60<br>120<br>180<br>360<br>420<br>180<br>240<br>360<br>420<br>480<br>540<br>581                             |

|     | 1 1  | 1 :                                   | 21                                     | 31                                     | 41                                     | 51                                      |                          |
|-----|--|---------------------------------------|--|--|--|---|--------------------------|
| 5 . | MQFRECSING M<br>NETELIKEHD L                                 | FFKAVSLCH '                           | TVQISNVQTD                             | CTGDGPWQSN                             | LAPSQLEYYA                             | SSPDEKALVE                              | 60<br>120                |
|     | AAARIGIVFI G<br>AESSILPKCI G<br>REEKLAAVFQ F<br>SLSCGHFHRT M | GEIEKTRIH '                           | VDEFALKGLR '<br>ATAVEDRLQD             | TLCIAYRKFT<br>KVRETIEALR               | Skeyeeidkr<br>Magikvwvlt               | ifeartalqq<br>GDKHETAVSV                | 180<br>240<br>300<br>360 |
| 10  | EKLFMEVCRN C<br>GIMGKEGRQA F<br>QFYCLFSOOT I                 | SAVLCCRMA<br>ARNSDYAIAR               | PLQKAKVIRL<br>FKFLSKLLFV               | IKISPEKPIT<br>HGHFYYIRIA               | LAVGDGANDV<br>TLVQYFFYKN               | SMIQEAHVGI<br>VCFITPQFLY                | 420<br>480<br>540        |
| 15  | SIKTFLYWTI I<br>MALETHPWTW I<br>ILMVVTCLFL I                 | GFSHAFIFF<br>INHLVTWGSI<br>DIIKKVFDRH | FGSYLLIGKD<br>IFYFVFSLFY<br>LHPTSTEKAQ | TSLLGNGQMF<br>GGILWPFLGS<br>LTETNAGIKC | GNWTFGTLVF<br>QNMYFVFIQL<br>LDSMCCFPEG | TVMVITVTVK<br>LSSGSAWFAI                | 600<br>660<br>720        |
|     | LERVIGROSP T   |                                       |  | LTLSTMDSST                             | C                                      |   | 761                      |
| 20  | Protein Acce   | ession #: X                           | P_087461.1                             |  | 41                                     | E1                                      |                          |
|     | MLPLLAALLA A   | AACPLPPVRG                            | 21<br>GAADAPGLLG                       | 31<br>VPSNASVNAS                       | 41<br> <br>  SAASPSPRGC                | 51<br> <br>  WPRRPPGPPS<br>  AFFAAAFHRV | 60<br>120                |
| 25  | GPPLLIEHLG :<br>AAEPPGPLWL<br>LIWPVPIIAG                     | LAAGGAQQDL<br>QGEPLHFCCL              | RLCVGCGWVR<br>DFSLEELQGE               | GRRTGRLRPA<br>PGWRLNRKPI               | AAPSAAAATA<br>ESTLVACFMT               | GAPTALPAYP<br>LVIVVWSVAA                | 180<br>240<br>299        |
| 30  | Seq ID NO:<br>Protein Acc                                    |                                       |  |  |  |   |                          |
|     | 1  | 11<br>                                | 21                                     | 31<br>  ·                              | 41<br>                                 | 51<br>                                  |                          |
| 35  | MDLHLFDYSB<br>ANSVVVWVNI                                     | QAKTTGYDTH                            | CYILNLAIAD                             | LWVVLTIPVW                             | VVSLVQHNQW                             | PMGELTCKVT                              | 60<br>120                |
|     | HLIFSINLFG<br>YYLKTVTSAS                                     | NNETYCRSFY                            | PEHSIKEWLI                             | GMELVSVVLG                             | FAVPFS11AV                             | FYFLLARAIS<br>HALFTALHVT                | 180<br>240<br>300        |
| 40  |  |                                       |  |  |  | ETEYSALEQS                              | 360<br>362               |
|     |  |                                       | in Sequence<br>NP_000341.1             |  |  |   |                          |
| 45  | 1  | 11                                    | 21                                     | 31<br>1                                | 41                                     | 51<br>I                                 |                          |
|     | MGFVRQIQLL<br>MPSAGMLPWL                                     | LWKNWTLRKR<br>OGIFCNVNNP              | QKIRFVVELV<br>CFOSPTPGES               | WPLSLPLVLI<br>PGIVSNYNNS               | WLRNANPLYS<br>ILARVYRDFQ               | HHECHFPNKA<br>ELLMNAPESQ                | 60<br>120                |
| 50  | HLGRIWTELH   | ILSQFMDTLR                            | THPERIAGRG                             | IRIRDILKDE                             | ETLTLFLIKN                             | IGLSDSVVYL<br>SLSQGTLQWI                | 180<br>240               |
|     | EDTLYANVDF<br>RPLMQNGGPE                                     | FKLFRVLPTL<br>TFTKLMGILS              | LDSRSQGINL<br>DLLCGYPEGG               | RSWGGILSDM<br>GSRVLSFNWY               | SPRIQEFIHR<br>BDNNYKAFLG               | PSMQDLLWVT<br>IDSTRKDPIY                | 300<br>360               |
|     | LEHVRKLVKA   | WEEVGPQIWY                            | FFDNSTQMNM                             | IRDTLGNPTV                             | KDFLNRQLGE                             | LKNANSTFEE<br>EGITAEAILN                | 420<br>480               |
| 55  | LLEENMFWAG   | VVFPDMYPWI                            | SSLPPHVKYK                             | IRMDIDVVER                             | C TNKIKDRYWI                           | ETQLTQRALS<br>SGPRADPVED                | 540<br>600               |
| •   | LAWIYSVSMT   | VKSIVLEKE                             | RLKETLKNOG                             | VSNAVIWCTV                             | FLDSPSIMS                              | LNRCFPIFMV<br>SIPLLTIFIM                | 660<br>720<br>780        |
| 60  | AWQDRMTABL   | KKAVSLLSPV                            | AFGFGTEYLV                             | RFEEQGLGL(                             | WSNIGNSPTE                             | TLYLPHILCF<br>GDEFSFLLSM                | 840<br>900               |
|     | TEETEDPEHP   | EGIHDSFFEE                            | EHPGWVPGVC                             | VKNLVKIFE                              | CGRPAVDRL                              | E ERALEKTEPL<br>N ITPYENQITA            | 960                      |
| 65  | AEHMLFYAQL   | KGKSQEEAQI                            | EMBAMLEDTO                             | LHHKRNEBA                              | DLSGGMQRK                              | HNILPHHLTV<br>L SVAIAFVGDA              | 1020                     |
| 65  | SGTPLFLKNC   | FGTGLYLTL                             | / RKMKNIQSQ                            | R KGSEGTCSC                            | S SKGFSTTCP                            | A HVDDLTPEQV                            | 1140<br>1200             |
|     | SPGISDTPLE   | EIFLKVTED:                            | S DSGPLFAGG                            | A QOKRENVNP                            | R HPCLGPREK                            | L EETLADLGLS<br>A GQTPQDSNVC            | 1260<br>1320             |
| 70  | SPGAPAAHPE<br>ATFVFLALML                                     | GOPPPEPECI<br>SIVILPFGE               | P GPQLNTGTQI<br>Y PALTLHPWI            | L VLQHVQALL<br>Y GQQYTFFSM             | V KRFQHTIRSI<br>D EPGSEQFTV            | H KDFLAQIVLP<br>L ADVLLNKPGF            | 1380<br>1440             |
|     | GNRCLKEGWI   | PEYPCGNST                             | P WKTPSVSPN                            | I TQLFQKQKW                            | T QVNPSPSCR                            | C STREKLTMLP<br>F WVNEQRYGGI            | 1500<br>1560             |
|     | SIGGKLPVVE   | ITGEALVGF                             | L SDLGRIMNV                            | S GGPITREAS                            | K EIPDFLKHL                            | E TEDNIKVWFN<br>E ITVLTTSVDA            | 1620<br>1680             |
| 75  | VVAICVIPSM   | SEVPASEVL                             | Y LIQERVNKS                            | K HLQFISGVS                            | P TTYWVTNFL                            | W DIMNYSVSAG                            | 1740                     |
|     | FIGINSSAIT   | PILELFONN                             | R TLLRFNAVL                            | R KLLIVFPHF                            | C LGRGLIDLA                            | T AYVALSCANL<br>L SQAVTDVYAR            | 1800<br>1860             |
|     | FGEEHSANPI   | HWDLIGKNL                             | F AMVVEGVVY                            | F LLTLLVQRH                            | P PLSQWIAEP                            | T KEPIVDEDDD<br>L LGVNGAGKTT            | 1920<br>1980             |
| 80  | TPKMLTGDTT   | T VTSGDATVA                           | G KSILTNISE                            | V HQNMGYCPQ                            | F DAIDELLTG                            | R EHLYLYARLR                            | 2040                     |
|     | MDPOARRML  | NVIVSIIRK                             | G RAVVLTSHS                            | M EECEALCTR                            | L AIMVKGAFR                            | P LVLLDEPTTG<br>C MGTIQHLKSK            | 2100<br>2160             |
|     | FGDGYIVTM  | K IKSPKDDLL                           | P DLNPVEQFF                            | Q GNFPGSVQR                            | E RHYNMLQFQ<br>L HPRAAGASR             | V SSSSLARIFQ                            | 2220<br>2273             |
|     | LLLSHKDSLI   | r ieearaloi                           | I PDOALANLY                            | v ččirounis                            | D 111.10.                              |   |                          |

|     |  | C332 Protei:<br>ession #: N  |  |  |  |  |                                       |
|-----|--|--|--|--|--|--|---------------------------------------|
| 5   | 1  | 11   | 21   | 31   | 41   | 51   |                                       |
|     | LKMMILPLVV   | <br>RDVCRRNGLL<br>SSLMSGLASL<br>PIMSSADALL                                       | DAKTSSRLGV   | LTVAYYLWTT   | FMAVIVGIFM   | VSIIHPGSAA   | 60<br>120<br>180                      |
| 10  | RILIYGVQEE<br>DSGAPLVSFC<br>VCGLVLHGLF<br>IDRRIARFVL | NGSHVQNFAL<br>QCLNESVMKI<br>ILPLLYFFIT<br>PVGATINMDG                             | DLTPPPEVVY<br>VAVAVWYFPF<br>KKNPIVFIRG<br>TALYBAVAAI | KSEPGTSDGM<br>GIVFLIAGKI<br>ILQALLIALA<br>FIAQVNNYEL | NVLGIVFFSA<br>LEMDDPRAVG<br>TSSSSATLPI<br>DFGQIITISI | TMGIMLGRMG<br>KKLGFYSVTV<br>TFKCLLENNH<br>TATAASIGAA | 240<br>300<br>360<br>420              |
| 15  | PARDTGTEKL<br>LPAASLNHCT                             |  | QEIVAAQQNG   | CVKSVAEASE   | INVLGDALAA<br>LTLGPTCPHH                             | VPVQVERDEE   | 480<br>540<br>560                     |
| 20. | Protein Acc  | C333 Protei<br>cession #: N  | P_005680.1   |  |  |  |                                       |
|     | 1  | 11   | 21<br>1  | 31<br>I  | 41   | 51<br>   |                                       |
| 25  | SLSWGAGPRI<br>GLWLLVVERS<br>GQQVQFSLWV<br>DFGRKLRLLS | EGPVGPAWMQ<br>SPYVLQLLLA<br>QARQRLAMGI<br>LRYVVSGGLP<br>GYLWPRGSPA<br>FLKPLQGGGT | TLQAALPLAG<br>WIKPRHSPGL<br>VLGLWAPGLR<br>LQLVVLICLG | LAGRVGTARG<br>LLLWTVAFAA<br>PQSYTLQVHE<br>LMGLERALNV | APLPSYLLLA<br>ENLALVSWNS<br>EDQDVERSQV<br>LVPIFYRNIV | SVLESLAGAC PQWWWARADL RSAAQQSTWR NLLTEKAPWN          | 60<br>120<br>180<br>240<br>300<br>360 |
| 30  | HLGRRTGEVL<br>MSLYLTLTIV<br>IKYQGLEWKS               | RIADRGTSSV<br>VTEWRTKFRR<br>SASLVLLNQT   | TGLLSYLVFN<br>AMNTQENATR<br>QNLVIGLGLL               | VIPTLADIII<br>ARAVDSLLNF<br>AGSLLCAYFV               | GIIYFSMFFN<br>ETVKYYNAES<br>TEQKLQVGDY               | AWFGLIVFLC<br>YEVERYREAI<br>VLFGTYIIQL               | 420<br>480<br>540                     |
|     |  |  |  |  |  | BFENVHFSYA<br>GQDISQVTQA                             | 600<br>660                            |
| 25  | SLRSHIGVVP   | QDTVLFNDTI   | ADNIRYGRVT   | AGNDEVEAAA   | QAAGIHDAIM   | AFPEGYRTQV   | 720                                   |
| 35  | GERGLKLSGG<br>VAHRLSTVVN                             | EKQRVAIART<br>ADOILVIKDG   | CIVERGRHEA   | DEATSALDTS<br>LLSRGGVYAD                             | NERALQASLA<br>MWQLQQGQEE                             | KVCANRTTIV<br>TSEDTKPQTM                             | 780<br>840                            |
|     | ER   |  |  |  |  |  | 842                                   |
| 40  |  | C334 Prote<br>cession #: :   | NP_000667.1  |  |  |  |                                       |
|     | 1  | 11<br>1  | 21<br>   | 31<br>   | 41<br>   | 51<br>   |                                       |
| 45  | MLLETQDALY<br>IPFAITISLG                             | VALELVIAAL<br>FCTDFYGCLF   | SVAGNVLVCA   | AVGTANTLQT   | PTNYFLVSLA<br>VDRYLAICVE                             | AADVAVGLFA<br>LRYKSLVTGT                             | 60<br>120                             |
|     | RARGVIAVLW<br>YMVYFNFFGC                             | VLAFGIGLTP<br>VLPPLLIMLV   | FLGWNSKDSA<br>IYIKIFLVAC                             | TNNCTEPWDG<br>RQLQRTELME                             | TINESCCLVI<br>HSRTTLQRE                              | CLPENVVPMS<br>HAAKSLAMIV                             | 180<br>240                            |
| 50  |  | HAVNCVTLFQ<br>CQADVKSGNG   |  |  | ANSVVNPIV  | AYRNRDFRYT   | 300<br>332                            |
| 30  |  | C335 Prote   |  | •  |  |  |                                       |
|     |  |  | _  |  | 0.2  |  |                                       |
| 55  | 1<br>  | 11<br>   | 21<br>   | 31<br>   | 41   | 51<br>   |                                       |
|     |  |  |  |  |  | TVKPPTSVAS   | 60<br>120                             |
|     |  |  |  |  |  | S TSTMIVTHNS<br>M YYSRRGIRYR                         | 180                                   |
| 60  | TIDEHDAII  |  |  |  |  |  | 189                                   |
| 00  |  | : C336 Prote   |  |  |  |  |                                       |
|     | ·1   | 11   | 21   | 31   | 41   | 51   |                                       |
| 65  | 1  | 1  |  | l  | 1  | 1  |                                       |
|     | MAQHGAMGAI<br>YPGRECCSE                              | F RALCGLALLA<br>W DCMCVOPEF  | C ALSIGORPT<br>H CGDPCCTTC                           | G GPGCGPGRL<br>R HHPCPPGOG                           | L LGTGTDARC<br>V OSOGKFSFG                           | C RVHTTRCCRD<br>F QCIDCASGTF                         | 60<br>120                             |
|     | <b>EGGHEGHCK</b>                                     | P WIDCIQFGF  | L TVFPGNKTH  | N AVCVPGSPP.   | a eplgwltvv  | L LAVAACVLLL   | 180                                   |
| 70  | TSAQLGLHI  | W QLRSQCMWP  | K ELÖPPPEAL  | P STEDARSCU  | r PEBBRGBRS  | A EEKGRLGDLW   | 240<br>241                            |
|     |  | : C337 Prot  |  |  |  |  |                                       |
| 75  | 1  | 11   | 21   | 31   | 41   | 51   |                                       |
|     | ĺ  | 1  | 1  | 1  | T. DI.BOOMEO   | T. DOTOMPPOO   | 60                                    |
|     |  |  |  |  |  | L PQISWVFFSQ<br>LS VMALAGLAMG                        | 120                                   |
| 80  | CIDTVANMQ  | L VRMYQKDSA  | V PLQVLHFFV  | G FGALLSPLI  | A DPFLSEANC  | l panstantts   | 180                                   |
| 30  | LSKERLLTC  | C PORRPLLLS  | A DELALETQE  | P EKEDASSLE  | P KFQSHLGHI  | D LPVPMAVLML<br>D LPSCCQRKNL                         | 300                                   |
|     | RGAPYSFFA  | I HITGALVLE  | M TDGLTGAYS  | a pvysyavek  | P LSVGHKVAC  | Y LPSLFWGFIT   | 360                                   |
|     |  |  |  |  |  | SL GLFLSSTFPS<br>SG VIFGCLAFTF                       |                                       |
|     |  |  |  |  |  |  |                                       |

|                            | YILLEPPHRM H  | ipglpsvptq   | DRSIGMENSE (   | YQR  |  |  | 514   |
|----------------------------|---|--|--|--|--|--|---|
| 5                          | Seq ID NO: 0  |  |  |  |  |  |   |
| J                          | 1 2   | 11   | 21 :   | 31 4   | 11   | și.  |   |
|                            | MGPERTGAAP I  | LDT.T.T.MT.AT.C  | CCTLNCCLAY I   | WGLDRAKIR 9  | REPSSENEGY   | )<br>AVOOPINPKG  | 60  |
|                            | NWLLVGSPWS (  | GFPENRMGDV   | YKCPVDLSTA   | CEKTNIOLS 1  | CSIPNVTEMK   | TNMSLGLILT   | 120   |
| 10                         | RNMGTGGFLT (  | CGPLWAQQCG   | NOYYTTGVCS   | DISPDFQLSA S   | FSPATQPCP  | SLIDVVVVCD   | 180   |
|                            | ESNSIYPWDA V  | VKNFLEKFVQ   | GLDIGPTKTQ '<br>KYAYSAASGG !   | VGLIQYANNP I   | RVVFNLNTYK   | TKEEMIVATS   | 240<br>300  |
|                            | HDNILREGIA V  | VLGYLNRNAL   | DTKNLIKEIK   | AIASIPTERY I   | FFNVSDEAAL   | LEKAGTLGEQ   | 360   |
| 1.5                        | IPSIEGTVQG (  | GDNFQMEMSQ   | VGFSADYSSQ I   | NDILMLGAVG A   | AFGWSGTIVQ   | Ktshghlipp   | 420   |
| 15                         | KQAFDQILQD I  | RNHSSYLGYS   | Vaaistgest  <br>DKDTITDVLL   | HFVAGAPRAN :   | KKEEGDAAI'E<br>KLGÖIAFAZA  | NENGNITVIQ<br>TIKKGILGOH   | 480<br>540  |
|                            |   |  | LSDINMDGFN   |  |  |  | 600   |
|                            | SQKILGSDGA  | FRSHLQYFGR   | SLDGYGDLNG :   | DSITDVSIGA   | FGQVVQLWSQ   | SIADVAIEAS   | 660   |
| 20                         |   |  | FSAKFRPTKQ :   |  |  |  | 720<br>780  |
| 20                         | FSIPFHKDCG  | EDGLCISDLV   | LDVRQIPAAQ   | EQPFIVSNQN 1   | KRLTFSVTLK   | NKRESAYNTG   | 840   |
|                            | IVVDFSENLF  | FASFSLPVDG   | TEVTCQVAAS   | QKSVACDVGY   | PALKREQQVT   | FTINFDFNLQ   | 900<br>960  |
|                            |   |  | KADNLVNLKI<br>SVPVSMATVI   |  |  |  | 1020  |
| 25                         | ADINPLKIGQ  | TSSSVSFKSE   | NFRHTKELNC   | RTASCSNVTC   | WLKDVHMKGE   | YFVNVTTRIW   | 1080  |
|                            |   |  | NTYNPEIYVI<br>RKYEKMTKNP   |  |  | PTGVIIGSII   | 1140<br>1181  |
|                            | AGIDDOMADA  | AIDWANGFFA   | KKIEMIIMI  |  |  |  |   |
| 30                         |   |  | in Sequence  |  |  |  |   |
| 30                         |   | ession #: 1<br>11  | NP_113648.1<br>21  | 31   | 41   | 51   |   |
|                            | 1   |  | 1  | 1  | 1  | 1  |   |
|                            |   |  | STVLLLLAYL<br>VVQAYKNGAS   |  |  |  | 60<br>120   |
| 35                         |   |  | IPLNLVVLNR   |  |  |  | 180   |
|                            | GSGALLSGLL  | LFLLLPPLLF   | SHMEGWSYTE   | GFYFAFITLS   | TVGFGDYVIG   | MNPSQRYPLW   | 240   |
|                            |   |  | KLILSQLETP<br>PSAHAAGCGK   |  | SKEDFKSQSW   | ROGPUREPES   | 300<br>332  |
| 40                         |   |  |  |  |  |  |   |
| 40                         |   |  | in Sequence  |  |  |  |   |
|                            | Protein Acc   | ession #:  | NP_004145.1  |  |  |  |   |
|                            |   |  |  |  |  |  |   |
|                            | i,  | 11   | 21   | 31   | 41   | 51   |   |
| 45                         | 1   | 1  |  | 1  | 1  | 1  | 60  |
| 45                         | <br>  MEWDNGTGQA<br>  TAVYTLNLAL  | <br>LGLPPTTCVY<br>ADLLYACSLP   | <br>RENFKQLLLP<br>LLIYNYAQGD   | PVYSAVLAAG<br>HWPPGDFACR   | <br>LPLNICVITQ<br>LVRFLFYANL   | <br>  ICTSRRALTR<br>  HGSILFLTCI   | 120   |
| 45                         | <br>  MEWDNGTGQA<br>  TAVYTLNLAL<br>  SFQRYLGICH  | LGLPPTTCVY<br>ADLLYACSLP<br>PLAPWHKRGG   | <br>RENFKQLLLP<br>LLIYNYAQGD<br>RRAAWLVCVA   | PVYSAVLAAG<br>HWPPGDFACR<br>VWLAVTTQCL   | <br>LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI   | <br>  ICTSRRALTR<br>  HGSILFLTCI<br>  QRNRTVCYDL   | 120<br>180  |
|                            | MEWDNGTGQA<br>TAVYTLNLAL<br>SPQRYLGICH<br>SPPALATHYM  | LGLPPTTCVY<br>ADLLYACSLP<br>PLAPWHKRGG<br>PYGMALTVIG   | <br>RENFKQLLLP<br>LLIYNYAQGD<br>RRAAWLVCVA<br>PLLPFAALLA   | PVYSAVLAAG<br>HWPPGDPACR<br>VWLAVTTQCL<br>CYCLLACRLC   | <br>LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI<br>RQDGPAEPVA   | <br>  ICTSRRALTR<br>  HGS1LFLTCI<br>  QRNRTVCYDL<br>  QERRGKAARM   | 120   |
| 45<br>50                   | MEWDNGTGQA<br>TAVYTLNLAL<br>SFQRYLGICH<br>SPPALATHYM<br>AVVVAAAFAI  | LGLPPTTCVY<br>ADLLYACSLP<br>PLAPWHKRGG<br>PYGMALTVIG   | <br>RENFKQLLLP<br>LLIYNYAQGD<br>RRAAWLVCVA<br>FLLPFAALLA<br>AYLAVRSTPG   | PVYSAVLAAG<br>HWPPGDPACR<br>VWLAVTTQCL<br>CYCLLACRLC   | <br>LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI<br>RQDGPAEPVA   | <br>  ICTSRRALTR<br>  HGS1LFLTCI<br>  QRNRTVCYDL<br>  QERRGKAARM   | 120<br>180<br>240   |
|                            | MEWDNGTGQA<br>TAVYTIMIAI<br>SFQRYLGICH<br>SPPALATHYM<br>AVVVAAAFAI<br>FYFTQKKFRR  | LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG SFLPFHITKT RPHELLQKLT  | RENFKQLLLP<br>LLIYNYAQGD<br>RRAAWLVCVA<br>FLLPFAALLA<br>AYLAVRSTPG<br>AKWQRQGR   | PVYSAVLAAG<br>HWPPGDPACR<br>VWLAVTTQCL<br>CYCLLACRLC   | <br>LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI<br>RQDGPAEPVA   | <br>  ICTSRRALTR<br>  HGS1LFLTCI<br>  QRNRTVCYDL<br>  QERRGKAARM   | 120<br>180<br>240<br>300  |
|                            | MEWDNGTGQA<br>TAVYTLNLAL<br>SFQRYLGICH<br>SPPALATHYM<br>AVVVAAAFAI<br>PYFTQKKFRR<br>Seq ID NO:  | LGLPPTTCVY<br>ADLLYACSLP<br>PLAPWHKRGG<br>PYGMALTVIG<br>SFLPPHITKT<br>RPHELLQKLT   | <br>RENFKQLLLP<br>LLIYNYAQGD<br>RRAAWLVCVA<br>FLLPFAALLA<br>AYLAVRSTPG   | PVYSAVLAAG<br>HWPPGDPACR<br>VWLAVTTQCL<br>CYCLLACRLC   | <br>LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI<br>RQDGPAEPVA   | <br>  ICTSRRALTR<br>  HGS1LFLTCI<br>  QRNRTVCYDL<br>  QERRGKAARM   | 120<br>180<br>240<br>300  |
| 50                         | MEWDNGTGQA<br>TAVYTINLAL<br>SPQRYLGICH<br>SPPALATHYM<br>AVVVAAAFAI<br>PYFTQKKFRR<br>Seq ID NO:<br>Protein Acc   | LGLPPTTCVY ADLIVACSU PLAPWHKRGG PYGMALITVIG SFLPFHITKT RPHELLQKLT  C341 Prote cession #:   | RENFKQLLLP<br>LLIYNYAQGD<br>RRAAWLVCVA<br>FLIPFAALLA<br>AYLAVRSTPG<br>AKWQRQGR<br>in Sequence<br>NP_009128.1   | PVYSAVLAAG<br>HWPFGDFACR<br>VWLAVTTQCL<br>CYCLLACRLC<br>VPCTVLEAFA   | <br>LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI<br>RQDGPAEPVA<br>AAYKGTRPFA   | ICTSRRALTR<br>HGSILFLTCI<br>QRNRTVCTDL<br>QERRGKAARM<br>SANSVLDPIL   | 120<br>180<br>240<br>300  |
|                            | MEWDNGTGQA<br>TAVYTLNLAL<br>SFQRYLGICH<br>SPPALATHYM<br>AVVVAAAFAI<br>PYFTQKKFRR<br>Seq ID NO:  | LGLPPTTCVY<br>ADLLYACSLP<br>PLAPWHKRGG<br>PYGMALTVIG<br>SFLPPHITKT<br>RPHELLQKLT   | RENFKQLLLP<br>LLIYNYAQGD<br>RRAAWLVCVA<br>FLLPFAALLA<br>AYLAVRSTPG<br>AKWQRQGR<br>in Sequence  | PVYSAVLAAG<br>HWPPGDPACR<br>VWLAVTTQCL<br>CYCLLACRLC   | <br>LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI<br>RQDGPAEPVA   | <br>  ICTSRRALTR<br>  HGS1LFLTCI<br>  QRNRTVCYDL<br>  QERRGKAARM   | 120<br>180<br>240<br>300  |
| 50                         | MEWDINGTGQA TAVYTLINLAL SFQRYLGICH SPPALATHYM AVVVAAAFAI FYFTQKKFRR Seq ID NO: Protein Acc  | <br>LGLPPTTCVY<br>ADLLYACSLP<br>PLAPWHKRGG<br>PYGMALTVIG<br>SFLPPHITKT<br>RPHELLQKLT<br>C341 Prote<br>cession #:<br>11<br> <br>VLQVMGSCAF  | RENFKQLLLP RENFKQLLLP LLIYNYAQGD RRAAWLVCVA FLLPFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1 21  | PVYSAVLAAG HWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP  | LPLNICVITQ<br>LVRFLFYANL<br>PTAIFAATGI<br>RQDGFAHPVA<br>AAYKGTRPFA   | ICTSRRALTR HGSILFLTCI ORNRTVCTDL OERRGKAARM SANSVLDPIL   | 120<br>180<br>240<br>300<br>328   |
| 50                         | MEWDNGTGQA TAVYTLNLAL SFQRYLGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  | <br>LGLPPTTCVY<br>ADLLYACSLP<br>PLAPMHKRGG<br>PYGMALTVIG<br>SFLPPHITKT<br>RPHELLQKLI<br>C341 Prote<br>Cession #:<br>11<br> <br>VLQVMGSCAF<br>FAPLVEYGCE  | RENFKQLLLP RENFKQLLLP LLIYNYAQGD RRAAWLVCVA FLLPFAALLA AYLAVRSTPG AKWQRQGR Lin Sequence NP_009128.1 21   LISSMDMERPG GHLRFFLCSL  | PVYSAVLAAG PVYSAVLAAG HWPFGDFACR VWLAVTTQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS  | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC   | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI   | 120<br>180<br>240<br>300<br>328   |
| 50                         | MEWDINGTGQA TAVYTLINLAL SFQRYLGICH SPPALATHYM AVVVAAAFAI FYFTOKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKWFD PLKXGGFGRG   | <br>LGLPPTTCVY<br>ADLLYACSLP<br>PLAPWHKRGG<br>PYGMALTVIG<br>SFLPPHITKT<br>RPHELLQKLT<br>C341 Prote<br>cession #:<br>11<br> <br>VLQVMGSCAF<br>FAPLVEYGCE<br>SLDCRKLPHR  | RENFKQLLLP RENFKQLLLP RENFKQLLLP RAWLVCVA FLLPFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1 21   1   1   1   1   1   1   1   1   1  | PVYSAVLAAG HWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTE CTPGDDVYWS   | LPLNICVITQ LVRFLFYANL PTAIFAATGI RQDGPABPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFR  | ICTSRRALTR HGS1LFLTCI ORNRTVCTDL OERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI PORPHSAQEH  | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240  |
| 50<br>55                   | MEWDINGTGQA TAVYTLNIAL SFQRYIGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKMPD PLKDGGPGRG SSAFTVLTFL   | <br>LGLPPTTCVY<br>ADLLYACSLP<br>PLAPMHKRGG<br>PYGMALTVIG<br>SFLPPHITKT<br>RPHELLQKLT<br>C341 Prote<br>cession #:<br>11<br>VLQVMGSCAF<br>YAPLVEYGCE<br>SLDCRKLPNI<br>GCDNPGKFHH<br>IDPARFRYPI   | RENFKQLLLP RENFKQLLLP RENFKQLLLP RRAWLVCVA FLLFFAALLA AYLAVRSTPG AKWQRQGR Lin Sequence NP_009128.1 21   LISSMDMERPG GHLRFFLCSL KNDPNYLCMEA LVEKSASCAPL RPIIFLSMCY  | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGVDVYWS CVYSVGYLIR   | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLFPPLFF REDKRPAVVM LPAGASSIAC  | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QEERGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI PORPHSAQEH LAIWAVLCFF DRDSGQLYVI  | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300   |
| 50                         | MEWDIGTGQA TAVYTLNIAL SPORYLGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  MORPGPRLWL MORPGPRLWL MEQFINFKMPD PLKDGGFGRG PLKDGGFGRG SAPTVLTFL OBSLESTGCT  | <br>LGLPPTTCYY<br>BADLLYACSLP<br>PLAPWHKRGG<br>PYGMALTVIG<br>SFLPPHITKT<br>RPHELLQKLI<br>C341 Protecession #:<br>11<br> <br>VLQVMGSCAF<br>FAPLVEYGCE<br>SLDCRKLPNE<br>GCUNPCKFHE<br>LUPFLVLYYEV<br>LVFLVLYYEV  | RENFKOLLLP RENFKOLLLP RENFKOLLLP RAMMIVCVA FLIPFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1 21   | PVYSAVLAAG HWPFGDFACR VWLAVTTQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGVDVYWS CVYSVGYLIR TLTWFLAAGK   | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAHPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFR REDKRFAVVW LPAGASSIAC  | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI PQRPHSAQEH LAIMAVLCFF LAIMAVLCFF DRDSGQLYVI SSYPHLAAWA  | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240  |
| 50<br>55<br>60             | MEWDINGTGQA TAVYTLNIAL SFQRYLGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKNFD PLKDGGPGRG SSAFTVLTFL QEGLESTGGT IPAVKTIGI FHIRRVMKTG   | LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLI  C341 Prote cession #:  11    VIQVMGSCAF PAPLVEYGCE SLDCRKLPNI GCNPGKFHE IDPARFRYPF LVFLVLYYFK VMRRVAGDEI GENTDKLEKG   | RENFKQLLLP RENFKQLLLP RENFKQLLLP RAWLVCVA FLLPFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1 21   ISSMDMERPG GHLRFFLCSL KNDPNYLCMEA TVEKSACAPL RPISTLSWCYGSML TGVCYVGSML MVRIGLFSVL  | PVYSAVLAAG PVYSAVLAAG PWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTFGDDYYMS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI   | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPABPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFR REDKRPAVW LFAGAESIAC KKGHEAIEAA PLACYLVIGT   | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI LAINAVLCFF DRDSCQLYVI SSYFILAANA SFILSGFVAL TYMKLLAAQHK   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480  |
| 50                         | MEWDIGTGQA TAVYTLNIAL SFQRYLGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Ac.  MQRPGPRLWL QREAAIQLHE MEQFIFKMPD PLKDGGPGGG SSAFTVLTFL QEGLESTGCT IPAVKTILIL FHIRRVMKTG CKOMNQTKTL  | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY PLAPMHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLI  C341 Prote Cession #:  11   VLQVMGSCAF FAPLVEYGCI SLDCRLPNI GCDNPGKFHH LDPARFRYPI LVFLVLYYFC VMRVAGDEI GENTDKLEKG CDCLMARSIFI CLCLMARSIFI CLCL | RENFKQLLLP RENFKQLLLP LLIYNYAQGD RRAAWLVCVA PLLPFAALLA AYLAVRSTPG AKWQRQGR LIN Sequence NP_009128.1 21   LISSMDMERPG GHLRFFLCSL KNDPNYLCMEA TOVEKSASCAPL RPIIFLSMCY MASSLWWVUL TGVCYVGSMU MYRIGLFSVL AVEIFMVKIFM   | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGVDVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA  | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFF REDKRFAVVW LFAGASSIAC KWGHEAIEAN PLACTIVIG CYPYERLING WIWTSKTLQS   | ICTSRRALTR HGSILFLTCI QENRTVCYDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI PQRPHSAQEH LAIWAVLCFF DRDSQLYVI SSYFHLAAWA SFILSGFVAL   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540   |
| 50<br>55<br>60             | MEWDIGTGQA TAVYTLNIAL SFQRYLGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Ac.  MQRPGPRLWL QREAAIQLHE MEQFIFKMPD PLKDGGPGGG SSAFTVLTFL QEGLESTGCT IPAVKTILIL FHIRRVMKTG CKOMNQTKTL  | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY PLAPMHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLI  C341 Prote Cession #:  11   VLQVMGSCAF FAPLVEYGCI SLDCRLPNI GCDNPGKFHH LDPARFRYPI LVFLVLYYFC VMRVAGDEI GENTDKLEKG CDCLMARSIFI CLCLMARSIFI CLCL | RENFKQLLLP RENFKQLLLP RENFKQLLLP RAWLVCVA FLLPFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1 21   ISSMDMERPG GHLRFFLCSL KNDPNYLCMEA TVEKSACAPL RPISTLSWCYGSML TGVCYVGSML MVRIGLFSVL  | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGVDVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA  | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFF REDKRFAVVW LFAGASSIAC KWGHEAIEAN PLACTIVIG CYPYERLING WIWTSKTLQS   | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI LAINAVLCFF DRDSCQLYVI SSYFILAANA SFILSGFVAL TYMKLLAAQHK   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480  |
| 50<br>55<br>60             | MEWDINGTGQA TAVYTINIAL SFQRYIGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKNFD PLKDGGPGRG SSAFTVLTFL QBGLESTGGT IPAVKTILI FHIRRVMKTG CKMNNQTKTL KKSRRKPASV  Seq ID NO:   | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY PLAPWHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLI C341 Prote cession #:  11   VIQVMGSCAF PAPLVEYGCE SLDCRLPNI CGCNPGKFHE IDPARFRYPF LVFLVLYYFK VMRRVAGDEI GENTDKLEKG CLMAASIPJ TISGGIYKK C342 Prote   | RENFKQLLLP RENFKQLLLP RENFKQLLLP RAWLVCVA FLLPFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1 21   ISSMDMERPG GHLRFFLCSL KNDPNYLCMEA TVEKSACAPL RPIIFLSMCY MARSLWWVVL TGVCYVGSML TGVCYVGSML WURIGLFSVL VEIFMVKIFM A QHPQKTHHGK ein Sequence   | PVYSAVLAAG PVYSAVLAAG PWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31    DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPFGDVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM  | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFF REDKRFAVVW LFAGASSIAC KWGHEAIEAN PLACTIVIG CYPYERLING WIWTSKTLQS   | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI LAINAVLCFF DRDSCQLYVI SSYFILAANA SFILSGFVAL TYMKLLAAQHK   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>540  |
| 50<br>55<br>60<br>65       | MEWDINGTGQA TAVYTINIAL SFQRYIGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKNFD PLKDGGPGRG SSAFTVLTFL QBGLESTGGT IPAVKTILI FHIRRVMKTG CKMNNQTKTL KKSRRKPASV  Seq ID NO:   | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY PLAPWHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLI C341 Prote cession #:  11   VIQVMGSCAF PAPLVEYGCE SLDCRLPNI CGCNPGKFHE IDPARFRYPF LVFLVLYYFK VMRRVAGDEI GENTDKLEKG CLMAASIPJ TISGGIYKK C342 Prote   | RENFKOLLLP RENFKOLLLP LLIYNYAQED RRAAWLVCVA FLLPFAALLA AYLAVRSTPG AKWORQGR in Sequence NP_009128.1 21  | PVYSAVLAAG PVYSAVLAAG PWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31    DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPFGDVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM  | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFF REDKRFAVVW LFAGASSIAC KWGHEAIEAN PLACTIVIG CYPYERLING WIWTSKTLQS   | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI LAINAVLCFF DRDSCQLYVI SSYFILAANA SFILSGFVAL TYMKLLAAQHK   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>540  |
| 50<br>55<br>60             | MEWDINGTGQA TAVYTINIAL SFQRYIGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKNFD PLKDGGPGRG SSAFTVLTFL QBGLESTGGT IPAVKTILI FHIRRVMKTG CKMNNQTKTL KKSRRKPASV  Seq ID NO:   | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY PLAPWHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLI C341 Prote cession #:  11   VIQVMGSCAF PAPLVEYGCE SLDCRLPNI CGCNPGKFHE IDPARFRYPF LVFLVLYYFK VMRRVAGDEI GENTDKLEKG CLMAASIPJ TISGGIYKK C342 Prote   | RENFKQLLLP RENFKQLLLP RENFKQLLLP RAWLVCVA FLLPFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1 21   ISSMDMERPG GHLRFFLCSL KNDPNYLCMEA TVEKSACAPL RPIIFLSMCY MARSLWWVVL TGVCYVGSML TGVCYVGSML WURIGLFSVL VEIFMVKIFM A QHPQKTHHGK ein Sequence   | PVYSAVLAAG PVYSAVLAAG PWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31    DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPFGDVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM  | LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFF REDKRFAVVW LFAGASSIAC KWGHEAIEAN PLACTIVIG CYPYERLING WIWTSKTLQS   | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI LAINAVLCFF DRDSCQLYVI SSYFILAANA SFILSGFVAL TYMKLLAAQHK   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>540  |
| 50<br>55<br>60<br>65       | MEWDNGTGQA TAVYTINIAL SFQRYLGICH SPPALATHYM AVVVAAAPAI PYFTOKKFRR Seq ID NO: PTOTEIN ACT  | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG STLPPHITKT RPHELLQKLT  C341 Prote cession #:  11    VLQVMGSCAP FAPLVEYGC: SLDCRKLPNN GCDNPGKFHH LUPFLVLYYFK VMRRVAGDEI CGENTDKLEKG DCLMAASIPJ TISGGIYKK  C342 Prote cession #:  11    1  | RENFKOLLLP RENFKOLLLP LLIYMYAQGD RRAAWLVCVA FLIFFAALLA AYLAVRSTPG AKWORQGR in Sequence NP_009128.1 21   ISSMDMERPG ISSMDMERPG INDENTICMEA VEKSASCAPL INDENTICMEA | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGVDVYWS CVYSYGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC  | LPLNICVITQ LPLNICVITQ LVRPLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPPLFF REDKRFAVVW LPAGASSIAC KWGHEAIEAN PLACTIVIGE CYPYERIGH WIWTSKTLQS V  | ICTSRRALTR HGS1LFLTCI QRNRTVCTDL QERRGKAARM SANSVLDPIL  51   FRMPNLMGHEN EQARLKCSPI EQARLKCSPI DRDSGQLYVI SSYFHLAAWA SSYFHLAAWA SFILSGVAL WQQVCSRRLK   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>581   |
| 50<br>55<br>60<br>65<br>70 | MEWDINGTGQA TAVYTLNIAL SFQRYLGICH SPPALATHYM AVVVAAAFAI FYFTOKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKWFD PLKDGGGGRG SSAFTVLTFL QEGLESTGCT IPAVKTILIF FHIRRWMETG CKMNNQTKTL KKSRRKPASV Seq ID NO: Protein Acc  1   MEVSRRKAPE SGSCLDOLDY  | LGLPPTTCVY ADLLYACSLP PLAPMHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLT  C341 Prote cession #:  VLQVMGSCAF PAPLVEYGCE SLDCRKLPNE GCDNPGKFHH LDFARFRYPH LVFLVLYYFK GCDNPGKFHH GENTDKLEKG DCLMAASIPH CCGSSION #:  11    C342 Prote ccession #:  21    PRPPRPAAPLL SERLESSEL  | RENFKQLLLP RENFKQLLLP RLIYNYAQGD RRAAWLVCVA FLLFFAALLA AYLAVRSTPG AKWQRQGR LIN Sequence NP_009128.1 21 LISHDMERPG GHLRFFLCSL NDENFLCSL VEKSASCAPL RPIIFLSMCY MORIGLESVI AVEIFMVKIFM AOHO SEQUENCE NP_005752.1 21 LISYLLALAM Y RDQAGNCTE  | PVYSAVLAAG PWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGUDYWNS CVYSVGYLIR TLIWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC   | LPLNICVITQ LPLNICVITQ LVRFLFYANL PTAIFAATGI RQDGPABPVA AAYKGTRPFA  41   MCKDIGYNMI TPIPACRVMC GSGLPPLFR REDKRFAVVW LFAGAESIAC KWGHEAIEAA PLACYLVIGG CYFYERLINMI WIWTSKTLQS V  41   RSEQAIGALI RSEQAIGALI RSEQAIGALI RSEQAIGALI   | ICTSRRALTR HGS1LFLTCI QENRTVCTDL QERGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI LAIWAVLCFF DRDSQLYVI SYPHLAAWA SYPHLAAWA SYHLAAWA WQQVCSRRLK  51   QUANTION OF THE CONTROL OF THE CONTRO | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>581  |
| 50<br>55<br>60<br>65       | MEWDINGTGQA TAVYTLNIAL SFQRYIGICH SPPALATHYM AVVVAAAFAI PYFTQKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKMPD PLKDGPGGGG SSAFTVLTFL QEGLESTGCT IPAVKTILIL KKSRRKPASV Seq ID NO: Protein Acc  1   MEVSRRKAPE SGSCLDQLDY GILLITGWTFI  | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY ADLLYACSLP PLAPMHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLI  C341 Prote cession #:  11   VIQVMGSCAF PAPLVEYGCE SLDCRKLPHH GCDNPGKFHH IDPARFRYPI LVFLVLYYK LVFLVLYYK C342 Prote cession #:  11   RPRRPAAPL P REFERSALE R SEHSLERL R SEHSLERL R SEGACEVRPL   | RENFKQLLLP RENFKQLLLP RENFKQLLLP LLIYNYAQGD RRAAWLVCVA FLLFFAALLA AYLAVRSTPG AKWQRQGR LIN Sequence NP_009128.1 21   ISSMDMERPG GHLRFFLCSL KNDPNYLCMEA LYEKSASCAPL RPIIFLSMCYU MASSLWWVUL LWIFMCYLYWSML MVRIGLFSVI AVEIFMVKIFW OHPQKTHHGK LIN Sequence NP_005752.1 21   LLAYLLALAM Y RDQAGNCTEI G MLSRNSLRN   | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGVDVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC  31   PGRGADEPVW VSLAPPARPE TTEVVSCHPQG  | LPLNICVITQ LPLNICVITQ LVRFLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41    MCKDIGYNMT TPIPACRVMC GSGLFPPLFR REDKRFAVVW LPAGARSIAC KKGHEALEAN PLACYLVIGT CYFYRELINMI WIWTSKTLQS V  41    RESEQAIGALI PGSSFSKLLI GSTAGVYYRA  | ICTSRRALTR HGS1LFLTCI QENRTVCTDL QERGKAARM SANSVLDPIL  51 RMPNLMGHEN EQARLKCSPI DADSCQLYVI SYPHLAAWA SFILSGFVAL WQQVCSRRLK  51 A ASQEDGVFVA L PYREGAAGIG RNNRWYLAVA  | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>360<br>420<br>480<br>581  |
| 50<br>55<br>60<br>65<br>70 | MEWDIGTGQA TAVYTINIAL SFQRYLGICH SPPALATHYM AVVVAAAFAI PYFTOKKFRR Seq ID NO: PTOTEIN ACI  MORPGPRLWL QREAAIQLHE MEQFNFKWPD PLKDGGFGRG SSAFTVLTFL FHIRRVMKTG COMNIQTKTL KKSRRKPASV Seq ID NO: PROTEIN ACI  MEVSRRKAPE SGSCLDQLD GLLTGWTFI ATYVLPEPE  | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG STLPPHITKT RPHELLQKLT  C341 Prote Ccession #:  11   VLQVMGSCAP FAPLVEYGGC SLDCRKLPMN GCDNPGKFHH IDPARRYPP LVFLVLYYPC VWRRVAGDEI GENTDKLEKI C342 Prote Ccession #:  11   PRPPRPAAPL CSLEHSLSRL CSRCEVRPL TASECNPAAS   | RENFKOLLLP RENFKOLLLP LLIYMYAQED RRAAWLVCVA FLLFFAALLA AYLAVRSTPG AKWORQGR LIN SEQUENCE NP_009128.1  21 LISMDMERPG I GHLRFFLCSL I NDPNYLCMEA I VEKSASCAPL I RENFILENCY I MASSLWWVIL L WEIFMVKIFW A OHPOKTHHEK PLIAYLLALAM Y ROQAGNCTEE P LLAYLLALAM Y ROQAGNCTEE G NLSRNSLRNG D HDTAIALKD  | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTTQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNINGSDEPTR CTPGVDVYWS CVYSVGYLIR YLTWFLAAGK VNALTGEVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC  31   PGRGADEPVW VSLAPPARPR TTEVVSCHPQC EGRSLATQEI  | LPLNICVITQ LVRFLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMI TPIPACRVMC GSGLEPPLER REDKRFAVVW LPAGASSIAC KWGHEAIEAN WIWTSKTLQS V  41   RESEQAIGALI RESEQAIGALI GREKLEGAVVYRA GREKLEGA   | ICTSRRALTR HGSILFLTCI QENRTVCYDL QERRGKAARM SANSVLDPIL  51 RMPNLMGHEN EQARLKCSPI LAIWAVLCFF DRDSGQLYVI SSYFHLAAWA SFILSGFVAL YWKILAAQHK WQQVCSRRLK  51 A ASQEDGVFVA L PYREGAAGLG G RNNRWYLAVA G SLHFVDAFLW   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>581  |
| 50<br>55<br>60<br>65<br>70 | MEWDINGTGQA TAVYTINIAL SFQRYIGICH SPPALATHYM AVVVAAAFAI PYFTOKKFRR Seq ID NO: Protein Acc  MQRPGPRLWL QREAAIQLHE MEQFNFKWPD PIKNGGGEGRG SSAFTVLTFL QEGILESTGCT IPAVKTILIT FHIRRWMETG CKMNQTKTL KKSRRKPASV  Seq ID NO: Protein Acc  1   MEVSRKAPE SGSCLDQLDY GLLLTGWTFL ATYVLPEPEI NGSIYFPYVI  | LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG SFLPPHITKT RPHELLQKLT  C341 Prote cession #:  11   VIQVMGSCAF PAPLVEYGCE SLDCKRLPNN GCDNPGKFHH IDPARFRYPH LVFLVLYYPE GCDNPGKFHH GENTDKLEKG DCLMAASIPH CCSSSION #:  11   RPPRPPAAPL CSSSION #:  2 REPSLSRL C SERSLPRAS C YNTYSGAAT F SAAAGEGGE  | RENFKQLLLP RENFKQLLLP RENFKQLLLP RAWLVCVA FLLFFAALLA AYLAVRSTPG AKWQRQGR in Sequence NP_009128.1  21     ISSMDMERPG I GHLRFFLCSL I VEKSACAPL I VEKSACAPL I TGVCYVGSML I TGVCYV | PVYSAVLAAG PVYSAVLAAG HWPFGDFACR VWLAVTIQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PRINGSDEPTR CTPGUDYWNS CVYSVGYLIR TLINFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC  31   PGRGADEPVW VSLAPPARFR TEVVSCHPQC EGRSLATQEI ETEVLFQGQAS FRMSEIQARF  | LPLNICVITQ LPLNICVITQ LVRFLFYANL PTAIFAATGI RQDGPABPVA AAYKGTRPFA  41   MCKDIGYNMT TPIPACRVMC GSGLPPLFM LPAGRAVMC LFAGAESIAC KWGHEAIEAN LYAGAESIAC KWGHEAIEAN WIWTSKTLQS V  41   RSEQAIGAII RSEQAIGAII RSEQAIGAII STAGVVYRAM GRIKLCEGAM L GRIKLCEGAM L KRVSWDFKT   | ICTSRRALTR HGS1LFLTCI ORNRTVCTDL OERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI DRDSQLYVI SYFHLAANA SYFILAANA SYFILAANA WQQVCSRRLK  51   ASQEDGVFVA L PYREGAAGLG G RNINRWYLAVA G SLHFVDAPLE G RRLLLSSLV A ESHCKEGDQP  | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>360<br>420<br>480<br>581  |
| 50<br>55<br>60<br>65<br>70 | MEWDIGTGQA TAVYTINIAL SFQRYLGICH SPPALATHYM AVVVAAAFAI PYFTOKKFRR Seq ID NO: PTOTEIN ACI  MORPGPRLWL QREAAIQLHE MEQFIFKMPD PLKDGGFGRG SSAFTVLTFL FHIRRVMKTG CKMINGTKLIL FHIRRVMKTG CKMINGTKLIL FHIRRVMKTG CKMINGTKLIL FHIRRVMKTG CKMINGTKAPASV  1   MEVSRKAPASV 1   MEVSRKAPE SGSCLDQLDY GLLLTGMTFI ATTYLPEPET NGSIYFPYYG ERLDVWAGVI ERVOPIASST | LGLPPTTCVY LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG SPLPPHITKT RPHELLQKLI  C341 Prote cession #:  VLQVMGSCAP FAPLVEYGG: SLDCRKLPNN GCDNPGKFHH LUPLVLYYP VMRRVAGDEI GENTDKLEKI DCLMAASIPI TISGGIYKKI C342 Prote C342 Pro | RENFKOLLLP RENFKOLLLP LLIYMYAQED RRAAWLVCVA FLLFFAALLA AYLAVRSTPG AKWORQGR  IN SEQUENCE NP_009128.1  21   ISSMDMERPG IGHLFFFLSKCY KSASCAPLE RPIFLSKCY MASSLWWVL LTGVCYVGSME LWYLIGHSVL AVEIFMVKIFW A OHPOKTHICK NP_005752.1  P LLAYLLALAW Y RDQAGNCTEE G NLSRNSLRNC D HDTAIALKD G WFSMARIAQE R RSPTTTALCI Y GTVVMNTVI  | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTTQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS ENINGSDEPTR CTPGVDVYWS CVYSVGYLIR YTVPATCVIA LLVVGITSGM YEIPAQSPTC  31   PGRGADEPVW VSLAPPARFR TTEVVSCHPQG TEVVSCHPQG TEGRSLATQEI TEVLFQQAR FRMSEIQAR FLGTGGGQU  | LPLNICVITQ LVRFLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMI TPIPACRVWC REDKRFAVW LPAGASSIAC KWGHEAIEAN PLACYLVIGS CYFYBRLNMI WIWTSKTLQS V  41   RESEQAIGALI RESEQAIGALI STAGSVYRAL GRIKLLEGAG LCGHGHPD KWLLEGAG KKVLEGENLT KVLLEGENLT  | ICTSRRALTR HGSILFLTCI QRNRTVCYDL QERRGKAARM SANSVLDPIL  51 RMPNLMGHEN EQARLKCSPI LAIWAVLCFF DRDSGQLYVI SSYFILAWA SFILSGFVAL YWKILAAQHK WQQVCSRRLK  51 A ASQEDGVFVA L PYREGAAGLG G RNNRWYLAVA G SLHFVDAPLW G SLHFVDAPLW G SLHFVDAPLW G RRLLLSSSLV A ESHCKEGDQP S NCPBVIYEIK   | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>360<br>420<br>480<br>581  |
| 50<br>55<br>60<br>65<br>70 | MEWDINGTGQA TAVYTLNLAL SPQRYLGICH SPPALATHYM AVVVAAAPAI PYFTOKKFRR Seq ID NO: Protein Act      MQRPGPRLWL QREAAIQLHE MEQFNFKWFD PLKDGGFGRG SSAPTVLTFL QBGLESTGCT IPAVKTILIL FHIRRVMKTG CKMNQTKTLI KKSRRKPASV Seq ID NO: Protein Act      MEVSRRKAPE SGSCLDQLDY GLILTGWTFL ATYVLPEPET NGSIYFPYYL EALDVWAGWU ERVQPIASST                           | LIGHPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG SFLPFHITKT RPHELLQKLT  | RENFKOLLLP RENFKOLLLP LLIYNYAQED RRAAWLVCVA FLLPFAALLA AYLAVRSTPG AKWORQGR  in Sequence NP_009128.1  21   ISSMDMERFG IGHLRFFLCSL CNDPNYLCMEA IVEKSASCAPL RENFLCSL MVRIGLFSVL AVEIFMVKIFM ADENOMINATION OF DEN FOR SETTIALCO G WESMARIAGI G WESM | PVYSAVLAAG PVYSAVLAAG HWPFGDFACR VWLAVTTQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNNGSDEPTR CTPGVJVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC 31   PGRGADEPVW VSLAPPARPR GTEVVSCHPQC GEGRSLATQEI GTEVLFQGQAS FRMSEIQARR FLGTGDGQLI CRVANCNKHKS   | LPLNICVITQ LVRELFYANL PTAIFAATGI RQDGPABPVA AAYKGTRPFA  41    MCKDIGYNMI TPIPACRVMC GSGLPPPLFF REDKRPAVW LFAGASIAC KURSTENION WINTSKTLQS V  41    RESQAIGALI RESQAIGALI RESQAIGALI RESCAIGALI RESCAIGA | ICTSRRALTR HGSILFLTCI QENRTVCYDL QERRGKAARM SANSVLDPIL  51 RMPNLMGHEN EQARLKCSPI DEPORTYCHE LATWAVLCFF CDRDSQLYVI SSYFHLAWA SFILSGFVAL WQQVCSRRLK  51 A ASQEDGVFVA L PYREGAAGLG G RNNRWILAVA G SLHFVDAFLW G RRLLLSSSLV A ESHCKEGDQP P NCPEVIYBIK P HCGWCHSLQR  | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>360<br>420<br>480<br>581  |
| 50<br>55<br>60<br>65<br>70 | MEWDIGTGQA TAVYTINIAL SFQRYLGICH SPPALATHYM AVVVAAAFAI PYFTOKKFRR Seq ID NO: PTOTEIN AC  MORPGPRLWL QREAAIQLHE MEOFIFKWFD PLKDGGPGRG SSAFTVLTFL QEGLESTGCT IPAVKTILIL FHIRRVMKTG COMNQTKTL KKSRRKPASV  Seq ID NO: PTOTEIN AC  1  MEVSRRKAPF SGSCLDQLDY GLLLTGWTFI ATTVLPEPET NGSIYFPYYKL CTFQGDCVHE SSRELCQNKS SSELCQNKS                        | LGLPPTTCVY LGLPPTTCVY LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG STPLPHITKT RPHELLQKLT  C341 Prote cession #:  11    VLQVMGSCAP FAPLVEYGG: SLDCRKLPNM GCDNPGKPHM LUPLVLYY VMRRVAGDEM LUPLVLYY VMRRVAGDEM LUPLVLYY LUPLVLY LUP | RENFKOLLLP RENFKOLLLP RENFKOLLLP LLIYMYAQGD RRAAWLVCVA FLIFFAALLA AYLAVRSTPG AKWORQGR  IN Sequence NP_009128.1  21   ISSMDMERPG I GHLRFFLCSH I VEKSASCAPL I ROPHYLCMEA I NUSKIFW I WESASCAPL I PLAYLLALAM I ROPHYLCMEA I NLSRNSLRN I HDTAIALAM I ROPHYLCMEA I NLSRNSLRN I HDTAIALAM I ROPHYLCMEA I RESPITTALCI I GTVMNRTVI I LTAGKEVRR I S SGAKKCPKI I PTRATYKDW   | PVYSAVLAAG PVYSAVLAAG HWPPGDFACR VWLAVTTQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS ENNIGSDEPTR CTPGVDVYWS CVYSVGYLIR TLTHFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC  31   PGRGADEPVW VSLAPPARPFE TEVVSCHPQG TEGRSLATQEI TEVLFQGQAE FRMSEIQARF FRMSEIQARF FRMSEIQARF FRMSEIQARF FRMSEIQARF TRINSKEKTT S VVNVMFSFGS           | LPLNICVITQ LVRFLFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41    MCKDIGYNMT TPIPACRVMC GSGLEPPLEF REDKRFAVVW LPAGASSIAC KWGHERLEAN PLACYLVIGI CYFYBRLINM WIWTSKTLQS V  41    RESQAIGALI E PESSFSKLLL S STAGVYFRA GRIKLCEGAN GELKLCEGAN GELKLCEGAN LOGHGHPD LKVILGERLT C VTMVGSFSP WINLSDRENF WINLSDRENF S WINLSDRENF  | ICTSRRALTR HGSILFLTCI QRNRTVCYDL QERRGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI DRDSQLYVI SSYPHLANN SSFILSGFVAL YWKILAAQHK WQQVCSRRLK  51   A ASQEDGVFVA A PYREGAAGLG G RNNRWILAVA E SHCHEGOQP S NCPBVIYEIK P HCGWCHSLQR K HSKCMVKNVD T NCSSLKECPA  | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>240<br>300<br>240<br>300<br>360<br>420<br>480<br>360<br>480<br>540<br>560 |
| 50<br>55<br>60<br>65<br>70 | MEWDINGTGQA TAVYTLNLAL SPQRYLGICH SPPALATHYM AVVVAAAPAI PYFTOKKFRR Seq ID NO: Protein Act      MQRPGPRLWL QREAAIQLHE MEQFNFKWPD PLKDGGFGRG SSAFTVLTFL PHIRRVMKTG CKONNQTKTL KKSRRKAPASV Seq ID NO: Protein Act      MEVSRRKAPE SGSCLDQLDY GLLLTGWTFI ATYVLPEPE NGSIYFPYYE EALDVWAGYU ERVQPIASST EETFVFYKLI CTFQGCVHE SKRELCONKS CVETGCAWCI      | LIGHPTTCVY LGLPPTTCVY LGLPPTTCVY ADLLYACSLP PLAPWHKRGG PYGMALTVIG SPLPPHITKT RPHELLQKLT  C341 Prote cession #:  VLQVMGSCAF FAPLVEYGCE SLDCRKLPNH GCDNPGKFHH LUFLVLYYPC VMRRVAGDEI GENTDKLEKI C342 Prote cession #:  11   PRPFRPAAPL C342 Prote cession #:  2 REPERSAPL C342 Prote C442 Prote C543 Prote C545 Prote | RENFKOLLLP RENFKOLLLP LLIYMYAQED RRAAWLVCVA FLLFFAALLA AYLAVRSTPG AKWORQGR  IN SEQUENCE NP_009128.1  21   ISSMDMERPG I GHLRFFLCSL I NDPNYLCMEA I VEKSASCAPL I RENFLUSL I MYRIGLFSVL I TGVCYVGSMD I GHLFFLSKOV I TGVCYVGSMD I HOTALALAI Y ROQAGNCTEI G NLSRNSLRW I HOTALALAI Y ROQAGNCTEI G NLSRNSLRW G WPSMARIAQI G WPSMARIAQI G WPSMARIAQI G WPSMARIAQI G WFSMARIAQI G TTVANTVU Y LTAGKEVRR S SGAKKCPKI I PTRATYKDV T ACDPSDYER   | PVYSAVLAAG PVYSAVLAAG HWPFGDFACR VWLAVTTQCL CYCLLACRLC VPCTVLEAFA  31   DGKCQPIEIP YAPMCTEQVS PNINGSDEPTR CTPGVDVYWS CVYSVGYLIR TLTWFLAAGK VNALTGFVLI YTVPATCVIA LLVVGITSGM YEIPAQSPTC  31   A PGRGADEPVW VSLAPPARPE G TEVVSCHPQC G EGRSLATQEI G TEVLFQQAS FRMSEIQARE FRMSEIQARE L FLGTGGGOLL RVANCNKHKS Q IIRSSKEKTT S VVNVMPSFGS N QEQCPVAVE | LPLNICVITQ LVRELFYANL PTAIFAATGI RQDGPAEPVA AAYKGTRPFA  41   MCKDIGYNMI TPIPACRVMC GSGLPPPLFF REDKRPAVW LFAGASIAC KWGHEAIEAN WWTSKTLQS V  41   RSEQAIGALI STAGVYRAC GRIKLEGAA GRIKLEGAA GRIKLEGAA GRIKLEGAA GRIKLEGAT GWYSESP E WNLSDRFNF VTWGSFSP E WNLSDRFNF C TSGGGRFKE   | ICTSRRALTR HGSILFLTCI QENRTVCTDL QERGKAARM SANSVLDPIL  51   RMPNLMGHEN EQARLKCSPI LAIWAVLCFF DRDSQLYVI SYPHLAAWA SYPHLAAWA SYHLAAWA WQQVCSRRLK  51   QUANTION OF THE CONTROL OF THE CONTRO | 120<br>180<br>240<br>300<br>328<br>60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>581   |

| 5<br>10<br>15 | MSVCLSGPLR<br>LNVVPEKIPE<br>QMGTRQKELL<br>HLILPDSEAP<br>PFAIKYFFDF<br>CLSVIAQAFM<br>EEFLTQESKK<br>EKKKCKWM<br>Seq ID NO: | LKGNINVSEY VBSEVDTELE VBSEVDTELE GIKTASTIAN KELSRKQSQQ GGFTHIFTED LTIALQTKLV ETVGEPFYLL NESADVCRNI DIDSSSVILE QDVQGKRHRG LDAQAENKKI DAFSLTEQQL HENEFNEEVA C343 Protei  | CVATYCCFLA VKIQKENDNF SSKKVRVKLG LELLESELRK MHNRDANDKN YLTSILEVLT VTTLNQKINK SVNVLDCDTI DGITKLNTIG KHKFKVKENY TDPDVVHINK GKEAPTNKLL LTEIYKYIVK  IN Sequence | PSLKSSKVRT NISKKDIEIT NILELYVEQES EIRDGFAELQ ESLTALDALI RDLMEQCSMM GPVDVITCKA GQAKEKIFQA HYEISNGSTI LTKLLSTKVA TNSLPLRFWV YAKDIPTYKE | NVTVKLRVQD LFHGENGQLN VPSTWYFLIV MDKLDVVDSF CNKSFLVTVI QPKLMLRRTE LYTLNEDWLL FLSKNGSPYG KVFKKIANFT IHSVLEKLF BILKNPQFVF EVKSYYKAIR | TYLDCGTLQY CSPENITRNQ LPVLLVIVIF GTVPFLDYKH HTLEKQKNFS SVVEKLLTNW MQVPEFSTVA LQLNEIGLEL SDVEYSDDHC SIWSLPNSRA DIKKTPHIDG DLPPLSSSEM | 780<br>840<br>900<br>960<br>1020<br>1140<br>1260<br>1320<br>1380<br>1440<br>1560<br>1568 |
|---------------|--|--|---|--|--|---|--|
| 20            |  | ession #: N  |   | •  | 41   | 51  |  |
| 25            | DPDVNTTNLE<br>IDLTTIVKPE<br>VNLSSTKLTL   | 11<br>VFSLLQVVSG<br>FEICGALVEV<br>APFDLSVIYR<br>LQRKLQPAAM<br>FSVALLVILA   | KCLNFRKLQB<br>EGANDFVVTF<br>YEIKVRSIPD  | IYFIETKKFL<br>NTSHLQKKYV<br>HYFKGFWSEW   | LIGKSNICVK<br>KVLMHDVAYR<br>SPSYYFRTPE   | SQHSLTCAPE<br>VGEKSLTCKK<br>QEKDENKWTH<br>INNSSGEMDP  | 60<br>120<br>180<br>240<br>300   |
| 30            | ESFLDCQIHR<br>FGRDSSLTCL   | VDDTOARDEV   | EGFLQDTFPQ<br>ILSSSRSLDC  | QLEESEKQRL<br>RESGKNGPHV   | GGDVOSPNCP   | SEDVVVTPES<br>TNSTLPPPPS  | 360<br>420<br>459  |
| ,             |  | C344 Protescession #: 1  | NP_002713.1   |  |  | _   |  |
| 35            | 1<br> <br>  MAAARLCLSL<br>  TRPRYGKRHK   | 11<br> <br>  LLLSTCVALL<br>  EDTLAPSEWG  | 21<br> <br>  LOPLLGAQGA<br>  SPHAAVPREL   | 31<br> <br>  PLEPVYPGDN<br>  SPLDL   | 41<br> <br>  ATPEQMAQYA  | 51<br> <br>  ADLRRYINML   | 60<br>95   |
| 40            |  | C345 Prote<br>cession #:   |   |  |  |   |  |
| 45            | VTGSAEGWGF<br>SECGALEHGA   | EEPLPYSRAF   | GEGASARPRO  | CRNGGTCVLC LQTPDRCDPI  | SFCVCPAHF. C DFLASHANG!  | 51<br>  | 60<br>120<br>180<br>223  |
| 50            |  | : C346 Prote<br>ccession #:  |   |  |  |   |  |
| 55            | 1<br> <br>  Marslvclgv<br>  Fltihrgqvv<br>  Vktdkwdfy0   | V YVFSKLKGRO   | 21<br> <br>P GVRGGPMPKI<br>G RLFWGGSVQ  | 31<br>  ADRKLCADQI<br>G DYYGDLAARI   | 41<br> <br>E CSHPISMAV<br>L GYFPSSIVR  | 51<br> <br>A LQDYMAPDCR<br>E DQTLKPGKVD   | 60<br>120<br>131   |
| 60            |  | : C347 Protectes : C347 |   | ce   |  |   |  |
| 65            | TETIKAPVK<br>TSRTKLSSI   | S TENPEKTAA  | V TKTIKPSVK<br>P YLNKDGSQK  | v tgdkslttt<br>G ihagomgen   | S SHLNKTEVI<br>D SPPAWAIVI   | 51<br> <br> P TENLENTILI<br> P QVPTGSFTLI<br> V VLVAVILLLV<br> Q IPSPR  | 60<br>120<br>180<br>235  |
| 70            |  | : C348 Prot<br>ccession #:   |   |  |  |   |  |
| 75            | TETIKAPVK<br>TSRTKLSSI   | S TENPEKTAA  | IV TKTIKPSVI<br>IP YLNKDGSQI  | (V TGDKSLTT)<br>(G IHAGQMGEN   | rs shlnktev<br>ND sppawaiv:  | 51.<br> <br>KP TENLGNTTLT<br>TH QVPTGSFTLI<br>IV VLVAVILLLV<br>GQ IPSPR   | 120  |
| 80            | Seq ID NO<br>Protein A   | ): C349 Prot<br>Accession #:   | ein Sequenc<br>FGENESH p  | ce<br>redicted   |  |   |  |
|               | 1  | 11<br>   | 21<br>  | 31<br>   | 41<br>   | 51<br> <br>1363   |  |

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MWPRLAFCCW GLALVSGWAT FQQMSPSRNF SFRLFPETAP GAPGSIPAPP APGDEAAGSR
       VERLGOAFRR RVRLLRELSE RLELVPLVDD SSSVGEVNFR SELMFVRKLL SDFPVVPTAT
                                                                                 120
       RVAIVTFSSK NYVVPRVDYI STRRARQHKC ALLLQEIPAI SYRGGGTYTK GAFQQAAQIL
       LHARENSTKV VFLITDGYSN GGDPRPIAAS LRDSGVEIFT FGIWQGNIRE LNDMASTPKE
                                                                                 240
 5
       EHCYLLHSFE EFEALARRAL HEDLPSGSFI QDDMVHCSYL CDEGKDCCDR MGSCKCGTHT
                                                                                 300
                                                                                 360
       GHFECICEKG YYGKGLOYEC TACPSGTYKP EGSPGGISSC IPCPDENHTS PPGSTSPEDC
       VCREGYRASG OTCELVHCPA LKPPENGYFI ONTCNNHFNA ACGVRCHPGF DLVGSSIILC
                                                                                 420
       LPNGLWSGSE SYCRVRTCPH LRQPKHGHIS CSTREMLYKT TCLVACDEGY RLEGSDKLTC
       QGNSQWDGPE PRCVERHCST FQMPKDVIIS PHNCGKQPAK FGTICYVSCR QGFILSGVKE
                                                                                 540
10
       MLRCTTSGKW NVGVQAAVCK DVEAPQINCP KDIEAKTLEQ QDSANVTWQI PTAKDNSGEK
                                                                                 600
       VSVHVHPAFT PPYLFPIGDV AIVYTATDLS GNQASCIFHI KVIDAEPPVI DWCRSPPPVQ
                                                                                 660
       VSEKVHAASW DEPOFSDNSG AELVITRSHT QGDLFPQGET IVQYTATDPS GNNRTCDIHI
                                                                                 720
       VIKGSPCEIP FTPVNGDFIC TPDNTGVNCT LTCLEGYDFT EGSTDKYYCA YEDGVWKPTY
                                                                                 780
       TTEWPDCAKK RFANHGFKSF EMFYKAARCD DTDLMKKFSE AFETTLGKMV PSFCSDAEDI
                                                                                 840
15
       DCRLEENLTK KYCLEYNYDY ENGFAIGPGG WGAANRLDYS YDDFLDTVQE TATSIGNAKS
SRIKRSAPLS DYKIKLIFNI TASVPLPDER NDTLEWENQQ RLLQTLETIT NKLKRTLNKD
                                                                                 900
                                                                                 960
       PMYSFQLASE ILIADSNSLE TKKASPFCRP GSVLRGRMCV NCPLGTYYNL EHFTCESCRI
                                                                                 1020
       GSYQDEEGQL ECKLCPSGMY TEYIHSRNIS DCKAQCKQGT YSYSGLETCE SCPLGTYQPK
                                                                                 1080
       FGSRSCLSCP ENTSTVKRGA VNISACGVPC PEGKFSRSGL MPCHPCPRDY YOPNAGKAPC
                                                                                 1140
20
       LACPFYGTTP FAGSRSITEC STSVLNITIF GGFGHLELLN CPSEVFHECF FNPCHNSGTC
                                                                                 1200
       QQLGRGYVCL CPLGYTGLKC ETDIDECSPL PCLNNGVCKD LVGEFICECP SGYTGQRCEE
                                                                                 1260
        NINECSSSPC LNKGICVDGV AGYRCTCVKG FVGLHCETEV NECQSNPCLN NAVCEDQVGG
                                                                                 1320
       FLCKCPPGFL GTRCGKNVDE CLSQPCKNGA TCKDGANSFR CLCAAGFTGS HCELNINECQ
                                                                                 1380
       SNPCRNQATC VDELNSYSCK CQPGFSGKRC ETEQSTGFNL DFEVSGIYGY VMLDGMLPSL
25
        HALTCTFWMK SSDDMNYGTP ISYAVDNGSD NTLLLTDYNG WVLYVNGREK ITNCPSVNDG
                                                                                 1500
       RWHHIAITWT SANGIWKVYI DGKLSDGGAG LSVGLPIPGG GALVLGQEQD KKGEGFSPAE
                                                                                 1560
       SFVGSISOLN LWDYVLSPOO VKSLATSCPE ELSKGNVLAW PDFLSGIVGK VKIDSKSIFC
                                                                                 1620
        SDCPRLGGSV PHLRTASEDL KPGSKVNLFC DPGFQLVGNP VQYCLNQGQW TQPLPHCERI
                                                                                 1680
        SCGVPPPLEN GFHSADDFYA GSTVTYQCNN GYYLLGDSRM FCTDNGSWNG VSPSCLDVDE
                                                                                 1740
30
       CAVGSDCSEH ASCLNVDGSY ICSCVPPYTG DGKNCAEPIK CKAPGNPENG HSSGEIYTVG
                                                                                 1800
        AGVTPSCQEG YQLMGVTKIT CLESGEWNHL IPYCKAVSCG KPAIPENGCI EELAFTFGSK
                                                                                 1860
        VTYRCNKGYT LAGDRESSCL ANSSWSHSPP VCEPVKCSSP ENINNGKYIL SGLTYLSTAS
                                                                                 1920
        YSCDTGYSLQ GPSIIECTAS GIWDRAPPAC HLVFCGEPPA IKDAVITGNN FTFRNTVTYT
                                                                                 1980
        CKEGYTLAGL DTIECLADGK WSRSDQQCLA VSCDEPPIVD HASPETAHRL FGDIAFYYCS
                                                                                 2040
35
        DGYSLADNSQ LLCNAQGKWV PPEGQDMPRC IAHFCEKPPS VSYSILESVS KAKFAAGSVV
                                                                                 2100
        SFKCMEGFVL NTSAKIECMR GGQWNPSPMS IQCIPVRCGE PPSIMNGYAS GSNYSFGAMV
                                                                                 2160
        AYSCNKGFYI KGEKKSTCEA TGQWSSPIPT CHPVSCGEPP KVENGFLEHT TGRIFESEVR
YOCNPGYKSV GSPVFVCQAN RHWHSESPLM CVPLDCGKPP PIQNGFMKGE NFEVGSKVQF
                                                                                 2220
                                                                                 2280
        PCNEGYELVG DSSWTCQKSG KWNKKSNPKC MPAKCPEPPL LENQLVLKEL TTEVGVVTFS
40
                                                                                 2400
        CKEGHVLQGP SVLKCLPSQQ WNDSFPVCKI VLCTPPPLIS FGVPIPSSAL HFGSTVKYSC
        VGGFFLRGNS TTLCOPDGTW SSPLPECVPV ECPOPEEIPN GIIDVQGLAY LSTALYTCKP
                                                                                 2460
        GFELVENTTT LCGENGHWLG GKPTCKAIEC LKPKEILNGK FSYTDLHYGO TVTYSCNRGF
                                                                                 2520
        RLEGPSALTC LETGDWDVDA PSCNATHCDS PQPIENGFVE GADYSYGAII IYSCFPGFQV
        AGHAMOTCEE SGWSSSIPTC MPIDCGLPPH IDFGDCTKLK DDQGYFEQED DMMEVPYVTP
                                                                                 2640
45
        HPPYHLGAVA KTWENTKESP ATHSSNFLYG TMVSYTCNPG YELLGNPVLI CQEDGTWNGS
APSCISIECD LPTAPENGPL RPTETSMGSA VOYSCKPGHI LAGSDLRLCL ENRKWSGASP
                                                                                 2700
                                                                                 2760
        RCBAISCKKP NPVMNGSIKG SNYTYLSTLY YECDPGYVLN GTERRTCODD KNWDEDEPIC
        IPVDC9SPPV SANGQVRGDE YTFQKEIEYT CNEGFLLEGA RSRVCLANGS WSGATPDCVP
                                                                                  2880
        VRCATPPOLA NGVTEGLDYG FMKEVTFHCH EGYILHGAPK LTCQSDGNWD AEIPLCKPVN
                                                                                 2940
 50
        CGPPEDLAHG FPNGFSFIHG GHIQYQCFPG YKLHGNSSRR CLSNGSWSGS SPSCLPCRCS
                                                                                  3000
        TPVIEYGTVN GTDFDCGKAA RIQCFKGFKL LGLSEITCEA DGQWSSGFPH CEHTSCGSLP
                                                                                  3060
        MIPNAFISET SSWKENVITY SCRSGYVIQG SSDLICTEKG VWSQPYPVCE PLSCGSPPSV
                                                                                  3120
        ANAVATGEAH TYESEVKLRC LEGYTMOTOT DTFTCOKDGR WFPERISCSP KKCPLPENIT
                                                                                  3180
        HILVHGDDFS VNRQVSVSCA EGYTFEGVNI SVCQLDGTWE PPFSDESCSP VSCGKPESPE
                                                                                  3240
 55
        HGFVVGSKYT PESTIIYQCE PGYELEGNRE RVCQENRQNS GGVAICKETR CETPLEPLNG
                                                                                  3300
        KADIENRITG PNVVYSCNRG YSLEGPSEAH CTENGTWSHP VPLCKPNPCP VPFVIPENAL
                                                                                  3360
        LSEKEFYVDO NVSIKCREGF LLOGHGIITC NPDETWTQTS AKCEKISCGP PAHVENAIAR
                                                                                  3420
        GVHYQYGDMI TYSCYSGYML EGFLRSVCLE NGTWTSPPIC RAVCRFPCQN GGICQRPNAC
                                                                                  3480
         SCPEGWMGRL CEEPICILPC LNGGRCVAPY QCDCPPGWTG SRCHTAVCQS PCLNGGKCVR
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 60
        PNRCHCLSSW TGHNCSR
                                                                                  3557
         Seq ID NO: C350 Protein Sequence
         Protein Accession #: FGENESH predicted
 65
        MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLCQPAPR CGDKIYNPLE
QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLKVQGV NSQCHSSPIS
                                                                                  120
                                                                                  129
 70
         Seg ID NO: C351 Protein Sequence
         Protein Accession #: AAH35671.1
                                 21
                                             31
                                                        41
                                                                    51
 75
         MVPGARGGGA LARAAGRGLL ALLLAVSAPL RLQAEELGDG CGHLVTYQDS GTMTSKNYPG
         TYPNHTVCEK TITVPKGKRL ILRLGDLDIE SQTCASDYLL FTSSSDQYGP YCGSMTVPKE
         LLLNTSEVTV RFESGSHISG RGFLLTYASS DHPDLITCLE RASHYLKTEY SKFCPAGCRD
                                                                                  180
         VAGDISONMV DGYRDTSLLC KAAIHAGIIA DELGGQISVL QRKGISRYEG ILANGVLSRD
GSLSDKRFLF TSNGCSRSLS FEPDGQIRAS SSWQSVNESG DQVHWSPGQA RLQDQGPSWA
                                                                                  240
 80
                                                                                   300
         SGDSSNNHKP REWLEIDLGE KKKITGIRTT GSTQSNFNFY VKSFVMNFKN NNSKWKTYKG
                                                                                   360
         IVNNEEKVFQ GNSNFRDPVQ NNFIPPIVAR YVRVVPQTWH QRIALKVELI GCQITQGNDS
                                                                                   420
         LVWRKTSQST SVSTKKEDET ITRPIPSEET STGINITTVA IPLVLLVVLV FAGMGIFAAF
                                                                                   480
         RKKKKKGSPY GSAEAQKTDC WKQIKYPFAR HQSAEFTISY DNEKEMTQKL DLITSDMAG
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Seg ID NO: C352 Protein Seguence
        Protein Accession #: Eos sequence
        MGFGAGORLR PVPAPRSSAE EAARPGOLRL GIRRGEABLA KLAPSGVMVP GARGGGALAR
        AAGRGLLALL LAVSAPLRLQ AEELGDGCGH LVTYQDSGTM TSKNYPGTYP NHTVCEKTIT
                                                                                            120
10
        VPKGKRLILR LGDLDIESQT CASDYLLFTS SSDQYGPYCG SMTVPKELLL NTSEVTVRFE
                                                                                            180
        SGSHISGRGF LLTYASSDHP DLITCLERAS HYLKTEYSKF CPAGCRDVAG DISGNMVDGY
                                                                                            240
        RDTSLLCKAA IHAGIIADEL GGQISVLQRK GISRYEGILA NGVLSRDGSL SDKRFLFTSN
                                                                                            300
        GCSRSLSFEP DGQIRASSSW QSVNESGDQV HWSPGQARLQ DQGPSWASGD SSNNHKPREW
                                                                                            360
        LEIDLGBEKKK ITGIRTTGST QSMFNFYVKS FVMMFKNNNS KWKTYKGIVN NEEKVFQGNS
NFRDPVQNNF IPPIVARYVR VVPQTWHQRI ALKVELIGCQ ITQGNDSLVW RKTSQSTSVS
TKKEDETITR PIPSEETSTG INITTVAIPL VLLVVLVPAG MGIFAAFRKK KKKGSPYGSA
                                                                                            420
15
                                                                                            480
                                                                                            540
        EAQKTDCNKQ IKYPFARHQS AEFTISYDNE KEMTQKLDLI TSDMAG
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        Seg ID NO: C353 Protein Sequence
20
        Protein Accession #: FGENESH predicted
        MFQRQERFLD LSSAEAVAAW ILHQHPDIIN KGDGCGHLVT YQDSGTMTSK NYPGTYPNHT
        VCEKTITVPK GKRLILRLGD LDIESQTCAS DYLLFTSSSD QYGMQKEEET EVLCLSVAGA
QRVDIPVQLL PSFLEGWKGH ADARGPYCGS MTVPKELLLN TSEVTVRFES GSHISGRGFL
25
                                                                                            120
                                                                                            180
         LTYASSDHPD LITCLERASH YLKTEYSKFC PAGCRDVAGD ISGNMVDGYR DTSLLCKAAI
                                                                                            240
        HAGIIADELG GQISVLQRKG ISRYEGILAN GVLSRDGSLS DKRFLFTSNG CSRSLSFEPD
                                                                                            300
         GQIRASSSWQ SYNESGDQVH WSPGQARLQD QGPSWASGDS SNNHKPREWL EIDLGEKKKI
TGIRTTGSTQ SNPNFYVKSF VMNPKNNNSK WKTYKGIVNN EEKVPQGNSN FRDPVQNNFI
                                                                                            360
30
         PPIVARYVRV VPQTWHQRIA LKVELIGCQI TQGNDSLVWR KTSQSTSVST KKEDETITRP
                                                                                            480
         IPSEETSTDA MPVQIVGDHT QMISQRENLG PDEGKIPFKG TAESMVRVVF AVVVNDLGML
                                                                                            540
         PLAHTPEEDI DHYCWKQIKY PFARHQSAEF TISYDNEKEM TQKLDLITSD MADYQQPLMI
GTGTVTRKGS TFRPMDTDAE EAGVSTDAGG HYDCPQRAGR HEYALPLAPP EPEYATPIVE
                                                                                            600
35
         RHVLRAHTFS AQSGYRVPGP QPGHKHSLSS GGFSPVAGVG AQDGDYQRPH SAQPADRGYD
                                                                                            720
         RPKAVSALAT ESGHPDSQKP PTHPGTSDSY SAPRDCLTPL NQTAMTALL
                                                                                            769
         Seq ID NO: C354 Protein Sequence
         Protein Accession #: NP_004607.1
40
                                                  31
         MAGVSACIKY SMFTFNFLFW LCGILILALA IWVRVSNDSQ AIFGSEDVGS SSYVAVDILI
                                                                                             60
         AVGAIIMILG PLGCCGAIKE SRCMLLLFFI GLLLILLLQV ATGILGAVFK SKSDRIVNET
                                                                                             120
45
         LYENTKLLSA TGESEKQFQE ALIVFQEEPK CCGLVNGAAD WGNNFQHYPE LCACLDKQRP
                                                                                             180
         CQSYNGKQVY KETCISFIKD FLAKNLIIVI GISFGLAVIB ILGLVFSMVL YCQIGNK
          Seq ID NO: C355 Protein Sequence
          Protein Accession #: NP_004608.1
 50
          MCTGGCARCL GGTLIPLAFF GFLANILLFF PGGKVIDDND HLSQBIWFFG GILGSGVLMI
          FPALVFLGLK NNDCCGCCGN EGCGKRFAMF TSTIFAVVGF LGAGYSFIIS AISINKGPKC
                                                                                             120
 55
          LMANSTWGYP PHDGDYLNDE ALWNKCREPL NVVPWNLTLF SILLVVGGIQ MVLCAIQVVN
                                                                                             180
          GLLGTLCGDC QCCGCCGGDG PV
          Seq ID NO: C356 Protein Sequence
          Protein Accession #: NP_002372.1
 60
          MPRPAPARRI PGLLLLIMPI LLLPSAAPDP VARPGFRRLE TRGPGGSPGR RPSPAAPDGA
PASGTSEPGR ARGAGVCKSR PLDLVFIIDS SRSVRPLEFT KVKTFVSRII DTLDIGPADT
                                                                                             60
 65
          RVAVVNYAST VKIEFQLQAY TDKQSLKQAV GRITPLSTGT MSGLAIQTAM DEAFTVEAGA
                                                                                              180
          REPSSNIPKV AIIVTDGRPQ DQVNEVAARA QASGIELYAV GVDRADMASL KMMASEPLEE
HVFYVETYGV IEKLSSRFQE TFCALDPCVL GTHQCQHVCI SDGEGKHHCE CSQGYTLNAD
KKTCSALDRC ALNTHGCEHI CVNDRSGSYH CECYEGYTLN EDRKTCSAQD KCALGTHGCQ
                                                                                              240
                                                                                              300
                                                                                              360
          HICVNDRTGS HHCECYEGYT INADKKTCSV RDKCALGSHG CQHICVSDGA ASYHCDCYPG
                                                                                              420
  70
          YTLNEDKKTC SATEEARRLV STEDACGCEA TLAFQDKVSS YLQRLNTKLD DILEKLKINE
                                                                                              480
                                                                                              486
          YGOIHR
          Seq ID NO: C357 Protein Sequence
          Protein Accession #: NP_057723.1
  75
          MARGSLRRLL RILVIGIWLA LLRSVAGEOA PGTAPCSRGS SWSADLDKCM DCASCRARPH
SDFCLGCAAA PPAPPRLLWP ILGGALSLTF VLGLLSGPLV WRRCRRREKF TTPIEBTGGE
                                                                                              120
  80
          GCPAVALIO
          Seq ID NO: C358 Protein Sequence
          Protein Accession #: NP_001810.1
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| 5<br>10<br>15 | 1   MQPTLLLSLL   LKTSRKDVKD   LKTSRKDVKD   SEEKHLEE   EEAGSQENHP   SEEKGHPQEE   RYRGRGSEEY   GRGQEPRAYF   GKWQQQGDLQ   MMNDNPLEGE   YDRVAQLDQL   AMDLELQKIA | GAVGLAAVNS KETTENENTK RERADEPQWS PGETQNAFLN QESKGQPRSQ SEESNVSMAS RAPRPQSEES MSDTREEKRP DTKENREEAR EENELTLNEK LHYRKKSAEF | MPVDNRNHNE FEVRLLRDPA FEVRLLRDPA LYPSDSQVSE ERKQASAIKK EESEEGEEDA LGEKRDHHST MDEEDKRNYP LGEGHRVQE FQDKQVSSHH NFFPEYNYDW | GMVTRCIIEV DASEAHESSS EVRTRHSEKS EELVARSETH TSEVDKRRTR HYRASEEPE SLELDKMAHG NOMDKARRHP TAEKRRLGE WEKKPFSEDV | LSNALSKSSA<br>RGEAGAPGEE<br>QREDEEEEG<br>AAGHSQEXTH<br>PRHHHGRSRP<br>YGEEIKGYPG<br>YGEESEEERG<br>QGAWKELDRN<br>LFNPYYDPLQ<br>NWGYEKRNLA | DIQGPTKADT ENYQKGERGE SREKSSQESG DRSSQGGSLP VQAPEDLEWE LEPGKGRHHR YLNYGEEGAP WKSSHFERRD RVPKLDLKRQ | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>677 |
|---------------|---|--|---|---|---|--|---|
| 13            | Seq ID NO:<br>Protein Acc   |  |   |   |   |  |   |
| 20            | <br>MKLLCEGLKQ  | 11<br> <br>PNCVLQTLRW<br>KLQKLNLQFS  | 21<br> <br>YRCLISSASC<br>LSVTAAKLPV   | 31<br> <br>GALAAVLSTS<br>GMVGNCSGFS   | 41<br> <br>QWLTELEFSE<br>GSLVQSHFGY   | 51<br> <br>TKLEASALKL<br>CQDSSFKCDL  | 60<br>120   |
| 25            | NYGSFRDLVD<br>QVTIPDGFVN<br>EAVKGTLDGQ<br>DVNNPPDFLG<br>LEGRDIVPVK  | LEVKAEPSLR<br>VTVGSNVTLI<br>QAELQIYFSQ<br>QNQGILNVSV<br>ENFNPTTGIL   | SPLSEGLNWA<br>KGGMDLQRPT<br>CIYTTTVASR<br>GGQAVAIGQF<br>LVKPSKPLCS<br>VIGNLTNFEQ  | LQVVLLCKIF<br>EQLSIQWSFF<br>KDRITGSNDP<br>VQGRPETGHT<br>GYYQCTAINR  | SLKLFLFIAL<br>HKKEMEPISS<br>GNASITISHM<br>ISLSCLSALG<br>LGNSSCEIDL  | PNSPGQVSVV<br>PWEEGKWPDV<br>QPADSGIYIC<br>TPSPVYYWHK<br>TSSHPEVGII                                 | 180<br>240<br>300<br>360<br>420<br>480  |
| 30            | TQLEVTLPSS  | IHETGPDTIQ   | ARNKAKAKAK<br>EPDYEPKPTQ<br>LSEDEKGVVK  | <b>EPAPEPAPGS</b>   |   |  | 540<br>600<br>631   |
| 35            | Protein Acc   |  | GENESH pred   |   | 41  | 51   |   |
| 40            | PPHKKEMEPI<br>DPGNASITIS<br>HTISLSCLSA<br>NRLGNSSCEI<br>ELEPMTKINP  | SSPWEEGKWP<br>HMQPADSGIY<br>LGTPSPVYYW<br>DLTSSHPEVG<br>RGESEAMPRE   | DVEAVKGTLD<br>ICDVNNPPDF<br>HKLEGRDIVP<br>IIVGALIGSL<br>DATQLEVTLP  | GQQAELQIYF<br>LGQNQGILNV<br>VKENFNPTTG<br>VGAAIIISVV<br>SSIHETGPDT  | SQGGQAVAIG<br>SVLVKPSKPL<br>ILVIGNLTNF<br>CPARNKAKAK<br>IQEPDYEPKP  | SREQLSIQWS QFKDRITGSN CSVQGRPETG EQGYYQCTAI AKERNSKTIA TQEPAPEPAP                                  | 60<br>120<br>180<br>240<br>300<br>360   |
| 45            | Seq ID NO:  | C361 Prote   | QSELEPEPEP<br>in Sequence<br>NP_003011.1  |   | EPLSEDERGV  | VKA  | 413   |
| 50            | PAHQAMNLVG<br>PVGKTDDGCL  | PQSIEGGAHE<br>ENTPDTAEFS   | GLOHLGPFGN  | IPNIVAELTC<br>DPEHDYPGLC  | DNIPKOPSEC  | 51<br> <br>  LGIARPRVEY<br>  QGYPDPPNPC<br>  MKGGERRKRR  | 60<br>120<br>180<br>211   |
| 55            |   |  | in Sequence<br>NP_076926.2  |   |   |  |   |
| 60            | MGITMMCMAS<br>SSVLAASGII  | NTYGSNPISV<br>INTFSLAFYS   | YIGYTIWGSV  | MFIISGSLS1<br>NSNNCHGTMS  | AAGIRTTKGI<br>ILMGLDGMVI  | 51<br> <br>V QILTALMSLS<br>L VRGSLGMNIT<br>L LLSVLEFCIA  | 60<br>120<br>180<br>220   |
| 65            | Seq ID NO:  | : C363 Prote   | in Sequence   |   |   |  |   |
| 70            | VSERGSLKQQ  |  | ARNLLGLIE   |   |   | 51<br> <br>M GKKSTGESSS<br>S WDSEDSSNFK  | 60<br>120<br>148  |
| 75            |   |  | ein Sequence<br>NP_036393.:   |   |   |  |   |
| 80            | EFAAKFIVP<br>FVKESHNMS:<br>ECQAQQTIS  | Y DVWASNYVD<br>K GPEATWRLS<br>L ASSDPQKTV  | L ITEQADIAL'<br>K VQFVYDSSE   | r RGAEVKGRC<br>K THFKDAVSA<br>P FDIISDFVF   | G HSQSELQVF<br>G KHTANSHHL<br>S EEHKCPVDE   | 51<br> <br>V RENGTTCLMA<br>W VDRAYALKML<br>S ALVTPAGKSY<br>R EQLEETLPLI                            | 60<br>120<br>180<br>240<br>280  |

|    |  | C365 Protei<br>ession #: N   |  |  |  |  |  |
|----|--|--|--|--|--|--|--|
| 5  | 1<br> <br>MLGLVLALLS<br>WCFKPLTRKT                                 | SSSAEEYVGL   | 21<br> <br>SANQCAVPAK  | 1  | 41<br> <br>TPKECNNRGC  | 51<br> <br>CFDSRIPGVP  | 60<br>74                                     |
| 10 |  | C366 Protei<br>ession #: N   |  |  |  |  |  |
| 15 |  | 11<br> <br>VPGPSGSLCA<br>AGPQCSKVEV  |  | <br>PGPLASAGPV   |  |  | 60<br>114                                    |
| 20 |  | C367 Protei<br>cession #: N  |  |  |  |  |  |
|    | 1<br> <br>   | 11<br> <br>  GAAILLAASL  | 21<br> <br> -  | BESKEDSI'IG  | 41<br> <br> -<br> -  | 51<br> <br> -<br>  KGVTVETVES  | 60   |
| 25 | VDEFSASVLT<br>DLLSVIWPPL<br>MGHSRKKANI<br>NYFLSLAIGV<br>TPSNLLLVVH | GKLTTVFLPI<br>KIAYHIHANN<br>AIGISLAIWL<br>FLFPAFLTAS<br>YPLIKSQGQS<br>QVSLTSKKHS | VYTIVFVVGL<br>WIYGEALCNV<br>LILLVTIPLY<br>AYVLMIRMLR<br>HVYALYIVAL | PSNGMALWVF<br>LIGFFYGNMY<br>VVKQTIFIPA<br>SSAMDENSEK<br>CLSTLNSCID | LFRTKKKHPA<br>CSILFMTCLS<br>LNITTCHDVL<br>KRKRAIKLIV             | VIYMANLALA<br>VQRYWVIVNP<br>PEQLLVGDMP<br>TVLAMYLICF   | 120<br>180<br>240<br>300<br>360<br>397       |
| 30 | Seq ID NO:   | C368 Protes  | in Seguence  |  |  |  |  |
| 35 | YIENLRQQAH   | KEESSPDYNP   | YQGVSVPLQQ   | KENGDESHLP   | ERDSLSEEDW   | 51<br> <br>PSPEMIRALE<br>MRIILEALRQ<br>EENSRDNPFK  | 60<br>120<br>180                             |
| 40 | RTNEIVEEQY<br>YEDVVGGEDW<br>DQLSDDVSKV<br>PPEDLIEMLK               | TPQSLATLES NPVEEKIESQ IAYLKRLVNA TGEKPNGSVE                                      | VFQELGKLTG<br>TQEEVRDSKE<br>AGSGRLQNGQ<br>PERELDLPVD               | PNNQKRERMD<br>NIGKNEQIND<br>NGERATRLFE<br>LDDISEADLD               | EEQKLYTDDE<br>EMKRSGQLGI<br>KPLDSQSIYQ<br>HPDLFQNRML             | DDIYKANNIA<br>QEEDLRKESK<br>LIEISRNLQI   | 240<br>300<br>360<br>420<br>480              |
| 45 | AAWIPHVENR   | QMAYENLNDK<br>LNQGSSQETD   | DOELGEYLAR   | MLVKYPEIIN   | SNOVKRVPGO   | GSSEDDLQEE<br>MKVLEYLNQE   | 540<br>600<br>617                            |
| 50 | Protein Ac   | C369 Prote<br>cession #:   | NP_112217.1  |  |  |  |  |
| 55 | DASGHFLSYO<br>KRYGNLSHVI<br>KHPLVEGGYI<br>SISKERWVET<br>LEEEEQGLKI | C LHYPITSSRE<br>C MMASSAPLCH<br>I PHIVYRRQKV<br>C LVVADTKMIE<br>I VHHAEKTLSS     | KRDLDGSEDW<br>LSGTVLQQGT<br>PETKEPTCGI<br>YHGSENVESY<br>FCKWQKSINI | VYYRISHEEK RVGTAALSAC KDSVNISQKQ ILTIMNMVTG KSDLNPVHHD             | DLFFNLTVNC<br>HGLTGFFQLI<br>ELWREKWERI<br>LFHNPSIGN<br>VAVLLTRKD | 51<br> <br>  EYHVVGPVRV<br>  GFLSNSYIME<br>  HGDFFIEPVK<br>  NLPSRSLSRR<br>  HIVVVRLIL<br>  CAGFNRPCBT | 60<br>120<br>180<br>240<br>300<br>360        |
| 60 | RQLQYDPTPI<br>QYGPNATFCX<br>IPGGWGRWSI<br>PTFRQMQCSI               | L TWSKCSEEYI  O EVENVOOTLW  P WSHCSRTCGA  E PDTVPYKNEI                           | TRFLDRGWGI CSVKGFCRSI GVQSAERLCI YHWFPIFNPI                        | CLDDIPKKKG LDAAADGTQC NPEPKFGGKY HPCELYCRPI                        | LKSKVIAPGY<br>GEKKWCMAGI<br>CTGERKRYRI<br>DGQFSEKMLI             | PVGRHPYIMS IYDVHHQCQL CITVGKKPES CNVHPCRSEA AVIDGTPCFE KEGSGYVDIG                                      | 420<br>480<br>540<br>600<br>660<br>720       |
| 65 | LIPKGARDII . EKLMATGPTI TGIRRQTAH GEKKRTVLC                        | R VMEIEGAGNI<br>N ESVWIQLLFO<br>C IKKGRGMVKA<br>I QTMVSDEQAA                     | F LAIRSEDPEI<br>O VTNPGIKYET<br>A TFCDPETQPI<br>L PPTDCQHLLI       | K YYLNGGFIIC<br>Y TIQKDGLDNI<br>N GRQKKCHEKA<br>K PKTLLSCNRI       | O VEQMYFWQYO<br>CPPRWWAGET<br>O ILCPSDWTVO                       | T VFQYDRKGDL<br>G HWTECSVTCG<br>W BACSATCGPH<br>G NWSECSVSCG<br>S NGKNPPTLKP                           | 780<br>840<br>900<br>960<br>1020             |
| 70 | VPPPTSRPRI<br>I STGSTSQP<br>PPYNTLTKG<br>PDLSRESWW                 | M LTTPTGPESI<br>I LTSQSLSIQI<br>P EMBIHSGSGI<br>P PFSTVMEGLI                     | M STSTPAISS<br>P SEENVSSSD<br>E EREQPEDKD<br>L PSQRPTTSE           | P SPTTASKEGI<br>I GPTSEGGLV/<br>E SNPVIWTKI<br>I GTPRVEGMV         | D LGGKQWQDS:<br>A TTTSGSGLS<br>R VPGNDAPVE<br>I EKPANTLLP        | S TQPELSSRYL<br>S SRNPITWPVT<br>S TEMPLAPPLT<br>L GGDHQPEPSG   | 1080<br>1140<br>1200<br>1260                 |
| 75 | WSECSTTCG<br>GGFKIREIQ<br>GVQERGVFC<br>EGNKTEDQD                   | L GAYWKRVEC<br>C VDSRDHRNL<br>P GGLCDWTKR<br>Q CLCDHKPRP                         | T TQMDSDCAA<br>R PFHCQFLAG<br>P TSTMSCNEH<br>P EFKKCNQQA           | I QRPDPAKRCI<br>I PPPLSMSCNI<br>L CCHWATGNWI<br>C KKSADLLCTI       | H LRPCAGWKV<br>P EPCEAWQVE<br>D LCSTSCGGG                        | G HGSAHWIVGN G NWSKCSRNCS P WSQCSRSCGG F QKRIVQCVPS T LKAMKKCSVP                                       | 1320<br>1380<br>1440<br>1500<br>1560<br>1593 |
| 80 | Seq ID NO  | : C370 Prot<br>ccession #:   | ein Sequenc  | e  |  |  | 1393   |
|    | 1  | 11   | 21   | 31   | 41   | 51   |  |

|     | 1  | 1                        | 1                        | 1                         | 1                            | i                             |                  |
|-----|--|--------------------------|--------------------------|---------------------------|------------------------------|-------------------------------|------------------|
|     | MRQSHQLPLV (<br>LKLVGIQIQT  <br>KLENKFQAEI | LMQKMIQQIK               | YNVKSRLSDV               | SSGELALIIL                | ALGVCRNAEE                   | NLIYDYHLTD                    | 60<br>120<br>180 |
| 5   | SQFSVDTGAM .<br>TFSTGEAMQA                 | AVLALTCVKK               | SLINGQIKAD               | egslknisiy                | TKSLVEKILS                   | EKKENGLIGN                    | 240<br>300       |
|     | DINKDSSCVS .                               | ASGNFNISAD               | EPITVTPPDS               | QSYISVNYSV                | RINETYFTNV                   | TVLNGSVPLS                    | 360<br>420       |
| 10  | RNGENLEVRW                                 |                          | SWGPITICIQ               | GLCANNNDRI                | IMEDUSGGEF                   | naganaa 1 v v                 | 433              |
| 10  | Seq ID NO:<br>Protein Acc                  |                          |                          |                           |                              |                               |                  |
| 15  | 1  | 11                       | 21                       | 31                        | 41                           | 51                            |                  |
| 15  | MCCTKSLLLA<br>NAIIFHTKKK                   |                          |                          |                           | LHPKFIVGFT                   | RQLANEGCDI                    | 60<br>96         |
| 20  | Seq ID NO:<br>Protein Acc                  |                          |                          |                           |                              |                               |                  |
|     | 1  | 11<br>                   | 21<br> -                 | 31<br>                    | 41<br>                       | 51                            |                  |
| 25  | MAGSPLLWGP                                 | RAGGVGLLVL               | LLLGLFRPPP               | ALCARPVKEP                | RGLSAASPPL                   | AETGAPRRFR<br>RVWGAPRNSD      | 60<br>120        |
| 23  | PALGLDDDDPD                                | APAAQLARAL               | LRARLDPAAL               | AAQLVPAPVP                | AAALRPRPPV                   | YDDGPAGPDA                    | 180              |
|     | EEAGDETPDV<br>RVKRLETPAP                   |                          | RILAGSADSE               | GVAAPRRLRR                | AADHDVGSEL                   | PPEGVLGALL                    | 240<br>260       |
| 30  |  | C373 Protes              |                          |                           |                              |                               |                  |
|     | Protein Acc                                | cession #: 1             | _                        |                           |                              |                               | •                |
| 0.5 | 1  | 11                       | 21                       | 31<br>                    | 41                           | 51<br>                        |                  |
| 35  | MLQSLAGSSC<br>RRFLEEHECL                   | VRLVERHRSA<br>SEOOLEOFLG | WCFGFLVLGY<br>RVLEASNYGV | LLYLVFGAVV                | PSSVELPYED<br>NWDFTSALFP     | LLRQELRKLK<br>ASTVLSTTGY      | 60<br>120        |
|     | GHTVPLSDGG                                 | KAFCIIYSVI               | GIPFTLLFLT               | AVVQRITVHV                | TRRPVLYFHI                   | RWGFSKQVVA<br>YVPGEGYNQK      | 180<br>240       |
| 40  | FRELYKIGIT                                 | CYLLLGLIAM               | LVVLETFCEL               | HELKKPRKMF                | AAKKDKDEDÖ                   | VHITEHDQLS                    | 300<br>336       |
| 40  |  | MKEDQKQNEP               |                          |                           |                              |                               | 330              |
|     |  | C374 Prote<br>cession #: |                          |                           |                              |                               |                  |
| 45  | 1  | 11                       | 21                       | 31                        | 41                           | 51                            |                  |
|     |  |                          |                          |                           |                              | PGRDDNSYMY                    | 60<br>103        |
| 50  |  | TVGSLILGYT               |                          |                           | SHI                          |                               | 203              |
| 30  | Protein Ac                                 | C375 Protecession #:     | NP_005236.1              | •                         | 41                           | 51                            |                  |
|     | 1  | 11<br>                   | 21<br>                   | 31<br>                    | 41                           |                               |                  |
| 55  | MGRHLALLLI<br>VYITHPAWEV                   | LLLLFQHFGE<br>RYKIVSGDSE | SDGSQRLEQ1               | C PLOFTHLEYN<br>GDFCFLRIR | V VTVQENSAAI<br>C KGGNTAILNI | R EVKDHYTLIV                  | · 60<br>120      |
|     | KALEKNTNVE                                 | : ARTKVRVQVI             | . DTNDLRPLFS             | PTSYSVSLP                 | e ntairtsia                  | R VSATDADIGT<br>K LYGSSGISSM  | 180<br>240       |
| 60  | AKLTVHIEQA                                 | NECAPVITAV               | TLSPSELDRI               | PAYAIVTVD                 | CDQGANGDI                    | A SLSIVAGDLL                  | 300<br>360       |
| 60  | KAGPVKFEKI                                 | VYRAEISEFA               | PPNTPVVMVI               | C AIPAYSHLR               | Y VFKRTPGKA                  | V KVIHVTSPQF<br>K FSLNYNTGLI  | 420              |
|     | SILEPVKRQ(                                 | AAHFELEVT                | SDRKASTKVI<br>SIANLNHVP  | VKVLGANSN: AIDHFTGAV:     | P PEFTQTAYK<br>S TSENLDYEL   | A AFDENVPIGT<br>M PRVYTLRIRA  | 480<br>540       |
| 65  | SOWGLPYRRE                                 | VEVLATITLE               | NLNDNTPLF                | KINCEGTIP                 | R DLGVGEQIT                  | T VSAIDADELQ<br>G ENPATPLYIN  | 600<br>660       |
| 03  | ITVAASHKLV                                 | / NLOCEETGV              | KMLAEKLLQ                | A NKLHNQGEV               | E DIFFDSHSV                  | N AHIPQFRSTL                  | 720              |
|     | DRETTDKYTI                                 | NITVYDLGI                | P QKAAWRLLH              | VVVDANDNP                 | P EFLQESYFV                  | E TGMLKILSPL<br>E VSEDKEVHSE  | 780<br>840       |
| 70  | IIQVEATDKI                                 | LGPNGHVTY                | S ILTDTDTFS              | I DSVTGVVNI               | a rpldrelqh                  | E HSLKIEARDQ<br>E AHDPDLGQSG  | 900<br>960       |
| , 0 | OVRYSLLDHO                                 | G EGNFDVDKL              | S GAVRIVOOL              | D FEKKQVYNL               | T VRAKDKGKP                  | V SLSSTCYVEV                  | 1020<br>1080     |
|     | VFKIGRETG                                  | V IETSDRLDR              | E STSHYWLTV              | F ATDQGVVPL               | S SPIBIYIEV                  | R YSIRDGSGVG<br>E DVNDNAPQTS  | 1140             |
| 75  | RKLDREOOD                                  | E HILEVIVID              | N GSPPKSTIA              | R VIVKILDEN               | D NKPQFLQKE                  | H PKTGLITTTS<br>Y KIRLPEREKP  | 1200<br>1260     |
|     | DRERNARRE                                  | P LYRVIATOK              | D EGPNAEISY              | S IEDGNEHGK               | F FIEPKTGVV                  | S SKRFSAAGEY<br>S DPVAHMIGVI  | 1320<br>1380     |
|     | SVEPPGIPL                                  | W FDITGGNYD              | S HFDVDKGTG              | T IIVAKPLDA               | E QKSNYNLTV                  | E ATDGTTTILT                  | 1440             |
| 80  | Gr. 100 VV.10                              | A TOSILVTSEK             | I. DHEAVSPAH             | I TVMVRDODV               | P VKRNFARI                   | I YTLQSSRDPL<br>V NVSDTNDHAP  | 1500<br>1560     |
|     | WFTASSYKG                                  | R VYESAAVGS              | V VLQVTALDK              | D KGKNAEVLY               | S IESGNIGNI                  | G NSFMIDPVLG<br>CF TSKEYSVELS | 1620<br>1680     |
|     | ETVSIGSFV                                  | G MVTAHSQSS              | V VYEIKDGNI              | G DAFDINPHS               | G TIITQKALL                  | OF ETLPIYTLII                 | 1740             |
|     | QGTNMAGLS                                  | T WILATARHTO             | P ENDNAPAL               | W WEITGHISH               | TO MOTING A A P.             | TD RNVPLVIRAA                 | 1300             |

|     | DADKDSNALL                | VYHIVEPSVH    | TYFAIDSSTG        | AIHTVLSLDY   | EETSIFHFTV ( | QVHDMGTPRL        | 1860 |
|-----|---------------------------|---------------|-------------------|--|--------------|-------------------|------|
|     | FAEYAANVTV                | HVIDINDCPP    | VFAKPLYEAS        | LLLPTYKGVK   | VITVNATDAD   | SSAFSQLIYS        | 1920 |
|     | ITEGNIGEKF                | SMDYKTGALT    | VQNTTQLRSR        | YELTVRASDG   | RFAGLTSVKI   | NVKESKESHL        | 1980 |
|     | KFTODVYSAV                | VKENSTEAET    | LAVITAIGSP        | INEPLEYHIL   | NPDRRPKISR ' | <b>TSGVLSTTGT</b> | 2040 |
| 5   | PFDREOOEAF                | DVVVEVIEEH    | KPSAVAHVVV        | KVIVEDQNDN   | APVFVNLPYY   | avvkvdtevg        | 2100 |
| _   | HVIRYVTAVD                | RDSGRNGEVH    | YYLKEHHEHF        | OIGPLGEISL   | KKQFELDTLN : | KEYLVTVVAK        | 2160 |
|     | DEGNEARSAE                | VIVPITVMNK    | AMPVEEKPEY        | SAEIAESIOV   | HSPVVHVQAN   | SPEGLKVFYS        | 2220 |
|     | TTDCDDESOF                | TINENTOVIN    | VIADIDERAH        | PAYKLSIRAT   | DSLTGAHAEV   | PVDIIVDDIN        | 2280 |
|     | TIDGDEFAGE                | TIMENTOWAN    | TOTOTOTO          | THENCEDNING  | ISYOMFGNHS   | KCHDHEHVDC        | 2340 |
| 10  |                           |               |                   |  | VDVTDLNGNP   |                   | 2400 |
| IO  | STGLISLLRT                | LDYEQSKORT    | IF V KAVDGGM      | PIDSSDVIVI   | WITDOM ST.   | m on must         | 2460 |
|     | RISEHAPHGH                | FVTCVKAYDA    | DSSDIDKLQY        | SILSGNORKH   | PVIDSATGII   | TUSNURANAD        |      |
|     | KPFYSLNLSV                | SDGVFRSSTQ    | VHVTVIGGNL        | HSPAFLQNEY   | BVELAENAPL   | HTLVMEVKIT        | 2520 |
|     | DGDSGIYGHV                | TYHIVNDFAK    | DRFYINERGQ        | IFTLEKLDRE   | TPAEKVISVR   | LMAKDAGGKV        | 2580 |
|     | AFCTVNVILT                | DDNDNAPQFR    | ATKYEVNIGS        | SAAKGTSVVK   | SASDADEGSN   | ADITYAIEAD        | 2640 |
| 15  | SESVKENLEI                | NKLSGVITTK    | ESLIGLENEF        | FTFFVRAVDN   | GSPSKESVVL   | VYVKILPPEM        | 2700 |
|     | OLPKFSEPFY                | TFTVSEDVPV    | <b>GTEIDLIRAE</b> | <b>HSGTVLYSLV</b>  | KGNTPESNRD   | ESFVIDRQSG        | 2760 |
|     | RLKLEKSLDH                | ETTKWYQFSI    | LARCTQDDHE        | MVASVDVSIQ   | VKDANDNSPV   | Fesspyeafi        | 2820 |
|     | VENLPGGSRV                | IQIRASDADS    | <b>GTNGQVMYSL</b> | DQSQSVEVIE   | SFAINMETGW   | ITTLKELDHE        | 2880 |
|     | KRDNYOIKVV                | ASDHGEKIOL    | SSTAIVDVTV        | TDVNDSPPRF   | TAEIYKGTVS   | EDDPQGGVIA        | 2940 |
| 20  | TLSTTDADSE                | EINROVTYFI    | TGGDPLGOFA        | VETIONEWKV   | YVKKPLDREK   | RDNYLLTITA        | 3000 |
|     | TOCTPOON                  | MEAKAT DAND   | NCDVCEKTI.Y       | SDTIPEDVIP   | GKLIMQISAT   | DADIRSNAEI        | 3060 |
|     | TVTLLCCAF                 | KEKLWEDIKE    | LKTSTPLDRE        | EOBANAHITAN  | ATDGGGRFCQ   | ASIVVTLEDV        | 3120 |
|     | TITINGSGAE                | DANTAGENA     | PROTEITEUR        | ATDADAGIND   | KILYSLIDSA   | DGOFSINELS        | 3180 |
|     | OTTO TWO I                | PERMITTE      | TAMPOUTED         | DITATCTUTU   | SVLDINDNPP   | VEEVREYGAT        | 3240 |
| 25  | GIIQUEKPLD                | KELVAVIIDS    | TUNNETUNO         | KRIMICAL   | SIDSKTGAVF   | TIENTDYESS        | 3300 |
| 23  | VSEDILVGTE                | VLQVYAASKD    | 1EANAEIIIS        | 113GNENGKP   | DIDOVIGUAL   | ILEOCALIAN        | 3360 |
|     | HEYYLTVEAT                | DGGTPSLSDV    | ATVNVNVTDI        | NUNTPVFSQD   | TYTTVISEDA   | ATECOACINGED      | 3420 |
|     | ADDADGPSNS                | HIRYSIIDGN    | QGSSFTIDPV        | RGEVKVTKLL   | DRETISGYTL   | TVQASDNGSP        |      |
|     | PRVNTTTVNI                | DVSDVNDNAP    | VFSRGNYSVI        | IQENKPVGFS   | VLQLVVTDED   | SSHNGPPPPP        | 3480 |
| 20  | TIVTGNDEKA                | PEANDOGATP    | TSSAIKRKEK        | DHYLLQVKVA   | DNGKPQLSSL   | TAIDIKAIRR        | 3540 |
| 30  | SIYPPAILPL                | EIFITSSGEE    | YSGGVIGKIH        | ATDQDVYDTL   | TYSLDPQMDN   | LPSVSSTGGK        | 3600 |
|     | LIAHKKLDIG                | OATTMASALD    | GKFTTVADIT        | VHIRQVTQEM   | LNHTIAIRFA   | NLTPEEFVGD        | 3660 |
|     | YWRNFQRALR                | NILGVRRNDI    | QIVSLQSSEP        | HPHLDVLLFV   | EKPGSAQIST   | Kollhkinss        | 3720 |
|     | VTDIEELIGV                | RILNVFQKLC    | AGLDCPWKFC        | DEKVSVDESV   | MSTHSTARLS   | FVTPRHHRAA        | 3780 |
|     | VCLCKEGRCP                | PVHHGCEDDP    | CPEGSECVSD        | PWEEKHTCVC   | PEGREGOCEG   | SSSMTLTGNS        | 3840 |
| 35  | YVKYRLTENE                | NKLEMKLTMR    | LRTYSTHAVV        | MYARGTDYSI   | LEIHHGRLQY   | KFDCGSGPGI        | 3900 |
|     | VSVOSTOVND                | GOWHAVALEV    | NGNYARLVLD        | OVHTASGTAP   | GTLKTLNLDN   | YVFFGGHIRQ        | 3960 |
|     | OCTRHCRSPO                | VGNGFRGCMD    | SIYLNGOELP        | LNSKPRSYAH   | IBESVDVSPG   | CPLTATEDCA        | 4020 |
|     | CALDUCARGA                | NDSDAGGVVC    | KCSALVIGTH        | CEISVNPCSS   | NPCLYGGTCV   | VDNGGFVCOC        | 4080 |
|     | PCI.VIYZOPCO              | LSDVCKDEDC    | KNGGTCFDSL        | DGAVCOCDSG   | FRGERCQSD1   | DECSGNPCLH        | 4140 |
| 40  | CAT CEMBERCO              | MONICOREA     | CDUCEDAADN        | OVVSTPWNTO   | LAEGIGIVVF   | VAGIFLLVVV        | 4200 |
| 70  | GALCENINGS                | INCNCORDIA    | WILL COMMEN       | OLAGIENTE  | KNIYSDIPPQ   | UDUDDIGVTD        | 4260 |
|     | FVLCRMISK                 | MANAGERAL S   | RAIGPAIAFE        | DEGMCRDEN  | UNICOUNDAIL. | DDDDDDGMGDG       | 4320 |
|     | SIPSDSRNNL                | DRNSFEGSAL    | PERPERSTEN        | PESVAGRANA   | VAVCSVAPNL   | CONCORROON        | 4380 |
|     | DSDSIQKPSW                | DFDYDTKVVL    | POLCTREKEL        | EERPSQPYSA   | RESLSEVQSL   | SSFQSESCUU        |      |
| A.C | ngyhwdtsdw                | MPSVPLPDIC    | EFPNYEVIDE        | QTPLYSADPA   | AIDTDYYPGG   | IDIESUPPP         | 4440 |
| 45  | PEDFPAADEI                | , pplppepsn(  | ) FESIHPPRDM      | PAAGSLGSSS   | RNRQRFNLNQ   | APDNEASTON        | 4500 |
|     | SEPQTKGTGE                | NSTCREPHAI    | YPPGYQRHFE        | S APAVESMPMS   | VYASTASCSD   | VSACCEVESE        | 4560 |
|     | VMMSDYESGI                | DGHFEEVTI     | PLDSQQHTEV        | 7  |              |                   | 4590 |
|     |                           |               |                   |  |              |                   |      |
|     | Seq ID NO:                | : C376 Prote  | in Sequence       | •  |              |                   |      |
| 50  | Protein Ad                | cession #:    | NP_055035.1       | L  |              |                   |      |
|     |                           |               | _                 |  |              |                   |      |
|     | 1                         | 11            | 21                | 31   | 41           | 51                |      |
|     | ī                         | ī             | ī                 | Ĭ  | 1            | 1                 |      |
|     | MCACACVOCA                | r cueractara  | . CTAANTLLVI      | PONGETKYASI  | R NHLSRFVWFF | SGIVGGGLLM        | 60   |
| 55  | **CIGRCARC                | r guantecto   | CIMMITED          | T.CCUT.AAT.T   | C TAGSGYCVIV | AALGLAEGPL        | 120  |
| 33  | CL DOL COLD               |               | J DENOGRACIO      | r cornitremi   | CT.PSTLLAL   | GIEFILCLIQ        | 180  |
|     | CITIZINGOMU               | TEASTEGQI     | L LDISINSEC.      | I DEMITARMIA   | v Sursznama. | Oldi Inchig       | 202  |
|     | VINGVLGGI                 | C GECCSHOOO.  | Y DC              |  |              |                   | 202  |
|     |                           |               |                   |  |              |                   |      |
| 60  |                           |               | ein Sequenc       |  |              |                   |      |
| 60  | Protein A                 | ccession #:   | NP_003750.        | 1  |              |                   |      |
|     |                           |               |                   |  |              |                   |      |
|     | 1                         | 11            | 21                | 31   | 41           | 51                |      |
|     |                           |               | 1                 |  |              |                   |      |
|     | MSTENVEGK                 | P SNLGERGRA   | R SSTFLRVVQ       | P MFNHSIFTS  | a vspaaeriri | 7 ILGEEDDSPA      | 60   |
| 65  | PPOLFTELD                 | E LLAVDGOEM   | E WKETARWIK       | P EEKVEQGGE  | R WSKPHVATL  | LHSLFELRTC        | 120  |
|     | MEKGSIMLD                 | R EASSLPQLV   | E MIVDHQIET       | G LLKPBLKDK  | V TYTLLRKHRI | 1 QTKKSNLRSL      | 180  |
|     | ADIGKTVSS                 | A SRMFTNPDN   | G SPAMTHRNL       | T SSSLNDISD  | K PEKDQLKNKI | MKKLPRDAEA        | 240  |
|     | SNVLVGEVD                 | F LDTPPIAFV   | R LOOAVMLGA       | L TEVPVPTRF  | L FILLGPKGK  | A KSYHEIGRAI      | 300  |
|     | ATIMSDEVE                 | H DIAYKAKDE   | H DLIAGIDEF       | L DEVIVLPPG  | E WDPAIRIEP  | P KSLPSSDKRK      | 360  |
| 70  | NMYSCGENU                 | O MNGDTPHTC   | G HGGGGHGDC       | E BLORTGREC  | G GLIKDIKRK  | a pffasdfyda      | 420  |
|     | TATTONTENT                | I. PIVI.AMM   | A TTEGGIA         | A TONMOGUT.E   | S FLOTAVSGA  | I PCLFAGQPLT      | 480  |
|     | TI-GOMODIA<br>THITÄUTIONT | TELEMENTAL IN | K LINDOLATE       | B IMIGINGAR  | L CLILVATDA  | S PLVQYFTRFT      |      |
|     | THOUSEN TO                | A LEVENTINES  | M TRIANVUNT       | N SNEKOGAMA  | L PSCTCVPPD  | P ANISISNDTT      | 600  |
|     | EEGFSSLIS                 | E TETIDALKE   | THE TANADITY      | TO DESCRIPTION OF THE PROPERTY | N NONETONIO  | , MSETT.DIATV     | 660  |
| 75  | LAPEYLPTM                 | S STUMYHNTI   | r DWAFLSKKE       | ~ DVIGONDAG  | N TANDONDO   | L MSFILFLGTY      | 720  |
| 13  | TSSMALKKE                 | K TSPYFPTTA   | K KLISDYAII       | T PINTONIA   | W TAGADIEUD  | I VPSEFKPTSP      | 780  |
|     | NRGWPVPPF                 | G ENPWWVCL    | A ALPALLVTI       | TEMPOOTTA  | A TANKYRUKT  | K KGAGYHLDLF      | 750  |
|     | WVAILMVIC                 | S LMALPWYVA   | A TVISIAHID       | S LKMETETSA  | TE GEOFKETGA | R EQRVTGTLVF      | 840  |
|     | ILTGLSVFM                 | A PILKFIPME   | V LYGVFLYMO       | V ASLNGVQFN  | ID KPKTFTWbr | K HQPDFIYLRH      | 900  |
| 00  | VPLRRVHLE                 | T FLOVLCLAI   | L WILKSTVA        | I IFPVMILAI  | O AVRKGMDYL  | P SQHDLSFLDD      | 960  |
| 80  | VIPEKDKK                  | CK EDEKKKKKI  | CK GSLDSDNDI      | S DCPYSEKVI  | S IKIPMDIME  | Q QPFLSDSKPS      | 1020 |
|     | DRERSPTFI                 |               |                   |  |              |                   | 1035 |
|     |                           |               |                   |  |              |                   |      |
|     |                           |               | ai- comione       |  |              |                   |      |

| 5    | MSTPGVNSSA<br>LAVTDLLGTL<br>INHAYFYSHY<br>HAAYSYMYAG<br>HPAASPALPR<br>SLEREVSKNP<br>OHCSDSORTS | SLSPDRLNSP<br>LVSPVTIATY<br>VDKRLAGLTL<br>FSSFLILATV<br>LSDFRRRSF<br>DLQAIRIASV<br>SAMSGHSRSF | MKGQWPGGQP<br>FAVYASNVLF<br>LCNVLVCGAL<br>RRIAGAEIQM<br>NPILDPWIYI<br>ISRELKEISS | 31   GVVGNLVAIV LCEYSTFILL CALPNMGLGS LRMHRQFMRR VILLIATSLV LLRKTVLSKA TSQTLLPDLS VLLVDEAGGS | VLCKSRKEQK<br>FFSLSGLSII<br>SRLQYPDTWC<br>TSLGTEQHHA<br>VLICSIPLVV<br>IEKIKCLFCR<br>LPDLSENGLG | CAMSVERYLA FIDWTTNVTA AAAASVASRG RVFVNQLYQP IGGSRRERSG GRNLLPGVPG                       | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>488 |
|------|--|---|--|--|--|---|--|
| 15   |  | C379 Protei<br>cession #: N   |  |  |  |   |  |
| 20   | ELVEKSCTHS<br>GSSDMSCERG<br>FHNNDTFHFL<br>MNQCLVATGT   | EKTNRTLSYR<br>RHQSLQCRSP<br>KCCNTTKCNE<br>HEPKNQSYMV  | TGLKITSLTE<br>EEQCLDVVTH<br>GPILELENLP   | 31<br> <br>NGDCRVEECA<br>VVCGLDLCNQ<br>WIQEGEEGRP<br>QNGRQCYSCK:<br>HAHLGDAFSM<br>TLLWT      | GNSGRAVTYS<br>KDDRHLRGCG<br>GNSTHGCSSE   | RSRYLECISC<br>YLPGCPGSNG<br>ETFLIDCRGP  | 60<br>120<br>180<br>240<br>300<br>335                      |
| . 25 | Seq ID NO:   | C380 Prote  | in Sequence  |  |  |   |  |
| 30   | MACSIGNITI   | QNLKDPVQIK  | IKHTRTQEVH   | LVRRAQFTFF<br>HPICAFWDLN   | KNKSFGGWNT   | SGCVAHRDSD  | 60<br>120<br>180   |
| 35   | EKLRRDYPSK<br>LEAIHMYIAL<br>DEFCWIQDPV<br>VVSLTFLLGM   | ILMNLSTALL VKVFNTYIRR IFYVTCAGYF TWGFAFFAWG   | FLNLLFLLDG<br>YILKFCIIGW<br>GVMFFLNIAM<br>PLNIPFMYLF                             | NTKVLTPISY<br>WITSFNVDGL<br>GLPALVVSVV<br>FIVVMVQICG<br>SIFNSLQGLP<br>SLSSSSIGSN             | CIAVAVLLHF<br>LASRNNNEVY<br>RNGKRSNRTL<br>IFIFHCAMKE   | FLLATFTWMG<br>GKESYGKEKG<br>REEVLRNLRS<br>NVQKQWRRHL                                    | 240<br>300<br>360<br>420<br>480                            |
| 40   | HTDNVSYEHS<br>Seq ID NO:   | FNKSGSLRQC  | FHGQVLVKTG<br>in Sequence<br>NP 000565.1   | PC .   |  |   | 512  |
| 45   | 1<br> <br>  MTVARPSVPA<br>  ITYKCEESFV   | 11<br> <br>  ALPLIGELPR   | 21<br> <br>  LLLLVLLCLE  | 31<br>AVWGDCGLPE   | PTRLNSASLE   | 51<br> <br>  GRTSFPEDTV<br>  QPYITQNYFP   | 60<br>120<br>180   |
| 50   | LFGATISFSC<br>DHYGYRQSVI<br>TVNVPTTEVS   | : NTGYKLFGST<br>T YACNKGPTMI  | SSFCLISGSS<br>GEHSIYCTVI<br>TTPNAQATRS   | VQWSDPLPEC NDEGEWSGPI  | REIYCPAPPO<br>PECRGKSLTS   | : NGQIDVPGGI<br>: IDNGIIQGER<br>: KVPPTVQKPT<br>: TTSGTTRLLS                            | 240<br>300<br>360<br>381                                   |
| 55   |  | ccession #:   | in Sequence<br>Eos sequene   | ce   | 0.   |   |  |
| 60   | PSNLSVFTS:<br>LQNNQLRHVI   | Y LDLSMNNIS( P TEALQNLRS)   | LLPNPLPSLI<br>LQSLRLDANH<br>TPDVAFGNI  | R PLEELRLAGI<br>I SYVPPSCFS:<br>S SLVVLHLHNI   | N ALTYIPKGA<br>3 LHSLRHLWL<br>N RIHSLGKKC  | 51<br>  DCSDLGLSEL<br>F TGLYSLKVLM<br>D DNALTEIPVQ<br>F DGLHSLETLD<br>G ASQITEPPDL      | 60<br>120<br>180<br>240                                    |
| 65   | TGTANLESL'<br>EIYEIKVDT<br>LTHLKLTGN<br>DLHKKDAGM  | T LTGAQISSL<br>F QQLLSLRSL<br>H ALQSLISSE<br>F QAQDERDLE                                      | P QTVCNQLPN<br>N FPELKVIEM<br>D FLLDFEEDL  | L QVLDLSYNL:<br>H PNAFSTLPS:<br>P YAYQCCAFG<br>K ALHSVQCSP                                   | L EDLPSFSVC<br>L IKLDLSSNL<br>V CENAYKISN<br>S PGPFKPCEH                                       | C KLQKIDLREN L SSFPITGLHG C WNKGDNSSMD L LDGWLIRIGV A GVDAPTFGSF                        | 360<br>420<br>480<br>540<br>600                            |
| 70   | ARHGAWWEN ILLCALLAL TKLYCNLDK LLVVVPLPA  | G VGCHVIGFL<br>T MAAVPLLGG<br>G DLENIWDCS<br>C LNPLLYILF                                      | S IFASESSVF<br>S KYGASPLCL<br>M VKHIALLLF<br>N PHFKEDLVS                         | L LTLAALERG<br>P LPFGEPSTM<br>T NCILNCPVA  | F SVKYSAKFE<br>G YMVALILLN<br>F LSFSSLINL<br>S KHPSLMSIN                                       | T KAPFSSLKVI<br>S LCFLMMTIAY<br>T FISPEVIKFI<br>S DDVEKQSCDS                            | 660<br>720<br>780<br>840<br>883                            |
| 75   |  |   | ein Sequenc<br>NP_003658.  |  |  |   |  |
| 80   | PSNLSVFTS<br>LQNNQLRHV<br>AFRSLSALQ  | TY LDLSMNNIS TO TEALQNLRS A MTLALNKIH   | Q LLPNPLPSI<br>L QSLRLDANI<br>H IPDYAFGNI  | r fleelrlag<br>II syvppscps<br>S slvvlhlhn   | R ALTYIPKGA<br>G LHSLRHLWI<br>IN RIHSLGKKO   | 51<br> <br>V DCSDLGLSEL<br>F TGLYSLKVLM<br>D DNALTEIPVQ<br>F DGLHSLETLD<br>D NPIQFVGRSA | 60<br>120<br>180<br>240<br>300                             |

| 5  | FOHLPELRTL TYNLLEDLPSF S LPSLIKLDLS S AFGVCENAYK C CSPSPGPFKP C AVMILTOVS A ERGFSVKYSA I STMGYMVALI I PVAFLSFSSL S WTRSKHPSLM S VAFVPCL | EVCQKLQKID 1<br>ENLLSSPPIT (<br>ISNQWNKGDN :<br>CEHLLDGWLI  <br>AVLAGVDAFT :<br>KPETKAPPSS :<br>LLNSLCFLMM ! | LRHNEIYEIK  3LHGLTHLKL SSMDDLHKKD RIGVWTIAVL FGSFARHGAW LKVIILLCAL TIAYTKLYCN IKFILLVVVP       | VDTFQQLLSL TGNHALQSLI AGMFQAQDER ALTCNALVTS WENGVGCHVI LALTMAAVPL LDKGDLENIW LPACLNPLLY    | RSLNLAWNKI SSENFPELKV DLEDFLLDFE TVFRSPLYIS GFLSIFASES LGGSKYGASP LCGSMVKHIAL ILFNPHFKED   | AITHPNAPST IEMPYAYQCC BDLKALHSVQ PIKLLIGVIA SVPLLTLAAL LCLPLPFGBP LLFTNCILNC LVSLRKQTYV  | 360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900 |
|----|---|--|--|--|--|--|--|
| 15 | Seq ID NO: (  |  |  |  |  |  |  |
| 13 | 1<br> <br> <br>  MEMFTFLLTC   | Ī  | 21   | 31<br> <br> -  | 41<br> <br>  | 51<br> <br>  OSTANVEMEN  | 60   |
| 20 | FLPLANLECS<br>LECDRLQYCD<br>CAPPCPNMYP<br>YSIVSLMYFI<br>VILTITWFLA  | PNIETFLCKA<br>ETVPVTFDPH<br>KSDELEFAKS<br>GFLLGDSTAC   | FVPTCIEQIH<br>TEFLGPQKKT<br>FIGTVSIFCL<br>NKADEKLELG   | VVPPCRKLCE<br>EQVQRDIGFW<br>CATLFTFLTF<br>DTVVLGSQNK                                       | KVYSDCKKLI<br>CPRHLKTSGG<br>LIDVRRFRYP<br>ACTVLFMLLY                                       | DTFGIRWPEE<br>QGYKPLGIDQ<br>ERPIIYYSVC<br>FFTMAGTVWW                                     | 120<br>180<br>240<br>300<br>360                                    |
| 25 | LYDLDASRYF<br>SGLYLVPLVT<br>LMTLIVGISA<br>KKHYKPSSHK<br>KADGASTPRL  | VLLPLCLCVF<br>LLGCYVYEQV<br>VFWVGSKKTC<br>LKVISKSMGT<br>REODCGEPAS   | VGLSLLLAGI<br>NRITWEITWV<br>TEWAGFFKRN<br>STGATANHGT<br>PAASISRLSG                             | ISLNHVRQVI<br>SDHCRQYHIP<br>RKRDPISESR<br>SAVAITSHDY<br>BQVDGKGQAG                         | QHDGRNQEKL<br>CPYQAKAKAR<br>RVLQESCEFF<br>LGQETLTEIQ<br>SVSESARSEG                         | PELALFMIKY<br>LKHNSKVKHK<br>TSPETSMREV   | 420<br>480<br>540<br>600<br>660                                    |
| 30 | TGLAQSNNLQ Seq ID NO:   | VPSSSEPSSL   | KGSTSLLVHP   | VSGVRKEQGG   | GCHSDT .   |  | 706  |
|    | 1   | 11   | 21   | 31   | 41   | 51   |  |
| 35 | PSKSNESHDH<br>DEPTDLEATE  | MDDMDDEDDD   | DHVDSQDSID   | SNDSDDVDDT   | DDSHQSDESH<br>RRPDIQYPDA   | KONLLAPOTL<br>HSDESDELVT<br>TDEDITSHME   | 60<br>120<br>180   |
| 40 | SEELNGAYKA<br>NEHSDVIDSQ  | IPVAQDLNAP<br>ELSKVSREFH   | SDWDSRGKDS   | LVVDPKSKEE   | DKHLKFRISH   | Lykrkandes<br>Eldsassevn   | 240<br>300   |
|    |   | C386 Prote<br>cession #:   |  | ,  |  |  |  |
| 45 | 1   | 11   | 21<br>   | 31<br>1  | 41   | 51<br>   |  |
| 50 | VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGPP VRLPTHGRVY SOLEEGKPGY  | PVQDTERRPA<br>LKHPASEAEI<br>GPEHSGLYSC<br>QPPPSLQWLF<br>IILEATLHLA<br>QKGHELVLAN<br>LDCLTOATPK               | QGSSLSFAAV<br>QPQTQVTLRC<br>CAHSAFGQAC<br>EDETPITNRS<br>EIEDMPLFEI<br>IAESDAGVYT<br>PTVVWYRNOM | DRLQDSGTF(<br>HIDGHPRPT)<br>SSQNFTLSII<br>RPPHLRRAT<br>RVFTAGSEE<br>CHAANLAGQ<br>LISEDSRFE | O CVARDDVTGE Y QWFRDGTPLS A DESFARVVLI V FANGSLLLTY R VTCLPPKGLI R RQDVNITVAT V FKNGTLRINS | LRCEVEAPGP BARSANASFN DEQSNHTVSS PODVVVARYE VRPRNAGIYR PEPSVWWEHAG VPSWLKKPQD VEVYDGTWYR | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480                |
| 55 | CMSSTPAGSI<br>GSSLPENVTD<br>TTVYQGHTAL<br>BYTCLAGNSO  | EAQARVQVLE NAGTLHFARV LQCEAQGDPF NIKHTRAPI   | KLKFTPPPQI TRDDAGNYT( PLIQWKGKDI VVDKPVPEE   | P QQCMEFDKE:<br>IASNGPQGQ<br>R ILDPTKLGP:<br>E EGPGSPPPY                                   | A TVPCSATGRI<br>I RAHVQLTVA'<br>R MHIFQNGSL'<br>K MIQTIGLSV                                | F KPTIKWERAD FITFKVEPER HIDVAPEDSG AAVAYIIAVL  | 540<br>600<br>660<br>720<br>780                                    |
| 60 | KRHSTSDKME<br>LDFRRELEME<br>PLSTKQKVAI<br>YHFROAWVPI  | FPRSSLQPIT GKLNHANVVI CTQVALGMEI RWMSPEAILI  | t tigksefget<br>R Ligicreae<br>H LSNNRFVHK<br>E GDFSTKSDV                                      | V FLAKAQGLE<br>P HYMVLEYVD<br>D LAARNCLVS<br>W APGVLMWEV                                   | E GVABTLVLVI<br>L GDLKQFLRI:<br>A QRQVKVSAL<br>F THGEMPHGG                                 | r SLGSGPAATN<br>K SLQTKDEQQQ<br>S KSKDEKLKSQ<br>G LSKDVYNSEY<br>Q ADDEVLADLQ             | 840<br>900<br>960<br>1020  |
| 65 | AGKARLPOPE<br>. Seq ID NO:  | GCPSKLYRLI   | M QRCWALSPR<br>ein Sequenc   | D RPSFSEIAS<br>e :   | a LGDSTVDSK  | P  | 1070   |
| 70 | ALFILYYTA<br>RDQKILNPS  | Q GEPFPNNLD<br>A LSLHSKLNA   | K LCGPNVTDF<br>T ADILRGLLS   | P PFHANGTER  | CA KLVELYRIV   | 51<br> <br>S QLAQLNGSAN<br>V YLGTSLGNIT<br>P DTSGKDVFQK                                  | 60<br>120<br>180   |
| 75 | Seq ID NO   | K YKQIIAVLA<br>: C388 Prot<br>ccession #:  | ein Sequenc  | e  |  |  | 202  |
| 80 | LYSLKILML<br>ALTEIPVRA  | Q NNQLGGIPA<br>L NNLPALOAM   | E ALWELPSLO<br>T LALNRISH  | S LRLDANLIS P DYAFONLTS  | SL VPERSFEGI<br>SL VVLHLHNNI   | 51<br> <br> L SHIPGQAFSG<br>LS SLRHLWLDDN<br>RI QHLGTHSFEG<br>PL LQTIHFYDNP              | 120<br>180   |

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IQFVGRSAFQ YLPKLHTLSL NGAMDIQEFP DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP
                                                                                  300
        RLRVLELSHN QIEELPSLHR CQKLEEIGLQ HNRIWEIGAD TFSQLSSLQA LDLSWNAIRS
                                                                                  360
       IHPEAFSTLH SLVKLDLTDN QLTTLPLAGL GGLMHLKLKG NLALSQAFSK DSFPKLRILE
                                                                                  420
       VPYAYQCCPY GMCASFFKAS GQWEAEDLHL DDEESSKRPL GLLARQAENH YDQDLDELQL
       EMEDSKPHPS VQCSPTPGPF KPCEYLFESW GIRLAVWAIV-LLSVLCNGLV LLTVFAGGPV
                                                                                  540
        PLPPVKFVVG AIAGANTLTG ISCGLLASVD ALTFGQFSEY GARWETGLGC RATGFLAVLG
                                                                                  600
        SEASVLLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG
                                                                                  660
        ASPLCLPYAP PEGQPAALGF TVALVMMNSF CPLVVAGAYI KLYCDLPRGD FEAVWDCAMV
                                                                                  720
        RHVAWLIFAD GLLYCPVAFL SFASMLGLFP VTPEAVKSVL LVVLPLPACL NPLLYLLFNP
                                                                                  780
10
        HFRDDLRRLR PRAGDSGPLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE
                                                                                  840
        TYGFPSVTLI SCQQPGAPRL EGSHCVEPEG NHFGNPQPSM DGELLLRAEG STPAGGGLSG
                                                                                  900
        GGGFQPSGLA FASHV
                                                                                  915
        Seg ID NO: C389 Protein Seguence
15
        Protein Accession #: NP_570901
        MASLVSLELG LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLINT LADRVHCTNG
                                                                                  60
20
        PCGKCLSVED ALGLGEPEGS GLPPGPVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA
                                                                                  120
        SHADHLLALL ESPKALTPGL SWLLQRMQAR AAGQTPKTAC VDIPQLLEEA VGAGAPGSAG
        GVLAALLDHV RSGSCFHALP SPQYFVDFVF QQHSSEVPMT LAELSALMQR LGVGREAHSD
                                                                                  240
        HSHRHRGASS RDPVPLISSS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP EAWAQLSPAL
                                                                                  300
        LQQQLSGACT SQSRPPVQDQ LSQSERYLYG SLATLLICLC AVFGLLLLTC TGCRGVAHYI
                                                                                  360
25
        LOTFLSLAVG ALTGDAVLHL TPKVLGLHTH SEEGLSPOPT WRLLAMLAGL YAPFLFENLF
                                                                                  420
        NLLLPROPED LEDGPCGHSS HSHGGHSHGV SLQLAPSELR QPKPPHEGSR ADLVAEESPE
                                                                                  480
                                                                                  540
        LINPEPRRLS PELRLIPYMI TLGDAVHNFA DGLAVGAAFA SSWKTGLATS LAVFCHELPH
        ELGDFAALLH AGLSVRQALL LNLASALTAF AGLYVALAVG VSEESEAWIL AVATGLFLYV
        ALCOMLPANL KVRDPRPWLL FLIHNVGLLG GWTVLLLLSL YEDDITF
                                                                                   648
30
        Seq ID NO: C390 Protein Sequence
        Protein Accession #: NP_061844
                                                         41
                                                                    51
35
        MANASEPGGS GGGEAAALGL KLATLSLLLC VSLAGNVLPA LLIVRERSLH RAPYYLLLDL
        CLADGLRALA CLPAVMLAAR RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLGVGVTR
                                                                                   120
        YLAIAHHRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL DGGGDDEDAP CALEQRPDGA PGALGFLLLL AVVVGATHLV YLRLLFFIHD RRKMRPARLV PAVSHDWTFH GPGATGQAAA
                                                                                   180
                                                                                   240
 40
        NWTAGFGRGP TPPALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LLFLLLWGPY
                                                                                   300
        VVASYLRVLV RPGAVPQAYL TASVWLTFAQ AGINPVVCFL FNRELRDCFR AQFPCCQSPR
                                                                                   360
                                                                                   375
        Sea ID NO: C391 Protein Sequence
 45
        Protein Accession #: NP_005622
                    11
                                 21
                                             31
                                                         41
                                                                     51
         MAAARPARGP ELPLIGLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP
 50
                                                                                   120
         LSHCGRAAPC EPLRYNVCLG SVLPYGATST LLAGDSDSQE EAHGKLVLWS GLRNAPRCWA
         VIOPLICAVY MPKCENDRVE LPSRTLCQAT RGPCAIVERE RGWPDFLRCT PDRFPEGCTN
                                                                                   180
         EVQNIKFNSS GQCEVPLVRT DNPKSWYEDV EGCGIQCQNP LFTEAEHQDM HSYIAAFGAV
                                                                                   240
         TGLCTLFTLA TFVADWRNSN RYPAVILFYV NACFFVGSIG WLAQFMDGAR REIVCRADGT
                                                                                   300
         MRLGEPTSNE TLSCVIIPVI VYYALMAGVV WFVVLTYAMH TSFKALGTTY QPLSGKTSYF
HLLTWSLPPV LTVAILAVAQ VDGDSVSGIC FVGYKNYRYR AGFVLAPIGL VLIVGGYFLI
                                                                                   360
 55
         RGVMTLFSIK SNHPGLLSEK AASKINETML RLGIFGFLAF GFVLITFSCH FYDFFNQAEW
                                                                                   480
         ERSFRDYVLC QANVTIGLPT KQPIPDCEIK NRPSLLVEKI NLFAMFGTGI AMSTWVWTKA
                                                                                   540
         TLLIWRRIWC RLIGOSDDEP KRIKKSKMIA KAPSKRHELL ONPGQELSPS MHTVSHDGPV
                                                                                    600
         AGLAFDLNEP SADVSSAWAQ HVTKMVARRG AILPQDISVT PVATPVPPEE QANLWLVEAE
                                                                                    660
 60
         ISPELOKRLG RKKKRRKRKK EVCPLAPPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG
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         AGDSCROGAW TLVSNPFCPE PSPPQDPFLP SAPAPVAWAH GRRQGLGPIH SRTNLMDTEL
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         MDADSDF
         Seq ID NO: C392 Protein Sequence
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         Protein Accession #: BAC04382
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         MGARSGARGA LLLALLLCWD PRLSQAGRKR SGEVLPDSFP SAPAEPLPYF LQEPQDAYIV
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         KNKPVELRCR AFPATOIYFK CNGEWVSOND HVTQEGLDEA TLGARGGLRV REVQIEVSRQ
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         QVEELFGLED YWCQCVAWSS AGTTKSRRAY VRIAYLRKNY DQEPLGKEVP LDHEVLLQCR
                                                                                    180
         PPEGYPVAEV EWLKNEDVID PTODTNPLLT IDHNIIRQA RISDTANYTC VARNIVAKRR
STTATVIVYV NGGWSSWAEW SPCSNRCGRG WOKRTRTCTN PAPLNGGAFC EGQAFOKTAC
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         TTICPVDGAW TEWSKWSACS TECAHWRSRE CMAPPPONGG RDCSGTLLDS KNCTDGLCMQ
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         NKKTLSDPNS HLLEASGDAA LYAGLVVAIF VVVAILMAVG VVVYRRNCRD FDTDITDSSA
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         ALTGGFHPVN FKTARPSNPQ LLHPSVPPDL TASAGIYRGP VYALQDSTDK IPMTNSPLLD
PLPSLKVEVY SSSTTGSGPG LADGADLLGV LPPGTYPSDF ARDTHFLHLR SASLGSQQLL
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                                                                                    600
         GLPRDPGSSV SGTFGCLGGR LSIPGTGVSL LVPNGAIPQG KFYEMYLLIN KAESTLPLSE
         GTOTYLSPSV TCGPTGLLLC RPVILTMPHC AEVSARDWIF QLKTQAHQGH WEEVVTLDEE
TLMTPCYCQL EPRACHILLD QLGTYVFTGE SYSRSAVKRL QLAVFAPALC TSLEYSLRVY
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  80
                                                                                    720
         CLEDTPVALK EVLELERTLG GYLVEEPKPL MFKDSYHNLR LSLHDLPHAH WRSKLLAKYQ
                                                                                    780
         EIPFYHIWSG SQKALHCTFT LERHSLASTE LTCKLCVRQV EGEGQIFQLH TTLABTPAGS
                                                                                    840
          LDTLCSAPGS TVTTQLGPYA FKIPLSIRQK ICNSLDAPNS RGNDWRMLAQ KLSMDRYLNY
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          FATKASPTGV ILDLWEALQQ DDGDLNSLAS ALEEMGKSEM LVAVATDGDC
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Seq ID NO: C393 Protein Sequence Protein Accession #: NP\_004616

| 5           | 1   | 11 :   | 21   | 31   | 41   | 51  |                                       |
|-------------|---|--|--|--|--|---|---------------------------------------|
| 10          | MNRKARRCLG VIGEGSQMGL AACTQGNLSD NLHNNEAGRK VRASRNKRPT ASGCDLMCCG | DECQFQFRNG  <br>CGCDKEKQGQ  <br>ILEENMKLEC  <br>PLKIKKPLSY         | RWNCSALGER<br>YHRDEGWKWG<br>KCHGVSGSCT<br>RKPMDTDLVY               | TVFGKELKVG<br>GCSADIRYGI<br>TKTCWTTLPQ<br>IEKSPNYCEE               | SREAAFTYAI<br>GFAKVFVDAR<br>FRELGYVLKD<br>DPVTGSVGTQ         | IAAGVAHAIT<br>EIKQNARTLM<br>KYNEAVHVEP  | 60<br>120<br>180<br>240<br>300<br>349 |
| 15          | Seq ID NO:<br>Protein Acc   |  |  |  |  |   |                                       |
|             | 1   | 11 .   | 21<br>   | 31<br>1  | 41   | 51<br>  |                                       |
| 20          | MDALCGSGEL<br>RGYIILSHLS<br>LLIQYERLQG<br>VLSALILACF              | KLKMVLGVLL<br>VOSSGVLIIF   | WCVSWADLFY<br>WFLCVVCAIV<br>NVDPNPYPET                             | SFHGLVHGRA<br>PFRSKILLAK<br>SAGFLSRLFF                             | PAPVFFVTPL<br>AEGEISDPFR<br>WWFTKMAIYG                       | VVGVTMLLAT<br>FTTFYIHFAL<br>YRHPLEEKDL  | 60<br>120<br>180<br>240<br>300        |
| 25          | KALLATEGSS  | PLISACPKLI<br>YHYIFVTGVK   | ODLLSFINPO   | LLSILIRFIS   | NPMAPSWWGP   | LVAGLMFLCS  | 360<br>420                            |
| <i>23</i> . | MDLAPFLNLL<br>MKLKDSRIKL<br>CSPFLVTLIT                            | WSAPLQIILA<br>MSEILNGIKV<br>LWVYVYVDPN                             | IYFLWQNLGP<br>LKLYAWEPSF<br>NVLDAEKAFV                             | SVLAGVAFMV<br>LKQVEGIRQG<br>SVSLFNILRL                             | LLIPLNGAVA<br>ELQLLRTAAY<br>PLNMLPQLIS                       | VKMRAFQVKQ<br>LHTTTTFTWM<br>NLTQASVSLK  | 480<br>540<br>600                     |
| 30          | GPVGCGKSSL<br>QQTLEACALL<br>VDSHVAKHIF                            | VSALLGEMEK<br>ADLEMLPGGD<br>DHVIGPEGVL                             | LEGKVHMKGS<br>QTEIGEKGIN<br>AGKTRVLVTH                             | VAYVPQQAWI<br>LSGGQRQRVS<br>GISFLPQTDF                             | QNCTLQENVL<br>LARAVYSDAD<br>IIVLADGQVS                       | VPKGALVAVV<br>FGKALNPKRY<br>IFLLDDPLSA<br>EMGPYPALLQ<br>DNDPVTYVVQ                | 660<br>720<br>780<br>840<br>900       |
| 35          | KQFMRQLSAL<br>DYAKAVGLCT<br>LOGFLVMLAA                            | SSDGEGQGRP<br>TLAICLLYVG<br>MAMAAGGIOA                             | VPRRHLGPSE<br>QSAAAIGANV<br>ARVLHOALLH                             | KVQVTEAKAD<br>WLSAWTNDAM<br>NKIRSPOSFF                             | GALTQEEKAA<br>ADSRQNNTSL<br>DTTPSGRILN                       | IGTVELSVFW<br>RLGVYAALGI<br>CFSKDIYVVD<br>ATSRQLKRLE                              | 960<br>1020<br>1080<br>1140           |
| 40          | SVSRSPIYSH<br>FVGNCVVLPA<br>KEYSKTETEA<br>IVGRTGAGKS              | FSETVTGASV<br>ALFAVIGRSS<br>PWVVEGSRPP<br>SMTLCLFRIL<br>SEEDIWWALE | IRAYNRSRDF<br>LNPGLVGLSV<br>EGWPPRGEVE<br>BAAKGEIRID<br>LSHLHTFVSS | EIISDTKVDA<br>SYSLQVTFAI<br>PRNYSVRYRI<br>GLNVADIGLE<br>OPAGLDFOCS | A NORSCYPYII  MWMIRMMSDI  GLDLVLRDLS  GLDLSVLRIII  EGGENLSVG | SNRWLSIGVE ESNIVAVERV LHVHGGEKVG ODPILFSGTL RQLVCLARAL                            | 1200<br>1260<br>1320<br>1380<br>1440  |
| 45          | LRKSRILVLD<br>VAEFDSPANL  | EATAAIDLET<br>IAARGIFYGM   | DNLIQATIRT<br>ARDAGLA  | QFDTCTVLT  | ( AHRLNTIMD)   | TRVLVLDXGV  | 1500<br>1527                          |
|             |   | C395 Prote   |  | •  | ;  |   | •                                     |
| 50          | 1<br> <br>  MRARPQVCEA  | 11<br> <br>  LLFALALQTG  | 21<br> <br>  VCYGIKWLAI  | 31<br> <br>  SKTPSALALI  | 41<br>N QTQHCKQLE  | 51<br> <br>  LVSAQVQLCR   | 60<br>120                             |
| 55          | AISHAIARAC<br>TGSQANKLME<br>YLSATKVVHI                            | TSGDLPGCSC<br>LHNSEVGRQA   | GPVPGEPPGI<br>LRASLEMKCI<br>KDLDIRPVKI                             | CHGVEGSCS CHGVEGSCS CHGVYLQSS                                      | n Lsyglimga<br>I RTCWKGLQE<br>P DFCMKNEKV                    | E SAFVYALSAA<br>K FSDAPMKVKK<br>L QDVAADLKTR<br>G SHGTQDRQCN<br>R YVCK            | 180<br>240<br>300<br>354              |
| 60          |   | : C396 Prote<br>ccession #:  |  | e  | · .  | •   |                                       |
|             | 1   | 11<br>   | 21<br>   | 31<br>   | 41   | 51<br>  |                                       |
| 65          | TQDEAGLEVI<br>LMRQYGFAW<br>GHGRPPGAR<br>VSSERHPLYI                | H QFWPLVEIQG<br>P DRMRCDRLPI<br>P PHRGGGRGG<br>N RVKTGQIANG        | C SPDLKFFLC<br>G QGNPDTLCM<br>G GGDAAAPPA<br>C ALPCHNPFF           | S MYTPICLED<br>D YNRTDLTTA<br>R GGGGGGKAR<br>S QDERAFTVE           | Y KKPLPPCRS<br>A PSPPRRLPF<br>LP PGGGAAPCE<br>W IGLWSVLCF    | Y TYMPNOFNHD V CERAKAGCAP P PPGEOPPSGS P GCOCRAPMVS V STFATVSTFL                  | 60<br>120<br>180<br>240<br>300<br>360 |
| 70          | GAAGAGAGG<br>WFLAAGMKW<br>LRGFVLAPL<br>TVPAAVVVA                  | P GGRGEYEELA<br>G NEALAGYSQ<br>V IYLFIGTMF:<br>C LFYFOHNRP         | 3 AVEQHVRYE<br>Y FHLAAWLVP<br>L LAGFVSLFR<br>R WEATHNCPC           | T TGPALCTVV<br>S VKSIAVLAI<br>I RSVIKQQDO<br>L RDLOPDQAI           | IP LLVYFFGMI<br>LS SVDGDPVAC<br>IP TKTHKLEKI<br>RR PDYAVFMLI | A GGAGGAAAGA LS SIWWVILSLT LI CYVGNQSLDN M IRLGLFTVLY CY FMCLVVGITS CG GPGGGGGPGG | 420<br>480<br>540                     |
| 75          | GGGSLYSDV   | S TGLTWRSGT.   | A SSVSYPKQM  | P LSQV   | 00010000   |   | 694                                   |
| 13          |   | : C397 Prot<br>ccession #:   |  | e  |  |   |                                       |
| 80          | PNLLGHETM   | IK EVLEQAGAW<br>IS AFGFPWPDM                                       | I PLVMKQCHI<br>L ECDRFPQDI   | PD TKKFLCSL<br>ND LCIPLASS   | PA PVCLDDLD:<br>DH LLPATEEA                                  | 51<br> <br>LC HGIEYQNMRL<br>ET IQPCHSLCVQ<br>PK VCEACKNKND<br>ER DLKKSVLWLK       | 120<br>180                            |
|             |   |  |  |  |  | 1373  |                                       |

|     | DSLQCTCEEM   | NDINAPYLVM  | GŐKŐGGELVI  | TSVKRWQKGQ   | REFKRISRSI   | RKLQC  | 295                                    |
|-----|--|---|---|--|--|--|--|
| · 5 |  | C398 Protei<br>ession #: N  |   |  |  |  |  |
| ,   | 1  | 11  | 21  | 31   | 41   | 51   |  |
| 10  | MQCKVYDSLL<br>GVLPLLAALL   | I<br>ALAVLGWLGT<br>ALPQDLQAAR<br>TLVPVSWSAN<br>YTATKVVYSA         | ALIVVAILLA<br>TIIRDFYNPV  | AFGLLVALVG<br>VPEAQKREMG                               | AQCTNCVQDD   | TAKAKITIVA   | 60<br>120<br>180<br>220                |
| 15  |  | C399 Protei<br>ession #: N  | •   |  |  |  |  |
|     | 1  | 11<br>i   | 21<br>  | 31<br>   | 41<br>   | 51<br>   |  |
| 20  | LQHTQELFPQ<br>VSITLLALVY<br>SYPMRRSYRY<br>VSDSLTWREF               | EELWKMKPRR WHLPIKIAAI LPGVIAAIVQ KLLNWAYQQV HYIQSKLGIV PCLRKKILKI | IASLTFLYTL<br>LHNGTKYKKP<br>QQNKEDAWIE<br>SLLLGTIHAL              | LREVIHPLAT<br>PHWLDKWMLT<br>HDVWRMEIYV<br>IFAWNKWIDI   | SHQQYFYKIP<br>RKQFGLLSFF<br>SLGIVGLAIL                 | ILVINKVLPM<br>FAVLHAIYSL<br>ALLAVTSIPS                             | 60<br>120<br>180<br>240<br>300<br>339  |
| 25  |  | C400 Protei   |   | ٠,   |  |  |  |
| 30  | ETVLARCVKY<br>KILLWSRIKD   | 11<br> <br>GDKPCCRLSR<br>TEIHPEMRHV<br>LAHQFTQVQR                 | DCQSVWDAFK<br>DMFTLEDTLL  | LVLILVVVLA<br>GAFISKHPCN<br>GYLADDLTWC                 | ITEEDYQPLM<br>GEFNTSKINY                               | KLGTQTVPCN<br>QSCPDWRKDC   | 60<br>120<br>180                       |
| 35  | WVIHGGREDS<br>Seq ID NO:   | TVSRRFAEAA<br>RDLCQDPTIK<br>C401 Protes                           | ELESIISKRN<br>in Sequence   |  |  | QPEKVQTLEA<br>PEDSSCTSEI   | 240<br>300                             |
| 40  | 1  | 11  | 21  | 31   | 41   | 51 :   |  |
| 40  | <b>FSEGSESNSR</b>  |   | YSDDPAPTTS  | PSSVQPREFG   | VMQGAPRARF   | TTRAKIFKRF<br>GSRTPPAAAE<br>RTRADPAGRR                             | 60<br>120<br>180                       |
| 45  | RRHPRSPAPG<br>LAKRYERPTL<br>PPLLPAPGVA<br>FGLMAQRRWQ               | GEGTCSEGPA<br>VELPHGHLRT<br>GTLLPPPTSS<br>HRSLKQFEWG              | PRRRMEBEMQ<br>PAQPPPASPA<br>SPPSPRPRPW<br>ILGSWGTWPC              | PAEEGPSVPK<br>ASSSSSFAAV<br>HAAAPRGGTS<br>GQDWLEKEGQ   | IYKQRSPYSV<br>VRLGAPPRPP<br>HTHMWRSQST<br>VAVLLPRSEG   | LKTFPSKRPA<br>RRGFRARGTI<br>LPGSDTMVSV<br>NTAPKKSRMI               | 240<br>300<br>360<br>420               |
| 50  | NVDIEMQYMQ<br>HTLENISLDS<br>LEDGIRSPVP                             | RKQQTSAFLR<br>TASLCKSRHL<br>LSCEALEMDL<br>YSCGLGKRKR              | VFTDSLQNYL<br>SREPPVKSDF<br>TSLGSKQLLN                            | LSGSFPTPNP<br>PNPLQQALAG<br>NYPVYITSKQ                 | SSASEYGHLA<br>GASRPFSGAQ<br>WDEAVNSSKK                 | GKGVHSQTSD<br>DVDPLSTSPV<br>QSIAYRVNSE<br>DGRRLLRYLI<br>VSPSVISPHR | 480<br>540<br>600<br>660<br>720<br>735 |
| 55  |  | C402 Prote<br>cession #:  |   |  | ٠  |  | : -                                    |
| 60  | EVARITFVFE   | TLCSVNCELY  | FMVGVNSRTN  | TPVETWKGSK   | GKQSYTYIIE   | 51<br> <br>QSVMADTENK<br>ENTITSFIWA<br>TSCPAGYYID                  | 60<br>120<br>180                       |
| 65  | RDSGTCHSCP<br>FSALANTVTL<br>SITAYVCQAV<br>PDVIFFYRSN<br>AAACPLCSVA | PNTILKAHQP AGGPSPTSKG IIPPEVTGYK DVTQSCSSGR DYHAIVSSCV            | YGVQACVPCG<br>LKYPHHFTLS<br>AGVSSQPVSI<br>STTIRVRCSE<br>AGIQKTTYV | PGTKNNKIHS LCGNQGRKMS ADRLIGVTTD QKTVPGSLLL REPKLCSGGI | LCYNDCTFSR VCTDNVTDLR MTLDGITSPA PGTCSDGTCL SLPEQRVTIC | NTPTRTFNYN IPPGESGFSK ELFHLESLGI GCNFHPLWES KTIDFWLKVG             | 240<br>300<br>360<br>420<br>480<br>540 |
| 70  | LIFTSKKSLF<br>Seq ID NO:   | GKIKSFTSKQ<br>C403 Prote  | PAPVTISLSE  | DS .   | ·  |  | 572                                    |
|     |  |   | -   | ,  | 41   | 51   |  |
| 75  | REPRAAASVO   | AVGCAAGALE  | PRCHGETPAC  | PRDSAAGKSP   | <br>  YDVSRLGRGE<br>  AYLCQAEWIV                       | <br>  RSLVLDLKQP<br>  PVQESFCRLA                                   | 60<br>120                              |
| 80  | GHDINYLALS<br>DANMVEGTAY<br>YELLIKGLGI<br>EEVVHHDHNI               | GVLSKIGRSG<br>LSSFLWKTQH<br>KSDELPNQMS                            | ENPYAPLNLA<br>SSLWEAPRG<br>TDDWPEMKKI<br>QDVSPRLAPI               | ADFAGGGLMO<br>NMLDGGAPFY<br>FADVFAKKTE                 | ALGIIMALFI<br>TTYRTADGBI<br>AEWCQIFDGT                 | O RTRTDKGQVI<br>P MAVGAIEPQP<br>T DACVTPVLTF<br>T EEILEEFGFS       | 180<br>240<br>300<br>360<br>382        |
| •   | Seq ID NO  | : C404 Prote  | ein Sequence  |  | _  |  |  |
|     |  |   |   |  |  | 2014   |  |

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Protein Accession #: XP 091332.1
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        MORWILWAAA FLILHSAQAF POIDISISPA LPELPLPSLC PLFWMEFKGH CYRFFPLNKT
        WAEADLYCSE FSVGRKSAKL ASIHSWEENV FVYDLVNSCV PGIPADVWTG LHDHRQEGQF
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        EWTDGSSYDY SYWDGSQPDD GVHADPEEED CVQIWYRPTS EQLQAPEPQL PLSISEATDV
                                                                                             180
        YLPEDFPAEP KLMDQSWVSR KSLKPSKSHL MEPPTPVAKH QKAKTRHRSL RGVWWPSGKA
                                                                                             240
        GSWKERMNAD YGRRRSAPR QEGRLRCRER RLRAASGGGR PEGGRKQRQQ ERQERGWEEL
GGVSPMRGAQ AWQHGLGAGS QRGAAPECGE NHQAPELGST WRGQRLQPQT AALCHFALRK
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10
        LPGNAHGLAA AFVQPALQVQ EEKNNRTRFS GAYFTMSDPT CDQDSKEQSL RRHGREAEKD
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        GPYRLVKKKR GPVACPSSFE LQSGGEVCLD PPVELRAGTW IAREPP
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        Protein Accession #: XP_054869.2
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        MHTCCPPVTL EQDLHRKMHS WMLQTLAFAV TSLVLSCAET IDYYGEICDN ACPCEERDGI
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        LTVSCENRGI ISLSEISPPR FPIYHLLLSG NLLWRLYPNE FVNYTGASIL HLGSNVIQDI
ETGAFHGLRG LRRLHLNNNK LELLRDDTFL GLENLEYLOV DYNYISVIEP NAFGKLHLLQ
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                                                                                             180
         VLILNDNLLS SLPNNLFRFV PLTHLDLRGN RLKLLPYVGL LQHMDKVVEL QLEENPWNCS
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         CELISLKOWL DSISYSALVG DVVCETPFRL HGRDLDEVSK QELCPRRLIS DYEMRPQTPL
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        STTGYLHTTP ASVNSVATSS SAVYKPPLKP PKGTRQPNKP RVRPTSRQPS KDLGYSNYGP
SIAYQTKSPV PLECPTACSC NLQISDLGLN VNCQERKIES IAELQPKPYN PKKMYLTENY
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         IAVVRRTDFL EATGLDLIHL GNNRISMIQD RAFGDLTNLR RLYLNGNRIE RLSPELFYGL
        QSLQYLFLQY NLIREIQSGT FDPVPNLQLL FLNNNLQAM PSGVFSGLTL LRLNLRSNHF
TSLPVSGVLD QLKSLIQIDL HDNFWDCTCD IVGMKLWVEQ LKVGVLVDEV ICKAPKKFAE
TDMRSIKSEL LCPDYSDVVV STPTPSSIQV PARTSAVTPA VRLNSTGAPA SLGAGGGASS
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30
         VPLSVLILSL LLVFIMSVFV AAGLFVLVMK RRKKNQSDHT STNNSDVSSF NMQYSVYGGG
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        GGTGGHPHAH VHHRGPALPK VKTPAGHVYE YIPHPLGHMC KNPIYRSREG NSVEDYKDLH
ELKVTYSSNH HLQQQQPPP PPQQPQQPP PQLQLQPGEE ERRESHHLRS PAYSVSTIEP
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                                                                                              840
         REDLLSPVQD ADRFYRGILE PDKHCSTTPA GNSLPEYPKF PCSPAAYTFS PNYDLRRPHQ
                                                                                              900
         YLHPGAGDSR LREPVLYSPP SAVFVEPNRN EYLELKAKLN VEPDYLEVLE KOTTFSQF
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         Seg ID NO: C406 Protein Seguence
         Protein Accession #: NP_000784.2
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         MGILSVDLLI TLQILPVFFS NCLFLALYDS VILLKHVVLL LSRSKSTRGB WRRMLTSEGL
         RCVWKSFLLD AYKQVKLGED APNSSVVHVS STEGGDNSGN GTQEKIAEGA TCHLLDFASP
                                                                                              120
         ERPLVVNFGS ATUPPFTSQL PAFRKLVEEF SSVADFLLVY IDEAHPSDGW AIPGDSSLSF
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         EVKKHONQED RCAAAQQLLE RFSLPPQCRV VADRMDNNAN IAYGVAFERV CIVQRQKIAY
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         LGGKGPFSYN LQEVRHWLEK NFSKRUKKTR LAG
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         MSSCVSSQPS SNRAAPQDEL GGRGSSSSES QKPCEALRGL SSLSIHLGME SFIVVTECEP
         GCAVDLGLAR DRPLEADGQE VPLD9SGSQA RPHLSGRKLS LQERSQGGLA AGGSLDMNGR
         CICPSLPYSP VSSPQSSPRL PRRPTVESHH VSITGMQDCV QLNQYTLKDE IGKGSYGVVK
                                                                                              180
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         LAYNENDNTY YAMKVLSKKK LIRQAGFPRR PPPRGTRPAP GGCIQPRGPI EQVYQEIAIL
KKLDHPNVVK LVEVLDDPNE DHLYMVPELV NQGPVMEVPT LKPLSEDQAR FYPQDLIKGI
                                                                                              .240
                                                                                              300
         EYLHYQKIIH RDIKPSNLLV GEDGHIKIAD FGVSNEFKGS DALLSNTVGT PAFMAPESLS
                                                                                              360
         ETRKIFSGKA LDVWAMGYTL YCFVFGQCPF MDERIMCLHS KIKSQALBFP DQPDIAEDLK
DLITRMLDKN PESRIVVPEI KLHPWYTRHG AEPLPSEDEN CTLVEVTEEE VENSVKHIPS
                                                                                              420
                                                                                              480
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         LATVILVKIM IRKRSFGNPF EGSRREERSL SAPGNLLIKK PIRECESLSE LKEARQRRQP
         PGHRPAPRGG GGSALVRGSP CVESCWAPAP GSPARMHPLR PERAMEPE
         Seg ID NO: C408 Protein Seguence
         Protein Accession #: NP_061116.2
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          MGLSLPKEKG LILCLWSKFC RWFQRRESWA QSRDEQNLLQ QKRIWESPLL LAAKDNDVQA
         LNKLLKYEDC KVHQRGAMGE TALHIAALYD NLEAAMVLMB AAPELVFEPM TSELYEGGTA
LHIAVVNONM NLVRALLARR ASVSARATGT AFRRSPCNLI YFGEHPLSFA ACVNSEEIVR
                                                                                               120
 70
                                                                                               180
          LLIEHGADIR AQDSLGNTVL HILILQPNKT FACQMYNLLL SYDRHGDHLQ PLDLVPNHQG
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          LTPFKLAGVE GNTVMFQHLM QKRKHTQWTY GPLTSTLYDL TEIDSSGDEQ SLLELIITTK
                                                                                               300
          KREARQILDQ TPVKELVSLK WKRYGRPYFC MLGAIYLLYI ICFTMCCIYR PLKPRTNNRT
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          SPRDNTLLQQ KLLQEAYMTP KDDIRLVGEL VTVIGAIIIL LVEVPDIFRM GVTRFFGQTI
LGGPFHVLII TYAPMVLVTM VMRLISASGE VVPMSFALVL GWCNVMYPAR GFQMLGPFTI
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                                                                                               480
          MIQKMIFGDL MRFCWLMAVV ILGFASAFYI IFQTEDPEEL GHFYDYPMAL PSTFELFLTI
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          IDGPANYNVD LPFMYSITYA APAIIATLLM LNLLIAMMGD THWRVAHERD ELWRAQIVAT
TVMLERKLPR CLWPRSGICG REYGLGDRWF LRVEDRODLN RQRIQRYAQA FHTRGSEDLD
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                                                                                               660
          KDSVEKLELG CPPSPHLSLP MPSVSRSTSR SSANWERLRQ GTLRRDLRGI INRGLEDGES
 80
          Seq ID NO: C409 Protein Sequence
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Protein Accession #: NP\_068710.1

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11
        MOKVILGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW
        RSSGEQAGRG WGSPPLTTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS
                                                                                        113
 5
        Seq ID NO: C410 Protein Sequence
        Protein Accession #: NP 005962.1
                     11
                                               31
10
        MQKVTLGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK
                                                                                        60
        CKCKFGQKSG HHPGETPPLI TPGSAQS
        Seg ID NO: C411 Protein Seguence
15
        Protein Accession #: NP_004952.1
                                                                         51
        MLSKYLPVLL GILLILOSRV EGPOTESKNE ASSRDVVYGP OPOPLENOLL SEETKSTETE
20
        TGSRVGKLPE ASRILNTILS NYDHKLRPGI GEKPTVVTVE IAVNSLGPLS ILDMEYTIDI IFSOTWYDER LCYNDTFESL VLNGNVVSOL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD
                                                                                        120
                                                                                        180
        GKVLYTIRMT IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIYKWENF KLEINEKNSW
                                                                                         240
        KLFQFDFTGV SNKTEIITTP VGDFMVMTIF FNVSRRFGYV AFQNYVPSSV TTMLSWVSFW
                                                                                        300
        IKTESAPART SIGITSVLTM TTLGTFSRKN PPRVSYITAL DFYIAICFVF CFCALLEFAV
LNFLIYNQTK AHASPKLRHP RINSRAHART RARSRACARQ HQEAFVCQIV TTEGSDGEER
                                                                                        360
25
                                                                                         420
        PSCSAQQPPS PGSPEGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL
        DNYSRVVFPV TFFFFNVLYW LVCLNL
                                                                                         506
        Seg ID NO: C412 Protein Sequence
30
         Protein Accession #: NP_068819.1
         MEYTIDIIFS OTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHBITMPNQ
35
         MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWENFKLE
                                                                                         120
         INEKNSWKLF OLDFIGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTTM
                                                                                         180
         LSWYSPWIKT ESAPARTSLG ITSVLTMTTL GTPSRKNFPR VSYITALDFY IAICFVFCFC
                                                                                         240
         ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE
                                                                                         300
         GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQARL
                                                                                         360
40
                                                                                         393
         CIHVYRLDNY SRVVPPVTFP PFNVLYWLVC LNL
         Seq ID NO: C413 Protein Sequence
         Protein Accession #: NP_068822.1
45
                                                31
         MEYTIDIIFS OTWISKRIHE HEITMPNOMV RIYKDGKVLY TIRMTIDAGC SLHMLRPPMD
         SHSCPLSPSS PSYPENEMIY KWENFKLEIN EKNSWKLFQF DFTGVSNKTE IITTPVGDFM
                                                                                         120
         VMTIPFNVSR RFGYVAFONY VPSSVTTMLS WVSFWIKTES APARTSLGIT SVLTMTTLGT
                                                                                         180
 50
         FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFII YNOTKAHASP KLRHPRINSR
AHARTRARSR ACARQHQEAF VCQIVTTEGS DGEERPSCSA QQPPSPGSPE GPRSLCSKLA
CCEWCKRFKK YFCMVPDCEG STWQQGRLCI HVYRLDNYSR VVFFVTFFFF NVLYWLVCLN
                                                                                         240
                                                                                         300
                                                                                         360
 55
         Seq ID NO: C414 Protein Sequence
         Protein Accession #: NP 068830.1
                                                31
                                                             41
 60
         MEYTIDIIFS OTWYDERLCY NOTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ
                                                                                          60
         MVRIYRDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWENFKLE
INEKNSWKLF QFDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTTM
LSWVSFWIKT ESAPARTSLG ITSVLTMTTL GTFSRKNFFR VSYITALDFY LAICFVFCFC
                                                                                          120
                                                                                          180
          ALLEPAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE
                                                                                          300
 65
          GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQGRL
                                                                                          360
          CIHVYRLDNY SRVVPPVTFF FFNVLYWLVC LNL
                                                                                          393
          Seq ID NO: C415 Protein Sequence
          Protein Accession #: NP_068591.1
 70
          MPAVSGPGPL FCLLLLLDP HSPETGCPPL RRFEYKLSFK GPRLALPGAG IPFWSHEGDA
          ILGLEEVRLT PSMRNRSGAV WSRASVPFSA WEVEVOMRVT GLGRRGAHGM AVWYTRGRGH
                                                                                          120
 75
          VGSVLGGLAS WDGIGIFFDS PAEDTQDSPA IRVLASDGHI PSEQPGDGAS QGLGSCHWDF
                                                                                          180
          RNRPHPFRAR ITYWGQRLRM SLNSGLTPSD PGEFCVDVGP LLLVPGGFFG VSAATGTLAD
                                                                                          240
          DHDVLSFLTF SLSEPSPEVP PQPFLEMQQL RLARQLEGLW ARLGLGTRED VTPKSDSEAQ
GEGERLFDLE ETLGRHRRIL QALRGLSKQL AQAERQWKKQ LGPPGQARPD GGWALDASCQ
                                                                                          300
                                                                                          360
          IPSTPGRGGH LSMSLNKDSA KVGALLHGQW TLLQALQEMR DAAVRMAAEA QVSYLPVGIE
                                                                                          420
 80
          HHFLELDHIL GLLQEELRGP AKAAAKAPRP PGQPPRASSC LQPGIFLFYL LIQTVGFFGY
                                                                                          480
          VHFRQELNKS LQECLSTGSL PLGPAPHTPR ALGILRRQPL PASMPA
          Seq ID NO: C416 Protein Sequence
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Protein Accession #: XP\_117036.1

|            | 1                        | 11                          | 21  | 31                       | 41                       | 51                                     |                   |
|------------|--------------------------|-----------------------------|---|--------------------------|--------------------------|--|-------------------|
| 5          | HRCPREAGQA               | PVGPSPETQG                  | I<br>LRHLCTGLQA<br>VAHVCSRARV<br>PAVARGSGDG | SVDEREPGGG               |                          |  | 60<br>120<br>156  |
| 10         |                          | C417 Protei<br>ession #: X  |   |                          |                          |  |                   |
| . •        | 1                        | 11                          | 21<br>I                                     | 31<br>1                  | 41<br>                   | 51<br>i                                |                   |
| 15         | KTKKKKKÖEK               | KNHTKFFHHT                  | PGVGIGGHCL<br>YPLSQQDFLF                    |                          |                          | KNFAAKRNEE                             | 60<br>108         |
|            |                          | C418 Protei<br>cession #: N |   |                          |                          |  |                   |
| 20         | 1                        | 11<br>                      | 21<br>                                      | 31<br>                   | 41                       | 51                                     |                   |
|            | LLMDFVFSLV               | NSFLGEFLRR                  | RNIFLKISII<br>IIGMQLITSL<br>MMNFQPPSKA      | GLQEFDIARN               | VLELIYAQTL               | VWIGIFFCPL                             | 60<br>120<br>180  |
| 25         | WRLKPSADCG               | PFRGLPLFIH                  | SIYSWIDTLS                                  | TRPGYLWVVW               | IYRNLIGSVH               | FFFILTLIVL                             | 240<br>300        |
| 23         |                          |                             | HEQIINEGKD<br>RSVQEGNPRA                    | KMFLIERLIK               | TYDMEKKAMP               | SSUVUERREV                             | 330               |
| 30         |                          |                             | in Sequence<br>Sos sequence                 | 2                        | (                        | •                                      |                   |
| 30         | 1                        | 11                          | 21  | 31                       | 41                       | 51                                     |                   |
|            | MLSDDHVNEI               | <br>  IIOVENVSSG            | VOSHPSSNQI                                  | FOEKVLLDSS               | INMVLSISDI               | <br>DVIDSQTVSK                         | 60                |
| 35         | RNDQKGNQVL               | RFSTSLNESM                  | SQTLHSLECM                                  | GIDTPGSSHE               | TVQGQKLIAS               | LIPMTSRDRI<br>SKNSLSEILN               | 120<br>180        |
| ,,         | SISLWQKTLK               | IIGGRFGTSV                  | LSYFNFLRWL                                  | LKFNIFSFIL               | NESFIIIPQF               | TVAKKNTLQF                             | 240               |
|            |                          |                             |   |                          |                          | TTCFFSLLFS<br>LSELRQENSK               | 300<br>360        |
| 40         | LTFNQLLTRF               | SVVWAVVVS                   | TGVAIACCAA                                  | VYYLAEYNLE               | FLKTHSNPGA               | VLLLPFVVSC                             | 420               |
| 40         |                          |                             |   |                          |                          | VALSGEECWE<br>VLELIYAQTL               | 480<br>540        |
|            | VWIGIFFCPL               | LPFIQMIMLF                  | IMFYSKNISL                                  | MMNFQPPSKA               | WRASOMMTFF               | IPLLFFPSFT                             | 600               |
|            |                          |                             |   |                          |                          | IYRNLIGSVH<br>LQDMEKKANP               | 660<br>720        |
| 45         |                          |                             | HDGSLDLRSR                                  |                          |                          |  | 760               |
|            |                          |                             | in Sequence<br>NP_002241.1                  |                          |                          |  | ٠.                |
| 50         | 1                        | 11                          | 21  | 31                       | 41                       | 51                                     | •                 |
|            | <br>                     |                             | OFFICE ACMAI                                | AL POMOTOL W             | THE WARMING              | <br>  GCSWALYLFL                       | 60                |
| 55         | VKCTISISTF<br>PVRGPPCVQD | LLLCLIVAFH<br>LGAPLTSPQP    | AKEVQLFMTE<br>WPGFLGQGEA                    | NGLRDWRVAL<br>LLSLAMLLRL | TGRQAAQIVI<br>YLVPRAVLLE | ELVVCGLHPA<br>SGVLLNASYR<br>VNATGHLSDT | 120<br>180<br>240 |
| <i>J J</i> | LWLIPITFLT               | GYGDVVPGT                   | MWGKIVCLCI                                  | GVMGVCCTAL               | LVAVVARKLE               | FNKAEKHVHN                             | 300               |
|            |                          |                             |   |                          |                          | FRQVRLKHRK STALGPRQLP                  | 360<br>420        |
| 60         | EPSQQSK                  | . 101011111111              |   |                          |                          |  | 427               |
| 00         |                          |                             | in Sequence<br>NP_079533.1                  |                          |                          |  | ;                 |
| CE         | 1                        | 11                          | 21  | 31                       | 41                       | 51                                     |                   |
| 65         |                          |                             |   |                          |                          | V VGIVAWLYGD<br>C PTPQVCVSSC           | 60<br>120         |
|            | PEDPWTVGK                | N EFSQTVGEVI                | YTKNRNFCL                                   | GVPWNMTVI                | SLQQELCPS                | F LLPSAPALGR                           | 180               |
| 70         |                          |                             |   |                          |                          | Y WILVALGVAL<br>I SQLGFTTNLS           | 240<br>300        |
|            | AYQSVQETWI               | L AALIVLAVLI                | AILLLVLIF                                   | L RQRIRIAIAI             | LKEASKAVG                | VJGYZMTSMM Ç                           | 360               |
|            |                          |                             |   |                          |                          | C NPTAHLVNSS<br>A FASFYWAFHK           | 420<br>480        |
| 75         | PQDIPTFPL:               | I SAFIRTLRY                 | I TGSLAFGAL                                 | LTLVQIARV                | LEYIDHKLR                | G VQNPVARCIM                           | 540               |
| 75         |                          |                             |   |                          |                          | V VVLDKVTDLL<br>A YVIASGFFSV           | 600<br>660        |
|            |                          |                             | N GSLDRPYYM                                 |                          |                          |  | 712               |
| 80         |                          |                             | ein Sequenc<br>NP_057264.                   |                          |                          |  | •                 |
|            | 1                        | 11                          | 21  | 31                       | 41                       | 51                                     |                   |
|            | 1                        | i                           | 1   | 1                        |                          | 1                                      | 60                |
|            | DAQDGNGDE                | " UTIVODADO                 | 2 ELDOAFELK                                 | " ETOKNILMÖ              | . A. LUREFUI             | A VEAAYVTPVL                           | 50                |

| 5  | LSVGLPSSLY S<br>LNGATVVAAL S<br>HYHALFTGFG OPLTEVAKGIP MTLKSLURAL S<br>LIYERGVEVG OVYSTLVLCSL S<br>CMVQLAQILV | IANPRRKLVW GALGYLLGAI PQQTPQDPPL VNMPPHYRYL CWGFCINSVF FGVMSSTLYT       | AISVTMIGVV<br>DWAHLELGRL<br>SSDGMYEYGS<br>CISHLIGWTA<br>SSLYSYFQKV<br>VPFNLITEYH | LFDFAADFID<br>LGTEFQVMFF<br>IEKVKNGYVN<br>FLSNMLFFTD<br>LVSYIGLKGL<br>REBEKBRQQA | GPIKAYLFDV<br>FSALVLTLCF<br>PELAMQGAKN<br>FMGQIVYRGD<br>YFTGYLLFGL<br>PGGDPDNSVR | CSHQDKEKGL<br>TVHLCSISEA<br>KNHAEQTRRA<br>PYSAHNSTEF<br>GTGFIGLFPN                          | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>530 |
|----|---|---|--|--|--|---|--|
| 10 | Seq ID NO:  |   |  |  |  |   |  |
| 15 | MEGFGGVGGR<br>PGKGTGRQRG<br>RGSATAAARH<br>AGAOGAGPAR  | AWGPRAEDGV<br>HVPPAPGGPF<br>GRSGEGSEWA                                  | RRRTLGMPRG<br>GPRAPAGSTR<br>RRGKGRPGPY   | SRRDVRAPCG<br>VPARAGGAVE<br>QSPLGPAVAE   | PAGSWGARGG<br>PTGAAAVARL<br>GQELKDKSRL   | RRRDGPSRRR<br>ARPAGGALPT<br>RYPINGFQAL  | 60<br>120<br>180<br>240                              |
| 20 | GNPIYDFFLG<br>NGFQLLYVGD<br>LPMASVICLI<br>RHPNYLGDLI  | RELNPRICFF<br>ALWHEEAVLT<br>NATGYYIFRG<br>MALAWSLPCG                    | PEMLLPLAFV<br>DFKYFCELRP<br>TMDITHDGFG<br>ANSQKNTFRK<br>VSHLLPYFYL               | GLIGWVLINL<br>FMLAFGDMAW<br>NPSDPRVAGL<br>LYPTALLVHR                             | ALLMKEAELR<br>VPFTYSLQAQ<br>ETISTATGRK<br>EARDERSACR                             | GSPSLAMWLV<br>FLLHHPQPLG<br>LLVSGWWGMV  | 300<br>360<br>420<br>480<br>540                      |
| 25 |   |   | GHVPTHPPAH<br>in Sequence  | PGPGASTHLG   | LKGLHPTQP  |   | 589  |
|    | Protein Acc   | ession #: 1   | NP_056535.1  |  | 42   | e1  |  |
| 30 | SEEPSETMGL  | GAGLGAPGSG  | FPSEENEESR   | ILQPPQYFWE   | EEEELNDSSL   | 51<br> <br>  LLPTGLEPLD<br>  DLGPTADYVF   | 60<br>120  |
| 35 | QEEEEEELL<br>PSLLLPSVTP<br>EEVPALPSFP<br>EGQAAEAQSR<br>LPRHGSGHHG   | PVNGSQEEAK<br>TTVTPGDQDS<br>QTTAPSGAEH<br>IPWDSTQVIC<br>AWHISLSKPS      | PQVRDFSLTS<br>TSQEAEATVL<br>PDEDPLGSRT<br>KDWSNLAGKN<br>EKEOHLLMTL               | SSQTPGATKS PAAGLGVEFE SASSPLAPGE YIILMMTENI VGEOGVVPTO                           | RHEDSGDQAS APQEASEEAT MELTPSSATL DCEVFRQHRG DVLSMLGDIR                           | EEREKEEVEK<br>SGVEVESSMG<br>AGAAGLSGQH<br>GQEDLNQQLL<br>PQLLALVEEV<br>RSLEEIGIQN            | 180<br>240<br>300<br>360<br>420<br>480               |
| 40 | YSTTSSCOAR  | ASOVRSDYGT  | LFVVLVVIGA   | . ICIIIIALGI   | <b>LYNCWORRLP</b>  | KLKHVSHGBE<br>RDPEDSDVFE  | 540<br>600<br>605                                    |
| 45 |   | C425 Prote<br>cession #:  | in Sequence<br>NP_001188.  |  | 41   | ,<br>51   |  |
| 50 | <br>  MSEVRPLSRD<br>  LACIGDEMDV  | <br>  ILMETLLYBO<br>  SLRAPRLAQI  | <br>  LLEPPTMEVI   | <br>  GMTDSEEDLI<br> - AFIYDQTED   | PMEDFDSLEC<br>RDVLRSFMDC   | <br>  MEGSDALALR<br>  FTTLKENIMR  | 60<br>120<br>160                                     |
|    |   | C426 Protecession #:  | ain Sequence<br>AAF76225.1   | 3  |  |   |  |
| 55 | 1<br> <br>  MATPLPPPSE  | 11<br> <br>  RHLRLLRLL  | 21<br> <br>L SGLVLGAALI  | 31<br> <br>R GAAAGHPDV   | 41<br> <br>A ACPGSLDCAI  | 51<br> <br>L KRRARCPPGA   | . 60   |
| 60 | DRORLPEPAT<br>DGLALVLILA<br>RLAOSAEMYH  | LGFSARGQGI<br>FCVAGAAAL   | L ELGLPSTPG<br>S VASLCWCRL<br>C LERHKEPPK  | r ptptphtsl<br>Q reirltqka   | G SPVSSDPVHI<br>D YATAKAPGS:   | SGQSTPPLPK SPLEPRGGQG AAPRISPGDQ PGLAPTGEME   | 120<br>180<br>240<br>300<br>325                      |
| 65 |   |   | ein Sequenc<br>NP_004436.  |  |  |   |  |
| 70 | HVAGAPPGTO<br>EEPDSPDSV:<br>VKERSFGPL   | G QDNWLQTHF<br>S SWHLKRWTK<br>I QRGFYVAFQ                               | V ERRGAQRAH<br>V DTIAADESF<br>D TGACLALVA  | I RLHFSVRAC<br>P SSSSSSSS<br>V RLFSYTCPA   | S SLGVSGGTC<br>S SAAWAVGPH<br>V LRSFASFPE  | 51<br> <br>Q RRLTRTFEAC<br>R ETFTLYYRQA<br>G AGQRAGLQLN<br>T QASGAGGASL<br>Y QPARGDKACQ     | 60<br>120<br>180<br>240<br>300                       |
| 75 | ACPRGLYKS:<br>LWFEVQGSA:<br>RQRGLTESR:<br>OVSRASNSI:  | S AGNAPCSPC<br>L MLHWRLPRE<br>V LVGGLRAHV<br>T VSWPOPDOT                | P ARSHAPNPA<br>L GGRGDLLFN<br>P YILEVQAVN<br>N GNILDYOLF                         | A PVCPCLEGE V VCKECEGRO G VSELSPDPE Y YDQAEDESE                                  | y rassdppea<br>E pasggggtc<br>Q aaainvsts<br>Is ftltsetni                        | P CTGPPSAPQE<br>H RCRDEVHFDP<br>H EVPSAVPVVH<br>PA TVTQLSPGHI                               | 360<br>420<br>480<br>540                             |
| 80 | AVVFQRKRR IGTGSFGEV GVVTKSRPL LSAHSVLVN SYGERPYWD   | G TGYTEQLQC<br>R QGRLQPRGF<br>M VLTEFMELG<br>S HLVCKVARI<br>M SEOEVLNAI | Y SSPGLGVKY<br>IR EQTVAIQAI<br>SP LDSFLRQRE<br>LG HSPQGPSCI<br>IE OEFRLPPPE      | TY IDPSTYEDS<br>W AGGAESLON<br>G QPSSLQLVI<br>LL RWAAPEVII<br>G CPPGLHLLM        | PC QAIRELARE<br>MT FLGRAAVIO<br>AM QRGVAAAMO<br>AH GKHTTSSDV<br>ML DTWQKDRAI     | A FLLLARITVL V DPAYIKIEEV Q FQHPNILRLE Y LSSFAFVHRS W SFGILMWEVM R PHFDQLVAAF TY QDNPSKFGLC | 720<br>780<br>840<br>900                             |

|          | TFSDVAQLSL I   | EDLPALGITL   | AGHQKKLLHH   | IQLLQQHLRQ  | QGSVEV  |  | 1006   |
|----------|--|--|--|---|---|--|--|
| 5        | Seq ID NO: (   |  |  |   |   |  |  |
| 10       | 1<br> <br>  MPFDFRRFDI T<br>PDKDSGGKID T<br>FSINKVPGNF P<br>PLASHDYILK<br>KYTERRQPLY T | <br>YRKVPKDLTQ<br>VSLNISLPNL<br>HVSTHSATAQ<br>IVPTVYEDKS                         | <br>PTYTGAIISI<br>HCELVGLDIQ<br>PQNPDMTHVI<br>GKQRYSYQYT                         | CCCLFILFLF<br>CCCLFILFLF<br>DEMGRHEVGH<br>HKLSFGDTLQ<br>VANKEYVAYS      | LSELTGFITT<br>IDNSMKIPLN<br>VQNIHGAFNA<br>HTGRIIPAIW  | NGAGCRFEGQ<br>LGGADRLTSN   | 60<br>120<br>180<br>240<br>290               |
| 15       | Seq ID NO:   |  |  |   |   |  |  |
| 20<br>25 | MAQKEGGRTV ARLMVFDKTE DEGRLPHTQR RYDGAHLCGG GGYLPFRDPN YYGQQAGVLQ                      | CSRPKVAA  GTWRLLCSSR  LLEVISVCDC  SLLSGDWVLT  SEENSNDIAL  EARVPIISND             | LTAGTLLLLT<br>SNARVAGLSC<br>PRGRFLAAIC<br>AAHCFPERNR<br>VHLSSPLPLT<br>VCNGADFYGN | EEMGPLRALT<br>QDCGRRKLPV<br>VLSRWRVFAG<br>EYIQPVCLPA<br>QIKPKMFCAG      | 41<br> <br>AVLLRSDQEP<br>HSELDVRTAG<br>DRIVGGRDTS<br>AVAQASPHGL<br>AGQALVDGKI<br>YPEGGIDACQ<br>FQAIKTHSEA | ANGTSGFFCV<br>LGRWPWQVSL<br>QLGVQAVVYH<br>CTVTGWGNTQ<br>GDSGGFFVCE   | 60<br>120<br>180<br>240<br>300<br>360<br>417 |
|          | Seq ID NO:<br>Protein Acc  |  |  |   |   |  |  |
| 30       | ]  | 11<br>   | 21<br>   | 31<br>  | 41<br>  | 51<br>   |  |
| 35       | EVARITFVFE<br>FQRTTFHEAS<br>RDSGTCHSCP<br>FSALANTVTL<br>SITAYVCQAV                     | TLCSVNCELY<br>RKYTNDVAKI<br>PNTILKAHQP<br>AGGPSFTSKG<br>IIPPEVTGYK               | FMVGVNSRTN<br>YSINVTNVMN<br>YGVQACVPCG<br>LKYPHHFTLS<br>AGVSSQPVSL               | TPVETWKGSK<br>GVASYCRPCA<br>PGTKNNKIHS<br>LCGNQGRKMS<br>ADRLIGVTTD      | TLVVPGFRPP<br>GKQSYTYIIE<br>LEASDVGSSC<br>LCYNDCTFSR<br>VCTDNVTDLR<br>MTLDGITSPA<br>PGTCSDGTCD            | ENTTTSFTWA<br>TSCPAGYYID<br>NTPTRTFNYN<br>IPEGESGFSK<br>ELFHLESLGI   | 60<br>120<br>180<br>240<br>300<br>360<br>420 |
| 40       | AAACPLCSVA<br>ISAGTCTAIL   | DYHAIVSSCV<br>LTVLTCYFWK   | AGIQKTTYVW   | REPKLCSGGI<br>KLVMNATLKD  | SLPEQRVTIC  | KTIDFWLKVG<br>IMEGEDVEDD   | 480<br>540<br>572                            |
| 45       |  |  | in Sequence<br>NP_004855.1<br>21   | 31  | 41  | 51   |  |
| 50       | MPGQELRTVN<br>EDLLTRLRAN<br>HRALFRLSPT<br>ELHLRPQAAR                                   | GSQMLLVLLV<br>QSWEDSNTDL<br>ASRSWDVTRP<br>GRRRARARNG                             | LSWLPHGGAL<br>VPAPAVRILT<br>LRRQLSLARP<br>DDCPLGPGRO                             | <br>SLAEASRASF<br>PEVRLGSGGH<br>QAPALHLRLS<br>CRLHTVRASL                | LHLRISRAAL<br>PPPSQSDQLL<br>EDLGWADWVL  | SRFRELRKRY PEGLPEASRL AESSSARPQL SPREVQVTMC GVSLQTYDDL   | 60<br>120<br>180<br>240<br>300<br>308        |
| 55       |  |  | in Sequence<br>NP_443090.1   |   |   |  |  |
| 60       | RDQERDGNRD<br>GLTWDAAAPP<br>EAEGLLECHK   | RNRDRERERE<br>GPAPWEAPER<br>CKYLCTGRAC   | RERDPDRGPR<br>PQPQRKGDPG<br>CQMLEVLLNI   | RDTHRDAGPE<br>RRRPESEPPS<br>LILACSSVS                                   | R AGEHGVWEKE<br>ERYLPSTPRE<br>SSTGGYTGIT  | 51<br>  RRRDGDRDPK<br>P RQSRTRDGAR<br>P GREEVEYYQS<br>SLGGIYYYQF   | 60<br>120<br>180<br>240                      |
| 65       | LLLVTEGLLD   | MLIAGGYIPA   | QFYQLKLPM<br>LYFYFHYLS<br>AIKGYRKVRI   | AYGSPVCKE   | R QALYQSKGYS  | GVLRVPWHCP<br>GFGCSFHGAD   | 300<br>360<br>401                            |
| 70       | Protein Ac   |  | ein Sequence<br>Eos sequence   |   | 41  | <b>51</b>  |  |
| 75       | GKTLLLTSSA<br>TIILYGRADE<br>ERSWGHRGVI<br>SRNLDDMARK                                   | <br>  PKAMLTISWI<br>  TVYSIHISEC<br>  GIQPDPYYGI<br>  VHVIDPKSGT<br>  AMTKLGSKHI | TLTCFPGATS GKLVIKDHDI KYIGVGKGGG VIHSDRFDT                                       | TVAAGCPDQ: TVAAGCPDQ: PIVLRTRHI LELHGQKKL RSKKESERL FLTVKGNPS           | S PELQPWNPGE L IDNGGELHAC S WTFLNKTLHI V QYLNAVPDGE   | <br>H DQDHHVHIGQ<br>G SALCPFQGNF<br>P GGMAEGGYFF<br>R ILSVAVNDEG<br>HRGSAAARVF                               | 120<br>180<br>240<br>300                     |
| 80       | IQATTMDGVN<br>STILNLEDNV<br>EIDGVDMRAE<br>GTELKHMGQQ<br>KDVVGYNSIA                     | I LSTEVVYKK<br>V QSWKPGDTL<br>VGLLSRNII<br>VGLLSRNII<br>VGQYPIHP<br>HCPFTEDGP    | G QDYRFACYD<br>V IASTDYSMY<br>V MGEMEDKCY<br>H LAGDVDERG<br>E ERNTFDHCL          | R GRACRSYRV<br>Q AEEFQVLPC<br>P YRNHICNFF<br>G YDPPTYIRD<br>G LLVKSGTLL | R FLCGKPVRPI<br>R SCAPNQVKVI<br>D FDTFGGHIKI<br>L SIHHTFSRC<br>P SDRDSKMCKI                               | H PGKICNRPIC<br>K LTVTIDTNVN<br>A GKPMYLHIGE<br>F ALGFKAAHLE<br>V TVHGSNGLLI<br>M ITEDSYPGYI<br>M YSPGYSEHIE | 420<br>480<br>540<br>600                     |

LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPPLSII SARYSPHQDA DPLKPREPAI 780 IRHFIAYKNQ DHGAMLRGGD VMLDSCHFRG EAQEGFLLTG MKAGGILLGG DEAASGMAQG 840 866

5

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

5

#### WHAT IS CLAIMED IS:

2

Tables 2A-80.

A method for determining the presence or absence of a pathological cell in a 1 1. patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% 2 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, 3 thereby determining the presence or absence of said pathological cell. 4 The method of Claim 1, wherein: 2. 1 a) said pathology is described in Table 1, including a cancer; and/or 2 b) said biological sample comprises isolated nucleic acids. 3 The method of Claim 1, wherein said biological sample is tissue from an organ 3. 1 which is affected by said pathology of Table 1, including a cancer. 2 The method of Claim 2, wherein said nucleic acids are mRNA 4. 1 5. The method of Claim 2: 1 a) further comprising a step of amplifying nucleic acids before said step of detecting 2 said nucleic acid; or 3 b) where said detecting is of a protein encoded by said nucleic acid. 4 1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as 2 described in Tables 2A-80. 7. The method of Claim 2, wherein: 1 a) said detecting step is carried out by: 2 i) using a labeled nucleic acid probe; 3 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence 4 5 as described in Tables 2A-80; or iii) detecting a polypeptide encoded by said nucleic acid; or 6 7 b) said patient is: i) undergoing a therapeutic regimen to treat said pathology of Table 1; or 8 9 ii) is suspected of having said pathology or cancer. An isolated nucleic acid molecule comprising a sequence as described in 1 8.

| 1 | 9. The nucleic acid molecule of Claim 8, which is labeled.                                  |
|---|---|
| 1 | 10. An expression vector comprising the nucleic acid of Claim 8.                            |
| 1 | 11. A host cell comprising the expression vector of Claim 10.                               |
| 1 | 12. An isolated polypeptide which is encoded by a nucleic acid molecule                     |
| 2 | comprising a sequence as described in Tables 2A-80.   |
| 1 | 13. An antibody that specifically binds a polypeptide of Claim 12.                          |
| 1 | 14. The antibody of Claim 13:   |
| 2 | a) conjugated to an effector component;   |
| 3 | b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a    |
| 4 | cytotoxic chemical;   |
| 5 | c) which is an antibody fragment; or  |
| 6 | d) which is a humanized antibody.   |
| 1 | 15. A method for specifically targeting a compound to a pathological cell in a              |
| 2 | patient, said method comprising administering to said patient an antibody of Claim 13,      |
| 3 | thereby providing said targetting.  |
| 1 | 16. A method for determining the presence or absence of a pathological cell in a            |
| 2 | patient, said method comprising contacting a biological sample with an antibody of Claim 13 |
| 1 | 17. The method of Claim 16, wherein:  |
| 2 | a) said antibody is conjugated to:  |
| 3 | i) an effector component; or  |
| 4 | ii) a fluorescent label; or   |
| 5 | b) said biological sample is a blood, serum, urine, or stool sample.                        |
| 1 | 18. A method for identifying a compound that modulates a pathology-associated               |
| 2 | polypeptide, said method comprising the steps of:   |

polypeptide, said method comprising the steps of:

| 3  | a) contacting said compound with a pathology-associated polypeptide, said          |
|----|--|
| 4  | polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence  |
| 5  | at least 80% identical to a sequence as described in Tables 2A-80; and             |
| 6  | b) determining the functional effect of said compound upon said polypeptide.       |
| 1  | 19. A drug screening assay comprising the steps of:                                |
| 2  | a) administering a test compound to a mammal having a pathology of Table 1 or a    |
| 3  | cell isolated therefrom; and   |
| 4  | b) comparing the level of gene expression of a polynucleotide that selectively     |
| 5  | hybridizes to a sequence at least 80% identical to a sequence as described in      |
| 6  | Tables 2A-80 in a treated cell or mammal with the level of gene expression of said |
| 7  | polynucleotide in a control cell or mammal, wherein a test compound that           |
| 8  | modulates said level of expression of the polynucleotide is a candidate for the    |
| 9  | treatment of said pathology.   |
| 10 |  |

## (19) World Intellectual Property Organization

International Bureau





#### (43) International Publication Date 22 May 2003 (22.05.2003)

**PCT** 

#### (10) International Publication Number WO 2003/042661 A3

(51) International Patent Classification<sup>7</sup>: C07H 21/02, 21/04

C12Q 1/68,

(21) International Application Number:

PCT/US2002/036810

(22) International Filing Date:

13 November 2002 (13.11.2002)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

13 November 2001 (13.11.2001) US 60/350,666 60/332,464 21 November 2001 (21.11.2001) US 60/334,393 29 November 2001 (29.11.2001) US 60/335,394 3 December 2001 (03.12.2001) US 60/340,376 14 December 2001 (14.12.2001) US 8 January 2002 (08.01,2002) 60/347.211 US 60/347,349 10 January 2002 (10.01.2002) US 60/355,250 8 February 2002 (08.02.2002) US 60/356,714 13 February 2002 (13.02.2002) US 20 February 2002 (20.02.2002) 60/359,077 US 60/368,809 29 March 2002 (29.03.2002) US 60/370,110 4 April 2002 (04.04.2002) US 60/372,246 12 April 2002 (12.04.2002) US 5 June 2002 (05.06.2002) 60/386,614 US 60/396,839 16 July 2002 (16.07.2002) US 60/397,775 22 July 2002 (22.07.2002) US 60/397,845 22 July 2002 (22.07.2002) US 60/409,450 9 September 2002 (09.09.2002) US

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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

#### Declaration under Rule 4.17:

of inventorship (Rule 4.17(iv)) for US only

#### Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
- (88) Date of publication of the international search report: 28 October 2004

#### (15) Information about Correction:

Previous Correction:

see PCT Gazette No. 42/2003 of 16 October 2003, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULA-TORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



#### INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

| A. CLASSIFICATION OF SUBJECT MATTER  IPC(7) : C12Q 1/68; C07H 21/02, 21/04  US CL : 435/6; 536/23.1, 24.3  A. Silva A. International Patent Classification (IPC) on to both national classification and IPC |   |  |  |  |  |  |
|---|---|--|--|--|--|--|
| According to International Patent Classification (IPC) or to both national classification and IPC  B. FIELDS SEARCHED   |   |  |  |  |  |  |
| Minimum documentation searched (classification system followed by classification symbols) U.S.: 435/6; 536/23.1, 24.3   |   |  |  |  |  |  |
| Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched   |   |  |  |  |  |  |
| Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WEST, PubMed   |   |  |  |  |  |  |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT  |   |  |  |  |  |  |
| Category * Citation of document, with indication, where appro   |   |  |  |  |  |  |
| A SATO, H. et al., Cloning and Expression of a Plasma M Exchange Transporter Composed of Two Distinct Prote Vol. 247, No. 17, pp. 11455-11458.  |   |  |  |  |  |  |
| A KIM, J. Y. et al., Human cystine/glutamate transporter by oxidative stress n glioma cells, B.B. Acta. June 2001   |   |  |  |  |  |  |
|   |   |  |  |  |  |  |
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| 8   |   |  |  |  |  |  |
| Further documents are listed in the continuation of Box C.  | See patent family annex.  |  |  |  |  |  |
| * Special categories of cited documents: "T"  | date and not in conflict with the application but cited to understand the   |  |  |  |  |  |
| "A" document defining the general state of the art which is not considered to be<br>of particular relevance   | principle or theory underlying the invention  |  |  |  |  |  |
| "E" earlier application or patent published on or after the international filing date   | document of particular relevance; the claimed invention cannot be<br>considered novel or cannot be considered to involve an inventive step<br>when the document is taken alone                      |  |  |  |  |  |
| "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)                                     | "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination |  |  |  |  |  |
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| "P" document published prior to the international filing date but later than the priority date claimed  |   |  |  |  |  |  |
|   | te of mailing of the international search report  |  |  |  |  |  |
| 04 August 2004(04.08.2004)  Name and resiling address of the ISA/IIS  Authorized officer  |   |  |  |  |  |  |
| Mail Stop PCT, Atm: ISA/US  | Teresa Strzelecka A. Roberts of Strzelecka  |  |  |  |  |  |
| P.O. Doy 1450   |   |  |  |  |  |  |
| Alexandria, Virginia 22313-1450  Facsimile No. (703) 872-9306   | lephone No. (571) 272-1600  |  |  |  |  |  |

Form PCT/ISA/210 (second sheet) (July 1998)

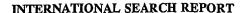
#### INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

| Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)  |  |  |  |  |
|--|--|--|--|--|
| This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:  |  |  |  |  |
| Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:   |  |  |  |  |
| Claim Nos.:  because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:   |  |  |  |  |
| Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule  |  |  |  |  |
| 6.4(a).  |  |  |  |  |
| Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)  |  |  |  |  |
| This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet  |  |  |  |  |
| <ol> <li>As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.</li> <li>As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.</li> <li>As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:</li> </ol> |  |  |  |  |
| 4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO: 19  Remark on Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.  |  |  |  |  |
| ;<br>  |  |  |  |  |

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)



PCT/US02/36810

#### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, drawn to a special technical feature of a method for determining presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

Group II, claim(s) 8-11, drawn to a special technical feature of an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, expression vector comprising the nucleic acid and a host cell comprising the expression vector.

Group III, claim(s) 12, drawn to a special technical feature of an isolated polypeptide which is encoded by an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

Group IV, claim(s) 13, 14, drawn to a special technical feature of an antibody which specifically binds to polypeptide of claim 12.

Group V, claim(s) 15, drawn to a special technical feature of a method for specifically targeting a compound to a pathological cell in a patient, comprising administering to a patient an antibody of claim 13.

Group VI, claim(s) 16, 17, drawn to a special technical feature of a method for determining the presence or absence of a pathological cell in a patient, comprising contacting a biological sample with an antibody of claim 13.

Group VII, claim(s) 18, drawn to a special technical feature of a method for identifying a compound that modulates a pathology-associated polypeptide by contacting the compound with a pathology-associated polypeptide encoded by a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 and determining the functional effect of the compound on the polypeptide.

Group VIII, claim(s) 19, drawn to a special technical feature of a drug screening assay comprising the steps of: administering a test compound to a mammal having pathology of Table 1 or a cell isolated therefrom; comparing the level of gene expression of a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal.

The inventions listed as Groups I-VIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: claim 8 is anticipated by a sequence with accession No. BB440042 (Table 2A, first entry) (July 25, 2000), therefore there is no contribution of claim 8 over prior art.

### CORRECTED VERSION

#### (19) World Intellectual Property Organization International Bureau



# 

#### (43) International Publication Date 22 May 2003 (22.05.2003)

#### PCT

#### (10) International Publication Number WO 03/042661 A2

| (51) | International Patent Classification?:     | G01N              | Richard   |
|------|---|-------------------|---|
| (21) | International Application Number:         | PCT/US02/36810    | CA 950<br>Balra Dr<br>E. [US/<br>(US). Zl<br>Alto, CA |
| (22) | International Filing Date:<br>13 November | 2002 (13.11.2002) |   |
| (25) | Filing Language:                          | English           | (74) Agents:  |
|      |   |                   | Townson   |

- (26) Publication Language: English
- (30) Priority Data: 60/350,666 13 November 2001 (13.11.2001) US 60/332,464 21 November 2001 (21.11.2001) US 29 November 2001 (29.11.2001) 60/334,393 US 60/335,394 3 December 2001 (03.12.2001) US 60/340,376 14 December 2001 (14.12.2001) US 60/347,211 8 January 2002 (08.01.2002) US 10 January 2002 (10.01.2002) 60/347,349 US 60/355,250 8 February 2002 (08.02.2002) US 60/356,714 13 February 2002 (13.02.2002) US 20 February 2002 (20.02.2002) 60/359,077 US 29 March 2002 (29.03.2002) 60/368,809 US 60/370,110 4 April 2002 (04.04.2002) US 60/372,246 12 April 2002 (12.04.2002) US 5 June 2002 (05.06.2002) US 60/386,614 60/396,839 16 July 2002 (16.07.2002) US 60/397,775 22 July 2002 (22.07.2002) US 60/397,845 22 July 2002 (22.07.2002) US 60/409,450 9 September 2002 (09.09.2002) US
- (71) Applicant (for all designated States except US): EOS BIOTECHNOLOGY, INC. [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): AFAR, Daniel [CA/US]; 435 Visitacion Avenue, Brisbane, CA 94005 (US). AZIZ, Natasha [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). GINSBURG, Wendy, M. [US/US]; 655 Page Street, San Francisco, CA 94117 (US). GISH, Kurt, C. [US/US]; 37 Artuna Avenue, Piedmont, CA 94611 (US). GLYNNE, Richard [GB/US]; 2691 Palomino Circle, La Jolla, CA 92037 (US). HEVEZI, Peter, A. [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). MACK, David, H. [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). MURRAY,

d [US/US]: 22643 Woodridge Court, Cupertino. 014 (US). WATSON, Susan, R. [GB/US]; 805 rive, El Cerrito, CA 94530 (US). WILSON, Keith, /US]; 219 Jeter Street, Redwood City, CA 94062 LOTNIK, Albert [US/US]; 507 Alger Drive, Palo A 94306 (US).

- : BASTIAN, Kevin, L. et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

#### **Declaration under Rule 4.17:**

of inventorship (Rule 4.17(iv)) for US only

- without international search report and to be republished upon receipt of that report
- (48) Date of publication of this corrected version:

16 October 2003

(15) Information about Correction: see PCT Gazette No. 42/2003 of 16 October 2003, Sec-

tion II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULA-TORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.





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